

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

091904968

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 14:59:58 ; Search time 0.001 Seconds
(without alignments)
119.944 Million cell updates/sec

Title: US-09-904-968A-3-COPY
Perfect score: 29
Sequence: 1 ccacccacctgtgtgacgtgtaaat 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 177 seqs, 2068 residues

Total number of hits satisfying chosen parameters: 354

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 177 summaries

Database : isedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	15.2	52.4	21	1	US-09-422-978-11421
C 2	14.8	51.0	20	1	US-09-422-978-9340
C 3	14.2	49.0	20	1	US-09-023-082A-97
C 4	14.2	49.0	20	1	US-09-218-444-18
C 5	14.2	49.0	20	1	US-09-248-998-97
C 6	14.2	49.0	20	1	US-09-853-666-18
C 7	14.2	49.0	20	1	US-09-610-651-97
C 8	14.2	49.0	20	1	US-09-345-373-97
C 9	14.2	49.0	20	1	US-09-075-446-97
C 10	13.4	46.2	19	1	US-09-422-978-6482
C 11	13.2	45.5	18	1	US-09-357-072-27
C 12	12.8	44.1	18	1	US-08-832-883-39
C 13	12.8	44.1	18	1	US-08-832-877-39
C 14	12.8	44.1	18	1	US-08-679-645-1205
C 15	12.8	44.1	18	1	US-09-809-920-34
C 16	12.4	42.8	17	1	US-09-866-108A-2171
C 17	12.4	42.8	17	1	US-09-866-108A-2172
C 18	12.4	42.8	17	1	US-09-866-108A-2173
C 19	12.4	42.8	17	1	US-09-866-108A-2174
C 20	12	41.4	17	1	US-09-866-108A-2169
C 21	12	41.4	17	1	US-09-866-108A-2170
C 22	11.2	38.6	16	1	US-09-112-096-13
C 23	11.2	38.6	16	1	US-09-371-772B-5660
C 24	10.8	37.2	15	1	US-08-182-968A-85
C 25	10.8	37.2	15	1	US-08-774-306A-85
C 26	10.8	37.2	15	1	US-09-064-156A-85
C 27	10.4	35.9	14	1	US-08-535-249-1
C 28	10.4	35.9	14	1	US-09-230-652-17
C 29	9.8	33.8	13	1	US-08-544-381B-25
C 30	9.8	33.8	13	1	US-08-778-794A-83
C 31	9.8	33.8	14	1	US-08-535-249-15
C 32	9.4	32.4	11	1	US-09-249-155A-54
C 33	9.4	32.4	11	1	US-09-249-155A-269

Sequence 27, Appl	US-08-367-175A-27	13	32.4	9.4
Patent No. 522537	522537-13	13	32.4	9.4
Sequence 73, Appl	US-08-481-658B-73	11	31.0	9
Sequence 73, Appl	US-08-477-504A-73	11	31.0	9
Sequence 73, Appl	US-08-486-756A-73	11	31.0	9
Sequence 73, Appl	US-08-485-862B-73	11	31.0	9
Sequence 73, Appl	US-08-787-739-73	11	31.0	9
Sequence 73, Appl	US-08-487-077A-73	11	31.0	9
Sequence 73, Appl	US-08-485-863A-73	11	31.0	9
Sequence 73, Appl	US-08-485-049D-73	11	31.0	9
Sequence 73, Appl	US-09-178-115-73	11	31.0	9
Sequence 73, Appl	US-09-177-776-73	11	31.0	9
Sequence 3, Appl	US-09-115-407-3	11	31.0	9
Sequence 30, Appl	US-09-772-719B-73	11	31.0	9
Sequence 30, Appl	US-10-286-387-30	12	30.3	8.8
Sequence 15, Appl	US-08-035-928-15	12	30.3	8.8
Sequence 29, Appl	US-08-250-740-29	12	30.3	8.8
Sequence 9, Appl	US-07-695-472B-9	12	30.3	8.8
Sequence 30, Appl	US-08-410-540-30	12	30.3	8.8
Sequence 69, Appl	US-08-441-887A-69	12	30.3	8.8
Sequence 9, Appl	US-09-106-375-9	12	30.3	8.8
Sequence 3, Appl	US-09-374-174B-3	12	30.3	8.8
Sequence 18, Appl	US-09-163-485-18	12	29.7	8.6
Sequence 23, Appl	US-08-367-175A-23	10	29.0	8.4
Sequence 78, Appl	US-08-388-353-78	10	29.0	8.4
Sequence 381, Appl	US-08-388-353-381	10	29.0	8.4
Sequence 782, Appl	US-08-388-353-782	10	29.0	8.4
Sequence 783, Appl	US-08-388-353-783	10	29.0	8.4
Sequence 784, Appl	US-08-388-353-784	10	29.0	8.4
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Sequence 129, Appl	US-09-245-041-129	10	29.0	8.4
Sequence 113, Appl	US-08-870-511-13	10	29.0	8.4
Sequence 118, Appl	US-09-508-753B-118	10	29.0	8.4
Sequence 8, Appl	US-10-042-111-8	10	29.0	8.4
Sequence 130, Appl	US-09-358-055B-130	10	29.0	8.4
Sequence 129, Appl	US-09-893-238-129	10	29.0	8.4
Sequence 15, Appl	US-08-800-036-15	11	29.0	8.4
Sequence 86, Appl	US-08-481-658B-86	11	29.0	8.4
Sequence 86, Appl	US-08-926-492-15	11	29.0	8.4
Sequence 86, Appl	US-08-477-504A-86	11	29.0	8.4
Sequence 86, Appl	US-08-486-756A-86	11	29.0	8.4
Sequence 86, Appl	US-08-485-862B-86	11	29.0	8.4
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Sequence 15, Appl	US-09-048-505-15	11	29.0	8.4
Sequence 86, Appl	US-08-487-077A-86	11	29.0	8.4
Sequence 86, Appl	US-08-485-863A-86	11	29.0	8.4
Sequence 86, Appl	US-08-485-049D-86	11	29.0	8.4
Sequence 86, Appl	US-09-178-115-86	11	29.0	8.4
Sequence 86, Appl	US-09-177-776-86	11	29.0	8.4
Sequence 113, Appl	US-09-249-155A-113	11	29.0	8.4
Sequence 285, Appl	US-09-249-155A-285	11	29.0	8.4
Sequence 86, Appl	US-09-772-719B-86	11	29.0	8.4
Sequence 76, Appl	US-08-435-350-76	12	29.0	8.4
Sequence 141, Appl	US-09-281-418-141	12	29.0	8.4
Sequence 191, Appl	US-09-281-418-191	12	29.0	8.4
Sequence 167, Appl	US-09-874-601-167	12	29.0	8.4
Sequence 77, Appl	US-09-875-453B-77	12	29.0	8.4
Sequence 11, Appl	US-08-634-350-11	10	27.6	8
Sequence 39, Appl	US-08-388-353-39	10	27.6	8
Sequence 40, Appl	US-08-388-353-40	10	27.6	8
Sequence 41, Appl	US-08-388-353-41	10	27.6	8
Sequence 785, Appl	US-08-388-353-785	10	27.6	8
Sequence 786, Appl	US-08-388-353-786	10	27.6	8
Sequence 788, Appl	US-08-388-353-788	10	27.6	8
Sequence 39, Appl	US-08-488-551B-39	10	27.6	8
Sequence 40, Appl	US-08-488-551B-40	10	27.6	8
Sequence 41, Appl	US-08-488-551B-41	10	27.6	8
Sequence 785, Appl	US-08-488-551B-785	10	27.6	8
Sequence 786, Appl	US-08-488-551B-786	10	27.6	8

Issued Patents NA

c 107	107	8	27.6	10	1	US-08-488-551B-788	Sequence 788, App
c 108	108	8	27.6	10	1	US-09-475-947A-279	Sequence 279, App
c 109	109	8	27.6	10	1	US-08-894-454-122	Sequence 122, App
c 110	110	8	27.6	10	1	US-10-042-111-23	Sequence 23, App1
c 111	111	8	27.6	11	1	US-09-249-155A-106	Sequence 106, App
c 112	112	8	27.6	11	1	US-08-836-734B-90	Sequence 90, App1
c 113	113	7.8	26.9	11	1	US-09-793-146-36	Sequence 36, App1
c 114	114	7.8	26.9	11	1	US-09-793-146-41	Sequence 41, App1
c 115	115	7.8	26.9	11	1	US-09-793-146-59	Sequence 59, App1
c 116	116	7.8	26.9	11	1	US-09-793-146-60	Sequence 60, App1
c 117	117	7.8	26.9	11	1	5256558-12	Patent No. 5256558
c 118	118	7.4	25.5	10	1	US-07-960-981-2	Sequence 2, App1
c 119	119	7.4	25.5	10	1	US-07-651-710A-40	Sequence 40, App1
c 120	120	7.4	25.5	10	1	US-08-335-565A-21	Sequence 21, App1
c 121	121	7.4	25.5	10	1	US-08-235-503B-24	Sequence 24, App1
c 122	122	7.4	25.5	10	1	US-08-545-253A-7	Sequence 7, App1
c 123	123	7.4	25.5	10	1	US-08-265-484B-13	Sequence 13, App1
c 124	124	7.4	25.5	10	1	US-08-388-353-77	Sequence 77, App1
c 125	125	7.4	25.5	10	1	US-08-388-353-79	Sequence 79, App1
c 126	126	7.4	25.5	10	1	US-08-388-353-140	Sequence 140, App
c 127	127	7.4	25.5	10	1	US-08-388-353-141	Sequence 141, App
c 128	128	7.4	25.5	10	1	US-08-388-353-142	Sequence 142, App
c 129	129	7.4	25.5	10	1	US-08-388-353-143	Sequence 143, App
c 130	130	7.4	25.5	10	1	US-08-388-353-380	Sequence 380, App
c 131	131	7.4	25.5	10	1	US-08-388-353-382	Sequence 382, App
c 132	132	7.4	25.5	10	1	US-08-388-353-770	Sequence 770, App
c 133	133	7.4	25.5	10	1	US-08-388-353-771	Sequence 771, App
c 134	134	7.4	25.5	10	1	US-08-388-353-781	Sequence 781, App
c 135	135	7.4	25.5	10	1	US-08-388-353-796	Sequence 796, App
c 136	136	7.4	25.5	10	1	US-08-388-353-797	Sequence 797, App
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c 138	138	7.4	25.5	10	1	US-08-488-551B-79	Sequence 79, App1
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c 141	141	7.4	25.5	10	1	US-08-488-551B-142	Sequence 142, App
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c 143	143	7.4	25.5	10	1	US-08-488-551B-380	Sequence 380, App
c 144	144	7.4	25.5	10	1	US-08-488-551B-382	Sequence 382, App
c 145	145	7.4	25.5	10	1	US-08-488-551B-770	Sequence 770, App
c 146	146	7.4	25.5	10	1	US-08-488-551B-771	Sequence 771, App
c 147	147	7.4	25.5	10	1	US-08-488-551B-781	Sequence 781, App
c 148	148	7.4	25.5	10	1	US-08-488-551B-786	Sequence 786, App
c 149	149	7.4	25.5	10	1	US-08-488-551B-797	Sequence 797, App
c 150	150	7.4	25.5	10	1	US-08-719-337-7	Sequence 7, App1
c 151	151	7.4	25.5	10	1	US-08-765-257A-13	Sequence 13, App1
c 152	152	7.4	25.5	10	1	US-08-522-384-18	Sequence 18, App1
c 153	153	7.4	25.5	10	1	US-08-522-384-120	Sequence 120, App
c 154	154	7.4	25.5	10	1	US-09-034-205-51	Sequence 51, App1
c 155	155	7.4	25.5	10	1	US-08-934-097A-51	Sequence 51, App1
c 156	156	7.4	25.5	10	1	US-08-677-218B-51	Sequence 51, App1
c 157	157	7.4	25.5	10	1	US-09-677-192-51	Sequence 51, App1
c 158	158	7.4	25.5	10	1	US-09-154-750A-14	Sequence 14, App1
c 159	159	7.4	25.5	10	1	US-09-229-007A-81	Sequence 81, App1
c 160	160	7.4	25.5	10	1	US-09-261-115-57	Sequence 57, App1
c 161	161	7.4	25.5	10	1	US-09-914-259-119	Sequence 119, App
c 162	162	7.4	25.5	10	1	US-09-914-259-120	Sequence 120, App
c 163	163	7.4	25.5	10	1	US-09-508-753B-67	Sequence 67, App1
c 164	164	7.4	25.5	10	1	US-09-508-753B-78	Sequence 78, App1
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c 167	167	7.4	25.5	10	1	US-09-508-753B-188	Sequence 188, App
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c 169	169	7.4	25.5	10	1	US-09-402-618B-51	Sequence 51, App1
c 170	170	7.4	25.5	10	1	US-09-825-574-51	Sequence 51, App1
c 171	171	7.4	25.5	10	1	US-10-113-424-81	Sequence 81, App1
c 172	172	7.4	25.5	10	1	US-09-821-694A-26	Sequence 26, App1
c 173	173	7.4	25.5	10	1	US-09-821-694A-30	Sequence 30, App1
c 174	174	7.4	25.5	10	1	US-10-053-883-70	Sequence 70, App1
c 175	175	7.4	25.5	10	1	PCT-US93-09634-2	Sequence 2, App1
c 176	176	7.4	25.5	10	1	PCT-US94-08023-14	Sequence 14, App1
c 177	177	7.4	25.5	10	1	PCT-US95-05265-24	Sequence 24, App1

ALIGNMENTS

RESULT 1

US-09-422-978-11421/c
; Sequence 11421, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11421
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-5747 for SEQ 3556, in compler
US-09-422-978-11421

Query Match 52.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 6.5;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGACC 21

Db 21 CATTGACTGCTGTGACC 2

RESULT 2

US-09-422-978-9340
; Sequence 9340, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9340
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-25387 for SEQ 1475, in compleme
US-09-422-978-9340

Query Match 51.0%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 7.3;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	DB	STRANDEDNESS: single	TOPOLOGY: linear	MOLECULE TYPE: cDNA	US-09-023-082A-97	Query Match	Best Local Similarity	Score 14.2;	DB 1;	Length 20;	Mismatches	Indels	Gaps
4	3	TCACCTGCTGTGTGACC 21			TCACCTGCTGTGTGACC 20	49.0%;	84.2%;	49.0%;	84.2%;	49.0%;	0;	0;	0;
3	4	TGCACCTGCTGTGTGACC 20			TGCACCTGCTGTGTGACC 21	49.0%;	84.2%;	49.0%;	84.2%;	49.0%;	0;	0;	0;
<p>RESULT 3</p> <p>US-09-023-082A-97</p> <p>; Sequence 97, Application US/09023082A</p> <p>; Patent No. 6077692</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: RUBEN, STEVEN M.</p> <p>; APPLICANT: JIMENEZ, PABLO</p> <p>; APPLICANT: DUAN, D. ROXANNE</p> <p>; APPLICANT: RAMPY, MARK A.</p> <p>; APPLICANT: MENDRICK, DONNA</p> <p>; APPLICANT: ZHANG, JUN</p> <p>; APPLICANT: NI, JIAN</p> <p>; APPLICANT: MOORE, PAUL A.</p> <p>; APPLICANT: COLEMAN, TIMOTHY A.</p> <p>; APPLICANT: GRUBER, JOACHIM R.</p> <p>; APPLICANT: DILLON, PATRICK J.</p> <p>; APPLICANT: GENTZ, REINER L.</p> <p>; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2</p> <p>; NUMBER OF SEQUENCES: 148</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.</p> <p>; STREET: 1100 NEW YORK AVE, NW, SUITE 600</p> <p>; CITY: WASHINGTON</p> <p>; STATE: DC</p> <p>; COUNTRY: USA</p> <p>; ZIP: 20005-3934</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; COMPUTER: IBM PC compatible</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/09/023,082A</p> <p>; FILING DATE: 13-FEB-1998</p> <p>; CLASSIFICATION: 435</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: PCT/US95/01790</p> <p>; FILING DATE: 14-FEB-1995</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US 08/461,195</p> <p>; FILING DATE: 05-JUN-1995</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US 60/023,852</p> <p>; FILING DATE: 13-AUG-1996</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US 60/039,045</p> <p>; FILING DATE: 28-FEB-1997</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US 08/862,432</p> <p>; FILING DATE: 23-MAY-1997</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US 08/910,875</p> <p>; FILING DATE: 13-AUG-1997</p> <p>; PRIOR APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US 60/055,561</p> <p>; FILING DATE: 13-AUG-1997</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: STEFFEE, ERIC K.</p> <p>; REGISTRATION NUMBER: 36,688</p> <p>; REFERENCE/DOCKET NUMBER: 1488.0360008/EKS</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: 202-371-2600</p> <p>; TELEFAX: 202-371-2540</p> <p>; INFORMATION FOR SEQ ID NO: 97:</p> <p>; SEQUENCE CHARACTERISTICS:</p> <p>; LENGTH: 20 base pairs</p> <p>; TYPE: nucleic acid</p>													

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACCACTGCAGGGTGAC 19

RESULT 6

US-09-853-666-18 Application US/09853666
; Sequence 18, Application US/09853666
; Patent No. 6653284
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Chopra, Arvind
; APPLICANT: Kaushal, Parveen
; APPLICANT: Spitznagel, Thomas
; APPLICANT: Unsworth, Edward
; APPLICANT: Khan, Fazal
; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations
; FILE REFERENCE: 1488.1030001
; CURRENT APPLICATION NUMBER: US/09/853,666
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/218,444
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-666-18

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACCACTGCAGGGTGAC 19

RESULT 7

US-09-610-651-97
; Sequence 97, Application US/09610651
; Patent No. 6693077
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jimenez, Pablo
; APPLICANT: Duan, D. Roxanne
; APPLICANT: Rampy, Mark A.
; APPLICANT: Mendrick, Donna
; APPLICANT: Zhang, Jun
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul A.
; APPLICANT: Coleman, Timothy A.
; APPLICANT: Gruber, Joachim R.
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Gentz, Reiner L.

FILE REFERENCE: 1488.036000J
; CURRENT APPLICATION NUMBER: US/09/610,651
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/US95/01790
; PRIOR FILING DATE: 1995-02-14
; PRIOR APPLICATION NUMBER: 08/461,195
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/696,135
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 08/862,432
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/023,852
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 60/039,045
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: 60/055,561
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 08/910,875
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/023,082
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 09/345,373
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/142,343
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/143,648
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/144,024
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/148,628
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149,935
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/163,375
; PRIOR FILING DATE: 1999-11-03
; PRIOR APPLICATION NUMBER: 60/171,677
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/205,417
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/198,322
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-610-651-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACCACTGCAGGGTGAC 19

RESULT 8

US-09-345-373-97
; Sequence 97, Application US/09345373
; Patent No. 6903072
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: JIMENEZ, PABLO
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: RAMPY, MARK A.
; APPLICANT: MENDRICK, DONNA
; APPLICANT: ZHANG, JUN
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL A.
; APPLICANT: COLEMAN, TIMOTHY A.
; APPLICANT: GRUBER, JOACHIM R.
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: GENTZ, REINER L.

TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE, NW, SUITE 600
; CITY: WASHINGTON

STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,373
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE:
PRIOR APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
|||
Db 1 CAACCACTGCAGGTGAC 19

RESULT 9
US-10-075-446-97
; Sequence 97, Application US/10075446
; Patent No. 6916786
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; JIMENEZ, PABLO
; DUAN, D. ROXANNE
; RAMPEY, MARK A.
; MENDRICK, DONNA
; ZHANG, JUN
; NI, JIAN
; MOORE, PAUL A.
; COLEMAN, TIMOTHY A.
; GRUBER, JOACHIM R.

TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/075,446
FILING DATE: 15-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-075-446-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
|||
Db 1 CAACCACTGCAGGTGAC 19

RESULT 10
US-09-422-978-6482/c
; Sequence 6482, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20

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; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6482
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19_bind
; OTHER INFORMATION: upstream amplification primer 99-11745 for SEQ 2548,
US-09-422-978-6482

Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CCACCTGCTGTGTA 19
Db      19 CCGCTGCTGTGTA 5

RESULT 11
US-09-357-072-27/c
; Sequence 27, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-27

Query Match          45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      9 CTGCTGTGTGACCTGGTA 26
Db      18 CTGGTGGCTGACCTGGTA 1

RESULT 12
US-08-832-883-39/c
; Sequence 39, Application US/08832883
; Patent No. 5807681
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; APPLICANT: Baldi, Alphonso
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
; TITLE OF INVENTION: OF CANCER
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
```

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; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,883
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-13 US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-832-883-39

Query Match          44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      13 TGTGTGACCTGGTAA 28
Db      17 TTTGTGACCTGGCAA 2

RESULT 13
US-08-832-877-39/c
; Sequence 39, Application US/08832877
; Patent No. 5840506
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,877
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-13 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
US-08-832-877-39

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGGTAAA 28
Db 17 TTGTGACCTGGCANA 2

RESULT 14
US-08-679-645-1205
; Sequence 1205, Application US/08679645
; Patent No. 6350934
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; APPLICANT: Edington, Brent E.
; APPLICANT: McSwiggen, James A.
; APPLICANT: Merlo, Patricia Ann Owens
; APPLICANT: Guo, Lining
; APPLICANT: Skokut, Thomas A.
; APPLICANT: Young, Scott A.
; APPLICANT: Folkerts, Otto
; APPLICANT: Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
; TITLE OF INVENTION: IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/679,645
; FILING DATE: July 12, 1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1205:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-679-645-1205

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

; MOLECULE TYPE: DNA (genomic)
US-09-809-920-34/c
; Sequence 34, Application US/09809920
; Patent No. 6812326
; GENERAL INFORMATION:
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
; EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
; THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/809,920
; FILING DATE: 16-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/156,191
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51902
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-809-920-34

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGAC 20
Db 18 CCACATGCTGTGTAC 3

RESULT 16
US-09-866-108A-2171
; Sequence 2171, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
```

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; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2171

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
Db 4 CCACCTGCTGTGAG 17

RESULT 17
US-09-866-108A-2172
; Sequence 2172, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2173

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
Db 3 CCACCTGCTGTGAG 16

RESULT 18
US-09-866-108A-2173
; Sequence 2173, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2173
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2173

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2169

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy 5 CCACCTGCTGTG 16
    |||||
Db 6 CCACCTGCTGTG 17
    |||||

RESULT 21
US-09-866-108A-2170
; Sequence 2170, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2174
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2174

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 5 CCACCTGCTGTG 18
    |||||
Db 1 CCACCTGCTGTG 14
    |||||

RESULT 20
US-09-866-108A-2169
; Sequence 2169, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

```

```
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 2170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-2170

Query Match      41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 16
Db 5 CCACCTGCTGTG 16

RESULT 22
US-09-112-096-13/c
; Sequence 13, Application US/09112096
; Patent No. 6194152
; GENERAL INFORMATION:
; APPLICANT: Reiner Laus
; APPLICANT: Michael H. Shapero
; APPLICANT: Larisa Tsavaler
; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
; FILE REFERENCE: 7636-0015.30
; CURRENT APPLICATION NUMBER: US/09/112,096
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: 60/056,110
; EARLIER FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(16)
; OTHER INFORMATION: oligonucleotide primer
US-09-112-096-13

Query Match      38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTGT 25
Db 16 TGCTGTGTGAAATTGT 1

RESULT 23
US-09-371-772B-5660
; Sequence 5660, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
```

```
; FILE REFERENCE: MHB00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5660

Query Match      38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTG 23
Db 1 CCUGCUGUGCGCGUG 16

RESULT 24
US-08-182-968A-85/c
; Sequence 85, Application US/08182968A
; Patent No. 5610054
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 497
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,968A
; FILING DATE: 13-JANUARY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,888
; FILING DATE: 14-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 205/277
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-182-968A-85

Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


QY 16 GTGACCTGGTAAAT 29
|||||
Db 15 GTGACCTGATACAT 2

RESULT 25

US-08-774-306A-85/c
; Sequence 85, Application US/08774306A

; Patent No. 5869253

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; TITLE OF INVENTION: METHOD AND REAGENT FOR

; TITLE OF INVENTION: INHIBITING HEPATITIS C

; TITLE OF INVENTION: VIRUS REPLICATION

; NUMBER OF SEQUENCES: 497

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/774,306A

; FILING DATE: December 26, 1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/182,968

; FILING DATE: January 13, 1994

; APPLICATION NUMBER: 07/882,888

; FILING DATE: May 14, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 223/227

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-774-306A-85

Query Match 37.2%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 31;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29

|||||

Db 15 GTGACCTGATACAT 2

RESULT 26

US-09-064-156A-85/c

; Sequence 85, Application US/09064156A

; Patent No. 6132966

; GENERAL INFORMATION:

; APPLICANT: Draper, Kenneth G.

; TITLE OF INVENTION: METHOD AND REAGENT FOR

; TITLE OF INVENTION: INHIBITING HEPATITIS C

; TITLE OF INVENTION: VIRUS REPLICATION

; NUMBER OF SEQUENCES: 498

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Suite 4700

; STATE: Los Angeles

; COUNTRY: California

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/064,156A

; FILING DATE: April 21, 1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/774,306

; FILING DATE: December 26, 1996

; APPLICATION NUMBER: 08/182,968

; FILING DATE: January 13, 1994

; APPLICATION NUMBER: 07/882,888

; FILING DATE: May 14, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/083

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 85:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-09-064-156A-85

Query Match 37.2%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 31;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29

|||||

Db 15 GTGACCTGATACAT 2

RESULT 27

US-08-535-249-1/c

; Sequence 1, Application US/08535249

; Patent No. 6455689

; GENERAL INFORMATION:

; APPLICANT: Schlengersiepen, Georg-Ferdinand

; APPLICANT: Brysch, Wolfgang

; APPLICANT: Schlengersiepen, Karl-Hermann

; APPLICANT: Schlengersiepen, Reimar

; APPLICANT: Bogdahn, Ulrich

; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of

; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (

; NUMBER OF SEQUENCES: 137

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jacobson, Price, Holman & Stern

; STREET: 400 Seventh St. N.W.

; CITY: Washington D.C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-535-249-1

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
Db 13 CTATCCACCTGC 2

RESULT 28
US-09-230-652-17/c
; Sequence 17, Application US/09230652A
; Patent No. 6537775
; GENERAL INFORMATION:
; APPLICANT: Tournier-Lasserre, Elisabeth
; APPLICANT: Joutel, Anne
; APPLICANT: Bousset, Marie-Germaine
; APPLICANT: Bach, Jean-Francois
; TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
; FILE REFERENCE: 03715.0048-00000
; CURRENT APPLICATION NUMBER: US/09/230,652A
; CURRENT FILING DATE: 1999-05-17
; EARLIER APPLICATION NUMBER: FR 96 09733
; EARLIER FILING DATE: 1996-08-01
; EARLIER APPLICATION NUMBER: FR 97 04680
; EARLIER FILING DATE: 1997-04-16
; EARLIER APPLICATION NUMBER: PCT/FR97/01433
; EARLIER FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; US-09-230-652-17

Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
Db 13 CTATCCACCTGC 12
```

```
Db 14 CCACCCACCTGC 3

RESULT 29
US-08-544-381B-25
; Sequence 25, Application US/08544381B
; Patent No. 6027880
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; TITLE OF INVENTION: Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/544,381B
; FILING DATE: 10-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-544-381B-25

Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 39;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGACCT 13
```

RESULT 30
US-08-778-794A-83
; Sequence 83, Application US/08778794A
; Patent No. 6309823
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles Garrett
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xishoua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, MacDonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes
; TITLE OF INVENTION: for Analyzing Biotransformation Genes
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,794A
; FILING DATE: 03-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: WO PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: US 08/544,381
; FILING DATE: 10-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-015700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0200
; TELEX:
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-778-794A-83

Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 39;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGACCT 13

RESULT 31

US-08-535-249-15
; Sequence 15, Application US/08535249
; Patent No. 6455689
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Schlingensiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta (1
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/535,249
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-535-249-15

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGTACT 13

RESULT 32
US-09-249-155A-54/c
; Sequence 54, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13

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; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-54

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTG 23
Db 11 TGTGTGCCTG 1

RESULT 33
US-09-249-155A-269
; Sequence 269, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-269

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGT 15
Db 1 CCACCTCCTGT 11

RESULT 34
US-08-367-175A-27
; Sequence 27, Application US/08367175A
; Patent No. 5631115
; GENERAL INFORMATION:
; APPLICANT: OHTSUKA, Eiko
; APPLICANT: KOIZUMI, Makoto
; TITLE OF INVENTION: Looped, hairpin ribozyme
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FRISHAUF, HOLTZ, GOODMAN,
; ADDRESSEE: LANGER & CHICK, P.C.
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-2023
; COMPUTER READABLE FORM:

; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-54

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTG 23
Db 11 TGTGTGCCTG 1

RESULT 33
US-09-249-155A-269
; Sequence 269, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-269

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 36;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGT 15
Db 1 CCACCTCCTGT 11

RESULT 34
US-08-367-175A-27
; Sequence 27, Application US/08367175A
; Patent No. 5631115
; GENERAL INFORMATION:
; APPLICANT: OHTSUKA, Eiko
; APPLICANT: KOIZUMI, Makoto
; TITLE OF INVENTION: Looped, hairpin ribozyme
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FRISHAUF, HOLTZ, GOODMAN,
; ADDRESSEE: LANGER & CHICK, P.C.
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-2023
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,175A
; FILING DATE: 29 Dec. 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOODMAN, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 920081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)319-4900
; TELEFAX: (212)319-5101
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHEICAL: N
; ANTI-SENSE: N
US-08-367-175A-27

Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 47;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGA 19
Db 3 CUGUGUGUGA 13

RESULT 35
5225537-13
; Patent No. 5225537
; APPLICANT: FOSTER, DONALD
; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
; PHOSPHOLIPID-BINDING PROTEINS
; NUMBER OF SEQUENCES: 14
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/459,082
; FILING DATE: 29-DEC-1989
; SEQ ID NO:13
; LENGTH: 13
5225537-13

Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TGACCTGGTAA 27
Db 3 TGACTTGGTAA 13

RESULT 36
US-08-481-658B-73/c
; Sequence 73, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
```

```
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
; US-08-481-658B-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 37
US-08-477-504A-73/c
; Sequence 73, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
; US-08-486-756A-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 38
US-08-486-756A-73/c
; Sequence 73, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
; US-08-486-756A-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 39

US-08-485-862B-73/c
; Sequence 73, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
US-08-485-862B-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 40

US-08-787-739-73/c
; Sequence 73, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,739
; FILING DATE: 24-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/486,756
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/481,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/485,862
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/485,863
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/487,077
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
US-08-787-739-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 41

US-08-487-077A-73/c
; Sequence 73, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder

STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,077A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3H
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 5' donor consensus splice sequence
US-08-487-077A-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 42
US-08-485-863A-73/c
Sequence 73, Application US/08485863A
Patent No. 6093548
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,863A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 5' donor consensus splice sequence
US-08-485-863A-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 43
US-08-485-049D-73/c
Sequence 73, Application US/08485049D
Patent No. 6204370
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-0332
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 5' donor consensus splice sequence
US-08-485-049D-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;

```
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 44
US-09-178-115-73/c
; Sequence 73, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 11
; TYPE: DNA
; ORGANISM: HUMAN
US-09-177-776-73

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 45
US-09-177-776-73/c
; Sequence 73, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 46
US-09-115-407-3
; Sequence 3, Application US/09115407A
; Patent No. 6410228
; GENERAL INFORMATION:
; APPLICANT: SCHWARTZ, ROBERT J.
; APPLICANT: EASTMAN, ERIC M.
; APPLICANT: LI, XUYANG
; APPLICANT: NORDSTROM, JEFF
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SYNTHETIC
; TITLE OF INVENTION: CELL-OR-TISSUE-SPECIFIC TRANSCRIPTIONAL
; FILE REFERENCE: 235/238
; CURRENT APPLICATION NUMBER: US/09/115,407A
; CURRENT FILING DATE: 1998-07-14
; EARLIER APPLICATION NUMBER: US 60/052,403
; EARLIER FILING DATE: 1997-07-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E-box binding site recognized by basic-helix-loop-helix
; OTHER INFORMATION: (bHLH) transcription factors.
US-09-115-407-3

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```
QY      6 CACCTGCTG 14
      |||||
Db      3 CACCTGCTG 11

RESULT 47
US-09-772-719B-73/c
; Sequence 73, Application US/09772719B
; Patent No. 6770438
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; Pastorekova, Silvia
; Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719B
; FILING DATE: 30-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 5' donor consensus splice sequence
; SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-09-772-719B-73

Query Match      31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CCACCTGCT 13
      |||||
Db      9 CCACCTGCT 1

RESULT 48
US-10-286-387-30
; Sequence 30, Application US/10286387
; Patent No. 6936443
; GENERAL INFORMATION:
; APPLICANT: Cytoc Corporation
; TITLE OF INVENTION: Detection and Typing of Human Papillomavirus Using PNA Probes
; FILE REFERENCE: cym-035CP
; CURRENT APPLICATION NUMBER: US/10/286,387
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 31
```

```
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PNA probe
US-10-286-387-30

Query Match      31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GCTGTGTGA 19
      |||||
Db      1 GCTGTGTGA 9

RESULT 49
US-08-035-928-15/c
; Sequence 15, Application US/08035928
; Patent No. 5538844
; GENERAL INFORMATION:
; APPLICANT: Duyao, Mabel P.
; APPLICANT: MacDonald, Marcy E.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: A No. 5538844el Transport Protein Gene from
; TITLE OF INVENTION: the Huntington's Disease Region
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/035,928
; FILING DATE: 19930323
; CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
US-08-035-928-15

Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ATCCACCTGCTG 14
      |||||
Db      12 ACCACCTACTG 1

RESULT 50
US-08-250-740-29
; Sequence 29, Application US/08250740
; Patent No. 5686240
; GENERAL INFORMATION:
; APPLICANT: Schuchman, Edward H.
; APPLICANT: Desnick, Robert J.
```

```
; TITLE OF INVENTION: Acid Sphingomyelinase Gene and Diagnosis
; TITLE OF INVENTION: of Niemann-Pick Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 27-MAY-1994
; APPLICATION NUMBER: US/08/250,740
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 6923-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-740-29

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No.55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12

RESULT 51
US-07-695-472B-9
; Sequence 9, Application US/07695472B
; Patent No. 5773278
; GENERAL INFORMATION:
; APPLICANT: Schuchman, Edward H.
; APPLICANT: Desnick, Robert J.
; TITLE OF INVENTION: The Acid Sphingomyelinase Gene and
; TITLE OF INVENTION: Diagnosis of Niemann-Pick Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19910503
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie

; TITLE OF INVENTION: Acid Sphingomyelinase Gene and Diagnosis
; TITLE OF INVENTION: of Niemann-Pick Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 27-MAY-1994
; APPLICATION NUMBER: US/08/250,740
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 6923-038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-740-29

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred.No.55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12

RESULT 52
US-08-410-540-30/c
; Sequence 30, Application US/08410540
; Patent No. 5807678
; GENERAL INFORMATION:
; APPLICANT: Miller, Walter L.
; APPLICANT: Lin, Dong
; APPLICANT: Straus III, Jerome F.
; TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
; TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,540
; FILING DATE: 23-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCAL-238/000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 853 5070
; TELEFAX: 415 857 0663
; TELEX: 380816CCOLEYPA
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-410-540-30
```

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 GACCTGTAAT 29
Db 12 GACCTGTTGAT 1

RESULT 53

US-08-441-887A-69
; Sequence 69, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)

US-08-441-887A-69

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGG 24
Db 1 TGTGTGCTGG 12

RESULT 54

US-09-106-375-9
; Sequence 9, Application US/09106375
; Patent No. 6541218
; GENERAL INFORMATION:
; APPLICANT: Schuchman, Edward H.
; APPLICANT: Desnick, Robert J.
; TITLE OF INVENTION: The Acid Sphingomyelinase Gene and
; TITLE OF INVENTION: Diagnosis of Niemann-Pick Disease
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,375
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/695,472
; FILING DATE: 03-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6923-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 7908864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..12

US-09-106-375-9

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12

RESULT 55

US-09-374-174B-3
; Sequence 3, Application US/09374174B
; Patent No. 6554985
; GENERAL INFORMATION:
; APPLICANT: Ruiz-Martinez, Maria C.

; APPLICANT: Berka, Jan
; APPLICANT: Simpson, John W.
; TITLE OF INVENTION: Methods and Formulations for the Separation of
; TITLE OF INVENTION: Biological Macromolecules
; FILE REFERENCE: Cura-31: Megabace (15966-531)
; CURRENT APPLICATION NUMBER: US/09/374,174B
; CURRENT FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: USSN 60/107,798

```
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Bacteriophage M13mp18
US-09-374-174B-3

Query Match          30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGT 15
Db 1 TCCACCTGGTTT 12

RESULT 56
US-09-163-485-18
; Sequence 18, Application US/09163485
; Patent No. 6277571
; GENERAL INFORMATION:
; APPLICANT: FILMORE, HELEN
; APPLICANT: BROADUS, WILLIAM
; APPLICANT: GILLIES, GEORGE
; TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
; FILE REFERENCE: VCUIP4B
; CURRENT APPLICATION NUMBER: US/09/163,485
; CURRENT FILING DATE: 1998-08-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide, consensus sequence from human
; OTHER INFORMATION: matrix metalloproteinases
US-09-163-485-18

Query Match          29.7%; Score 8.6; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 60;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 4 CTGCTGTGY 12

RESULT 57
US-08-367-175A-23
; Sequence 23, Application US/08367175A
; Patent No. 5631115
; GENERAL INFORMATION:
; APPLICANT: OHTSUKA, Eiko
; APPLICANT: KOIZUMI, Makoto
; TITLE OF INVENTION: Looped, hairpin ribozyme
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FRISHAUF, HOLTZ, GOODMAN,
; ADDRESSEE: LANGER & CHICK, P.C.
; STREET: 767 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-2023
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,175A
; FILING DATE: 29 Dec. 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GOODMAN, Herbert
; REGISTRATION NUMBER: 17081
; REFERENCE/DOCKET NUMBER: 920081
; TELEPHONE: (212)319-4900
; TELEFAX: (212)319-5101
; TELEX: 236268
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: N
; ANTI-SENSE: N
US-08-367-175A-23

Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19
Db 1 UGUUGUGUGA 10

RESULT 58
US-08-388-353-78/c
; Sequence 78, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-78

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
||| |||||
Db 10 CCATCTGCTG 1

RESULT 59
US-08-388-353-381/c
; Sequence 381, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 381:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-381

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGCTG 17
||| |||||
Db 10 CCTGCTGCTG 1

RESULT 60
US-08-388-353-782
; Sequence 782, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:

; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 782:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-782

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
||| |||||
Db 1 CTGTTGTGTG 10

RESULT 61
US-08-388-353-783
; Sequence 783, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 783:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-783

Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TGCTGTGTGA 19
Db      1 TGTGTGTGA 10

RESULT 62
US-08-388-353-784
; Sequence 784, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 784:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

```
US-08-388-353-784

Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 GCTGTGTGAC 20
Db      1 GTTGTGTGAC 10

RESULT 63
US-08-488-551B-78/c
; Sequence 78, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-78

Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CCACCTGTGTG 14
Db      10 CCATCTGTGTG 1

RESULT 64
US-08-488-551B-381/c
```

; Sequence 381, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 381:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-381

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CTGCTGTGTG 17
Db 10 CCTGGTGTGT 1

RESULT 65
US-08-488-551B-782
; Sequence 782, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK

; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 782:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-782

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18
Db 1 CTGTTGTGTG 10

RESULT 66
US-08-488-551B-783
; Sequence 783, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994

Query Match	29.0%;	Score 8.4;	DB 1;	Length 10;
Best Local Similarity	90.0%;	Pred. No. 49;		
Matches	9;	Conservative	0; Mismatches	1; Indels
			0; Gaps	0;
QY	10	TGCTGTGTGA	19	
DB	1	TGTTGTGTGA	10	
<p>RESULT 67</p> <p>US-08-488-551B-784</p> <p>Sequence 784, Application US/08488551B</p> <p>Patent No. 6015661</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Nicholas J. Deacon</p> <p>APPLICANT: Dale A. McPhee</p> <p>APPLICANT: David Cooper</p> <p>TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1</p> <p>NUMBER OF SEQUENCES: 841</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER</p> <p>STREET: 400 GARDEN CITY PLAZA</p> <p>CITY: GARDEN CITY</p> <p>STATE: NEW YORK</p> <p>COUNTRY: U.S.A.</p> <p>ZIP: 11530-0299</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/488,551B</p> <p>FILING DATE: 07-JUN-1995</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: PM3864 (AU)</p> <p>FILING DATE: 14-FEB-1994</p> <p>APPLICATION NUMBER: PM4002 (AU)</p> <p>FILING DATE: 21-FEB-1994</p> <p>APPLICATION NUMBER: PM0284 (AU)</p> <p>FILING DATE: 23-DEC-1994</p> <p>APPLICATION NUMBER: US 08/388,353</p> <p>FILING DATE: 14-FEB-1995</p> <p>APPLICATION NUMBER: PM3021/95</p> <p>FILING DATE: 17-MAY-1995</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: FRANK S. DIGIGLIO</p> <p>REFERENCE/DOCKET NUMBER: 9606Z</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: (516) 742-4343</p> <p>TELEFAX: (516) 742-4366</p> <p>INFORMATION FOR SEQ ID NO: 783:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 10 base pairs</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: DNA</p> <p>US-08-488-551B-783</p>				
Query Match	29.0%;	Score 8.4;	DB 1;	Length 10;
Best Local Similarity	90.0%;	Pred. No. 49;		
Matches	9;	Conservative	0; Mismatches	1; Indels
			0; Gaps	0;
QY	10	TGCTGTGTGA	19	
DB	1	TGTTGTGTGA	10	
<p>RESULT 68</p> <p>US-09-245-041-129/c</p> <p>Sequence 129, Application US/09245041</p> <p>Patent No. 6274339</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Moore, K.</p> <p>APPLICANT: Nagle, D.</p> <p>TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT</p> <p>TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY</p> <p>FILE REFERENCE: 7853-136</p> <p>CURRENT APPLICATION NUMBER: US/09/245,041</p> <p>CURRENT FILING DATE: 1999-02-05</p> <p>EARLIER APPLICATION NUMBER: 60/093,630</p> <p>EARLIER FILING DATE: 1998-07-21</p> <p>EARLIER APPLICATION NUMBER: 60/104,978</p> <p>EARLIER FILING DATE: 1998-10-20</p> <p>NUMBER OF SEQ ID NOS: 131</p> <p>SOFTWARE: FastSeq for Windows Version 3.0</p> <p>SEQ ID NO 129</p> <p>LENGTH: 10</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p> <p>FEATURE:</p> <p>OTHER INFORMATION: Primer</p> <p>US-09-245-041-129</p>				
Query Match	29.0%;	Score 8.4;	DB 1;	Length 10;
Best Local Similarity	90.0%;	Pred. No. 49;		
Matches	9;	Conservative	0; Mismatches	1; Indels
			0; Gaps	0;
QY	12	CTGTGTGACC	21	
DB	10	CTGTGTGTCC	1	
<p>RESULT 69</p> <p>US-08-870-511-13</p> <p>Sequence 13, Application US/08870511</p> <p>Patent No. 6287763</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Lee, Frank</p> <p>APPLICANT: Huszar, Dennis</p> <p>APPLICANT: Gu, Wei</p> <p>TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE</p> <p>TITLE OF INVENTION: REGULATION OF BODY WEIGHT</p> <p>FILE REFERENCE: 7853-083</p> <p>CURRENT APPLICATION NUMBER: US/08/870,511</p> <p>CURRENT FILING DATE: 1997-06-06</p> <p>NUMBER OF SEQ ID NOS: 45</p> <p>SOFTWARE: PatentIn Ver. 2.0</p> <p>SEQ ID NO 13</p> <p>LENGTH: 10</p> <p>TYPE: DNA</p> <p>ORGANISM: Artificial Sequence</p>				

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-08-870-511-13

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACTGC 12
|||||
Db 1 ATCCACTGC 10

RESULT 70

US-09-508-753B-118/c
; Sequence 118, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 118
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-118

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GTGACCTGGT 25
|||||
Db 10 GTGACCTGT 1

RESULT 71

US-10-042-111-8
; Sequence 8, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-8

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTG 11
|||||
Db 1 CATCCCCCTG 10

RESULT 72

US-09-358-055B-130/c
; Sequence 130, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
; TITLE OF INVENTION: OBESITY
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION NUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 130
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-358-055B-130

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CTGTGTGACC 21
|||||
Db 10 CTGTGTGTCC 1

RESULT 73

US-09-893-238-129/c
; Sequence 129, Application US/09893238
; Patent No. 6727348
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-893-238-129

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 49;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACC 21
|||||
Db 10 CTGTGTGTCC 1

RESULT 74

US-08-800-036-15
; Sequence 15, Application US/08800036
; Patent No. 5830661

GENERAL INFORMATION:

APPLICANT: Safarazi, Mansoor

TITLE OF INVENTION: Diagnosis and Treatment of Glaucoma

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David E. Brook, Esq.

STREET: Hamilton, Brook, Smith & Reynolds, Two

STREET: Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,036

FILING DATE: 13-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: UCT97-01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-9540

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-800-036-15

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 58;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAA 28
|||
Db 1 ACCAGGTAAA 10

RESULT 75

US-08-481-658B-86/c

; Sequence 86, Application US/08481658B

; Patent No. 5955075

GENERAL INFORMATION:

APPLICANT: Zavada, Jan

APPLICANT: Pastorekova, Silvia

APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leona L. Lauder

STREET: 6 Mariposa Court

CITY: Tiburon

STATE: California

COUNTRY: USA

ZIP: 94920

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,658B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 86:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: 3' acceptor consensus splice sequence

US-08-481-658B-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 58;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTCT 17
|||
Db 10 CCTTCTGTCT 1

RESULT 76

US-08-926-492-15

; Sequence 15, Application US/08926492

; Patent No. 5962230

GENERAL INFORMATION:

APPLICANT: Safarazi, Mansoor

TITLE OF INVENTION: Diagnosis and Treatment of Glaucoma

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: David E. Brook, Esq.

STREET: Hamilton, Brook, Smith & Reynolds, Two

STREET: Militia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/926,492

FILING DATE: 10-SEP-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/800,036

FILING DATE: 13-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: UCT97-01A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

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; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-926-492-15

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      19 ACTGCTGATAA 28
      ||| |||||
Db       1 ACCAGGTAAA 10

RESULT 77
US-08-477-504A-86/c
; Sequence 86, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-477-504A-86

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| |||||
Db       10 CCTTCTGTGT 1

RESULT 78
US-08-477-504A-86
; Sequence 86, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-477-504A-86

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| |||||
Db       10 CCTTCTGTGT 1

RESULT 79
US-08-486-756A-86/c
; Sequence 86, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-486-756A-86

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| |||||
Db       10 CCTTCTGTGT 1

RESULT 79
US-08-485-862B-86/c
; Sequence 86, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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```
;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
; US-08-485-862B-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
Db 10 CCTTCTGTGT 1

RESULT 80
US-08-787-739-86/c
; Sequence 86, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,739
; FILING DATE: 24-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/486,756
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
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;
;
; APPLICATION NUMBER: US 08/481,658
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,862
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,863
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,077
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
; US-08-787-739-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
Db 10 CCTTCTGTGT 1

RESULT 81
US-09-048-505-15
; Sequence 15, Application US/09048505
; Patent No. 6046009
; GENERAL INFORMATION:
; APPLICANT: Sarfarazi, Mansoor
; TITLE OF INVENTION: Diagnosis and Treatment of Glaucoma
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David E. Brook, Esq.
; STREET: Hamilton, Brook, Smith & Reynolds, Two
; STREET: Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,505
; FILING DATE: 26-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/926,492
; FILING DATE: 10-SEP-97
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/800,036
; FILING DATE: 13-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: UCT97-01A2
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (781) 861-6240
TELEFAX: (781) 861-9540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-048-505-15

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAA 28
Db 1 ACCAGGTAAA 10

RESULT 82
US-08-487-077A-86/c
; Sequence 86, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-487-077A-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db 10 CCTTCTGTGT 1

RESULT 83
US-08-485-863A-86/c
; Sequence 86, Application US/08485863A
; Patent No. 6093548
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,863A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: 3' acceptor consensus splice sequence
US-08-485-863A-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db 10 CCTTCTGTGT 1

RESULT 84
US-08-485-049D-86/c
; Sequence 86, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,049D
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 3' acceptor consensus splice sequence
US-08-485-049D-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
||| |||||
Db 10 CCTTCTGTGT 1

RESULT 85
US-09-178-115-86/c
; Sequence 86, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589

; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: HUMAN
US-09-178-115-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
||| |||||
Db 10 CCTTCTGTGT 1

RESULT 86
US-09-177-776-86/c
; Sequence 86, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
; LENGTH: 11
; TYPE: DNA
; ORGANISM: HUMAN
US-09-177-776-86

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
||| |||||
Db 10 CCTTCTGTGT 1

```
RESULT 87
US-09-249-155A-113
; Sequence 113, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-113

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 1 CTGCTTGTG 10

RESULT 88
US-09-249-155A-285
; Sequence 285, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-285

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 1 CTGCTTGTG 10

RESULT 89
US-09-772-719B-86/c
; Sequence 86, Application US/09772719B
; Patent No. 6770438
; GENERAL INFORMATION:
```

```
APPLICANT: Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Leona L. Lauder
STREET: 465 California Street, Suite 450
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/09/772,719B
FILING DATE: 30-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3A-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: 3' acceptor consensus splice sequence
SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-772-719B-86

Query Match          29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
Db 10 CCTTCTGTGT 1

RESULT 90
US-08-435-350-76/c
; Sequence 76, Application US/08435350
; Patent No. 5599704
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF BREAST CANCER
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,350
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936,531
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/245
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-350-76

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 10 CCATCCACTT 1

RESULT 91
US-09-281-418-141
; Sequence 141, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 141
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-141

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 92
US-09-281-418-191/c
; Sequence 191, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,350
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936,531
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/245
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-350-76

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 10 CCATCCACTT 1

RESULT 91
US-09-281-418-141
; Sequence 141, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 141
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-141

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 92
US-09-281-418-191/c
; Sequence 191, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F

; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 141
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-191

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13
Db 1 UCCACCAGCU 10

RESULT 94
US-09-875-453B-77
; Sequence 77, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu H.

; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 191
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-191

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
Db 11 CCACCTCTTG 2

RESULT 93
US-09-874-601-167
; Sequence 167, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(7)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-167

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 66;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13
Db 1 UCCACCAGCU 10

RESULT 94
US-09-875-453B-77
; Sequence 77, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu H.
```



```
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135-US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Escherichia coli
; US-09-875-453B-77

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CTTGGTAAAT 29
    |||||
Db 3 CTTGATAAAT 12

RESULT 95
US-08-634-350-11
; Sequence 11, Application US/08634350
; Patent No. 5911982
; GENERAL INFORMATION:
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: H2-1 VIRUS PERSISTENCE-ASSOCIATED
; TITLE OF INVENTION: GENE 1(pagl) PROMOTER, USES
; TITLE OF INVENTION: THEREFOR, AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING SAME OR PRODUCTS
; TITLE OF INVENTION: THEREFROM
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,350
; FILING DATE: 18-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, William F.
; REGISTRATION NUMBER: 28,029
; REFERENCE/DOCKET NUMBER: 516450-2008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-634-350-11

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTGGTAAA 28
    |||||
Db 3 CTGGTAAA 10

RESULT 96
US-08-388-353-39
; Sequence 39, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SAMS UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-39

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCTGCTGT 15
    |||||
Db 3 CCTGCTGT 10

RESULT 97
US-08-388-353-40
; Sequence 40, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
```

```

; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: /08/388,353
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-40

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCTGCTGT 15
Db 2 CCTGCTGT 9

RESULT 98
US-08-388-353-41
; Sequence 41, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-41

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCTGCTGT 15
Db 1 CCTGCTGT 8

RESULT 99
US-08-388-353-785
; Sequence 785, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 785:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

```

US-08-388-353-785

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGTGTGAC 20
Db 2 TGTGTGAC 9

RESULT 100

US-08-388-353-786
; Sequence 786, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 786:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-786

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGTGTGAC 20
Db 1 TGTGTGAC 8

RESULT 101

US-08-388-353-788
; Sequence 788, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.

; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 788:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-788

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGTGTGAC 20
Db 1 TGTGTGAC 8

RESULT 102

US-08-488-551B-39
; Sequence 39, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)

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; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-39

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
DB 3 CCTGCTGT 10

RESULT 103
US-08-488-551B-40
; Sequence 40, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-41

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
DB 2 CCTGCTGT 9

RESULT 104
US-08-488-551B-41
; Sequence 41, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-41

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-40

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCTGCTGT 15
DB 2 CCTGCTGT 9

RESULT 104
US-08-488-551B-41
; Sequence 41, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-41

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCTGCTGT 15
|||||

Db 1 CCTGCTGT 8

RESULT 105

US-08-488-551B-785
; Sequence 785, Application US/08488551B
; Patent No. 6015661

GENERAL INFORMATION:

; APPLICANT: Nicholas J. Deacon

; APPLICANT: Dale A. McPhee

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

; NUMBER OF SEQUENCES: 841

; CORRESPONDENCE ADDRESS: 841

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 GARDEN CITY PLAZA

; CITY: GARDEN CITY

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 11530-0299

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,551B

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PM3864 (AU)

; FILING DATE: 14-FEB-1994

; APPLICATION NUMBER: PM4002 (AU)

; FILING DATE: 21-FEB-1994

; APPLICATION NUMBER: PN0284 (AU)

; FILING DATE: 23-DEC-1994

; APPLICATION NUMBER: US 08/388,353

; FILING DATE: 14-FEB-1995

; APPLICATION NUMBER: PN3021/95

; FILING DATE: 17-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: FRANK S. DIGIGLIO

; REFERENCE/DOCKET NUMBER: 9606Z

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 785:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-488-551B-785

Query Match 27.6%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGTGTGAC 20

|||||

Db 2 TGTGTGAC 9

RESULT 106

US-08-488-551B-786

; Sequence 786, Application US/08488551B

; Patent No. 6015661

GENERAL INFORMATION:

; APPLICANT: Nicholas J. Deacon

; APPLICANT: Dale A. McPhee

; APPLICANT: David Cooper

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

; NUMBER OF SEQUENCES: 841

; CORRESPONDENCE ADDRESS: 841

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 GARDEN CITY PLAZA

; CITY: GARDEN CITY

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 11530-0299

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,551B

; FILING DATE: 07-JUN-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PM3864 (AU)

; FILING DATE: 14-FEB-1994

; APPLICATION NUMBER: PM4002 (AU)

; FILING DATE: 21-FEB-1994

; APPLICATION NUMBER: PN0284 (AU)

; FILING DATE: 23-DEC-1994

; APPLICATION NUMBER: US 08/388,353

; FILING DATE: 14-FEB-1995

; APPLICATION NUMBER: PN3021/95

; FILING DATE: 17-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: FRANK S. DIGIGLIO

; REFERENCE/DOCKET NUMBER: 9606Z

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; INFORMATION FOR SEQ ID NO: 786:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-08-488-551B-786

Query Match 27.6%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGTGTGAC 20

|||||

Db 1 TGTGTGAC 8

RESULT 107

US-08-488-551B-788

; Sequence 788, Application US/08488551B

; Patent No. 6015661

GENERAL INFORMATION:

; APPLICANT: Nicholas J. Deacon

; APPLICANT: Dale A. McPhee

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

; NUMBER OF SEQUENCES: 841

; CORRESPONDENCE ADDRESS: 841

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 GARDEN CITY PLAZA

; CITY: GARDEN CITY

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 11530-0299

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/488,551B
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PM3864 (AU)
;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: PM4002 (AU)
;; FILING DATE: 21-FEB-1994
;; APPLICATION NUMBER: PN0284 (AU)
;; FILING DATE: 23-DEC-1994
;; APPLICATION NUMBER: US 08/388,353
;; FILING DATE: 14-FEB-1995
;; APPLICATION NUMBER: PN3021/95
;; FILING DATE: 17-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FRANK S. DIGIGLIO
;; REFERENCE/DOCKET NUMBER: 9606Z
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; INFORMATION FOR SEQ ID NO: 788:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-488-551B-788

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 TGTGTGAC 20
|||
Db 1 TGTGTGAC 8

RESULT 108

US-09-475-947A-279/c
; Sequence 279, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0867
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 279
; LENGTH: 10
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-279

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCAC 8
|||
Db 8 CCATCCAC 1

RESULT 109

US-08-894-454-122
; Sequence 122, Application US/08894454

;; Patent No. 6544784
;; GENERAL INFORMATION:
;; APPLICANT: VAN DEN VEN, W.J.M.
;; APPLICANT: SCHOENMAKERS, H.F.P.M.
;; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRANT GROWTH
;; GENES
;; NUMBER OF SEQUENCES: 164
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: The Webb Law Firm
;; STREET: 700 Koppers Building, 436 Seventh Avenue
;; CITY: Pittsburgh
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 15219-1818
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/894,454
;; FILING DATE: 15-AUG-1997
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/EP/00716
;; FILING DATE: 19-FEB-1996
;; APPLICATION NUMBER: 95200390.3
;; FILING DATE: 17-FEB-1995
;; APPLICATION NUMBER: 95201951.1
;; FILING DATE: 14-JUL-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Johnson, Barbara E
;; REGISTRATION NUMBER: 31,198
;; REFERENCE/DOCKET NUMBER: 702-971100
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 412-471-8815
;; TELEFAX: 412-471-4094
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 122:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-894-454-122

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCTGCTG 14
|||
Db 3 ACCTGCTG 10

RESULT 110

US-10-042-111-23/c
; Sequence 23, Application US/10042111
; Patent No. 6551476
; GENERAL INFORMATION:
; APPLICANT: ZHEJIANG ACADEMY OF AGRICULTURAL SCIENCES
; APPLICANT: CHEN, Jinqing
; TITLE OF INVENTION: A METHOD FOR CONTROLLING RATIO OF PROTEINS/LIPIDS IN CROP SEEDS
; FILE REFERENCE: ref.
; CURRENT APPLICATION NUMBER: US/10/042,111
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: CN 99124511.3
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA

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; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: primer
US-10-042-111-23

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 60;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      9 CTGCTGTG 16
Db      9 CTGCTGTG 2

RESULT 111
US-09-249-155A-106
; Sequence 106, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-106

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 69;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      12 CTGTGTGA 19
Db      2 CTGTGTGA 9

RESULT 112
US-08-836-734E-90/c
; Sequence 90, Application US/08836734E
; Patent No. 6846623
; GENERAL INFORMATION:
; APPLICANT: BECKMANN, JACQUES
; APPLICANT: RICHARD, ISABELLE
; TITLE OF INVENTION: LGMD GENE CODING FOR A CALCIUM DEPENDENT PROTEASE
; FILE REFERENCE: 960-29 AFMB2628AD/FL/SDU
; CURRENT APPLICATION NUMBER: US/08/836,734E
; CURRENT FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: PCT/EP95/04575
; PRIOR FILING DATE: 1995-11-21
; PRIOR APPLICATION NUMBER: EP 94402668.1
; PRIOR FILING DATE: 1994-11-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: MS Word
; SEQ ID NO 90
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)

; OTHER INFORMATION: /label= Table 2
US-08-836-734E-90

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 69;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      5 CCACCTGC 12
Db      9 CCACCTGC 2

RESULT 113
US-09-793-146-36/c
; Sequence 36, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-36

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 76;
Matches      9; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

QY      5 CCACCTGTGT 15
Db      11 CGACCTGATGT 1

RESULT 114
US-09-793-146-41
; Sequence 41, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-41
```

Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 76; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14
||| |||||
Db 1 TCCTCTGCGG 11

RESULT 115

US-09-793-146-59
; Sequence 59, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-59

Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 76; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14
||| |||||
Db 1 TCCTCTGCGG 11

RESULT 116

US-09-793-146-60
; Sequence 60, Application US/09793146
; Patent No. 6919441
; GENERAL INFORMATION:
; APPLICANT: UHLMANN, EUGEN
; APPLICANT: BREIPOHL, GERHARD
; TITLE OF INVENTION: POLYAMIDE-OLIGONUCLEOTIDE DERIVATIVES, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; FILE REFERENCE: 02481.1437-02
; CURRENT APPLICATION NUMBER: US/09/793,146
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: P 44 08 528.1
; PRIOR FILING DATE: 1994-03-14
; PRIOR APPLICATION NUMBER: 08/402,838
; PRIOR FILING DATE: 1995-03-13
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PNA
US-09-793-146-60

Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 76; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 2; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14
||| |||||
Db 1 TCCTCTGCGG 11

RESULT 117

5256558-12/c
; Patent No. 5256558
; APPLICANT: CORUZZI, GLORIA M.; TSAI, FONG-YING
; TITLE OF INVENTION: GENE ENCODING PLANT ASPARAGINE SYNTHETASE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/514,816
; FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 347,302
; FILING DATE: 03-MAY-1989
; SEQ ID NO:12:
; LENGTH: 11
5256558-12

Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 76;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGT 15
||| |||||
Db 11 CTACGTGCTGT 1

RESULT 118

US-07-960-981-2/c
; Sequence 2, Application US/07960981
; Patent No. 5322801
; GENERAL INFORMATION:
; APPLICANT: Kingston, Robert E.
; APPLICANT: Bunker, Christopher
; TITLE OF INVENTION: Protein Partner Screening Assays and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/960,981
; FILING DATE: 19921014
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michelle A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.3630004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 833-7533
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-960-981-2


```
Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CCACCTGCT 13
      ||| |||||
Db      9 CCAGCTGCT 1

RESULT 119
US-07-651-710A-40
; Sequence 40, Application US/07651710A
; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nam-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-40

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      16 GTGACCTGG 24
      ||||| |||
Db      1 GTGACCTGG 9

RESULT 120
US-08-335-565A-21/c
; Sequence 21, Application US/08335565A
; Patent No. 5527671
; GENERAL INFORMATION:
; APPLICANT: Li, Kening
; APPLICANT: Rouse, Douglas I.
; APPLICANT: German, Thomas L.
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles and Brady
; STREET: 1 South Pinckney St., PO BOX 2113
; CITY: Madison

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      17 TGACCTGGT 25
      ||||| |||
Db      10 TCACCTGGT 2

RESULT 121
US-08-235-503B-24
; Sequence 24, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
; APPLICANT: Strulovici, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-235-503B-24

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 2 CCATCTGCT 10

RESULT 122
US-08-545-253A-7
; Sequence 7, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Anerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-545-253A-7

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTG 16
Db 2 CCAGCTGTG 10

; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-235-503B-24

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 2 CCATCTGCT 10

RESULT 123
US-08-265-484B-13/c
; Sequence 13, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION/DOCKET NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-265-484B-13

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCT 10
Db 10 CATCCACTT 2

RESULT 124
US-08-388-353-77/c
; Sequence 77, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA: /08/388,353
/ APPLICATION NUMBER: US/08/388,353
/ FILING DATE: 14-FEB-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: DiGiglio, Frank S.
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 9606
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ TELEX: 230 901 SANS UR
/ INFORMATION FOR SEQ ID NO: 77:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-77

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCACCTGCTG 14
Db 10 CATCTGCTG 2

RESULT 125
US-08-388-353-79/c
; Sequence 79, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-79

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CCACCTGCTG 14
Db 10 CATCTGCTG 2

RESULT 125
US-08-388-353-79/c
; Sequence 79, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
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```
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-79

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCATCTGCT 1

RESULT 126
US-08-388-353-140/c
; Sequence 140, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 140:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
/ US-08-388-353-140

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 10 CTGCTGTAT 2

RESULT 127
US-08-388-353-141/c
; Sequence 141, Application US/08388353
; Patent No. 6010895
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-141

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 9 CTGCTGTAT 1

RESULT 128
US-08-388-353-142/c
; Sequence 142, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-141
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;
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 142:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-142

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGT 15
Db 10 AGCTGCTGT 2

RESULT 129
US-08-388-353-143/c
; Sequence 143, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-143
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; MOLECULE TYPE: DNA (genomic)
US-08-388-353-143

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGT 15
Db 9 AGCTGCTGT 1

RESULT 130
US-08-388-353-380/c
; Sequence 380, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: US/08/388,353
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-380

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 10 CTGCTGTGT 2

RESULT 131
US-08-388-353-382/c
; Sequence 382, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.

```

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; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: US/08/388,353
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-382

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTG 16
Db 9 CCTGCTGTG 1

RESULT 132
US-08-388-353-770
; Sequence 770, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353

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```
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 770:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-770

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      13 TGTGTGACC 21
Db      2 TGTGTGCCC 10

RESULT 133
US-08-388-353-771
; Sequence 771, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 781:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-781

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTGCTGTGT 17
Db      2 CTGTTGTGT 10

RESULT 135
US-08-388-353-796
; Sequence 796, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
```

;
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 796:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-796

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGGTAAAT 29
|||
Db 2 CTGGTAACT 10

RESULT 136
US-08-388-353-797
; Sequence 797, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

;
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 797:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-797

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGGTAAAT 29
|||
Db 1 CTGGTAACT 9

RESULT 137
US-08-488-551B-77/c
; Sequence 77, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO

REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-141

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 9 CTGCTGTAT 1

RESULT 141
US-08-488-551B-142/c
Sequence 142, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)

FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-142

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGT 15
Db 10 AGCTGCTGT 2

RESULT 142
US-08-488-551B-143/c
Sequence 143, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-143

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGT 15
Db 9 AGCTGCTGT 1

RESULT 143
US-08-488-551B-380/c
; Sequence 380, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 380:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-380

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGT 15
Db 9 AGCTGCTGT 1

RESULT 144
US-08-488-551B-382/c
; Sequence 382, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-382

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTG 16
Db 9 CCTGCTGTG 1

RESULT 145
US-08-488-551B-770
; Sequence 770, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
```

APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994

APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995

APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO

REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 770:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-488-551B-770

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACC 21
|||||

Db 2 TGTGTGCCC 10
|||||

RESULT 146
US-08-488-551B-771

Sequence 771, Application US/08488551B
Patent No. 6015661

GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon

APPLICANT: Dale A. McPhee
APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B

FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)

FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)

FILING DATE: 23-DEC-1994

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994

APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995

APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO

REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 771:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-488-551B-771

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACC 21
|||||

Db 1 TGTGTGCCC 9
|||||

RESULT 147
US-08-488-551B-781

Sequence 781, Application US/08488551B
Patent No. 6015661

GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon

APPLICANT: Dale A. McPhee
APPLICANT: David Cooper

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B

FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)

FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)

FILING DATE: 23-DEC-1994

```
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 781:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-781

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGGT 17
Db 2 CTGTGTGT 10

RESULT 148
US-08-488-551B-796
; Sequence 796, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 796:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-796

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGGT 17
Db 2 CTGTGTGT 10

RESULT 149
US-08-488-551B-797
; Sequence 797, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 797:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-797

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGGTAAAT 29
Db 2 CTGGTAACT 10
```

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-796

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGGTAAAT 29
Db 2 CTGGTAACT 10

RESULT 149
US-08-488-551B-797
; Sequence 797, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 797:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-797

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 CTGGTAAAT 29
Db 1 CTGGTAACT 9
```

RESULT 150
US-08-719-337-7
; Sequence 7, Application US/08719337
; Patent No. 6054634
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 6054634th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/719,337
; FILING DATE: 25-SEP-1996
; CLASSIFICATION: 047
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,567
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-719-337-7
Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CCTGCTGTG 16
Db 2 CCAGCTGTG 10
RESULT 151
US-08-765-257A-13/c
; Sequence 13, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza

; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH, 1.44MB
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-13
Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CATCCACTT 10
Db 10 CATCCACTT 2
RESULT 152
US-08-522-384-18
; Sequence 18, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; APPLICANT: NIGAM, SANJAY KUMAR
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-18
Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 CACTGCTGTG 14
Db 1 CATCTGCTG 9
RESULT 153
US-08-522-384-120
; Sequence 120, Application US/08522384
; Patent No. 6110667

; GENERAL INFORMATION:
 ; APPLICANT: LOPEZ-NIETO, CARLOS E
 ; APPLICANT: NIGAM, SANJAY KUMAR
 ; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
 ; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
 ; FILE REFERENCE: 2458-4029
 ; CURRENT APPLICATION NUMBER: US/08/522,384
 ; CURRENT FILING DATE: 1996-11-15
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 120
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Unknown Organism
 ; FEATURE:
 ; OTHER INFORMATION: Description of Unknown Organism: Primer
 US-08-522-384-120

Query Match 25.5%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 78;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTG 14
 |||||
 Db 2 CATCTGCTG 10

RESULT 154
 US-09-034-205-51/c
 ; Sequence 51, Application US/09034205
 ; Patent No. 6194149
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor I.
 ; APPLICANT: Brow, Mary Ann D.
 ; APPLICANT: Fors, Lance
 ; APPLICANT: Neri, Bruce P.
 ; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 ; TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
 ; NUMBER OF SEQUENCES: 68
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: MEDLEN & CARROLL, LLP
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/034,205
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MacKnight, Kamrin T.
 ; REGISTRATION NUMBER: 38,230
 ; REFERENCE/DOCKET NUMBER: FORS-03268
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 397-8338
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "DNA"
 US-09-034-205-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 78;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19
 |||||
 Db 9 GCTGTGTGA 1

RESULT 155
 US-08-934-097A-51/c
 ; Sequence 51, Application US/08934097A
 ; Patent No. 6210880
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor I.
 ; APPLICANT: Brow, Mary Ann D.
 ; APPLICANT: Fors, Lance
 ; APPLICANT: Neri, Bruce P.
 ; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
 ; TITLE OF INVENTION: Structure Probing With Structure-Bridging
 ; TITLE OF INVENTION: Oligonucleotides.
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: MEDLEN & CARROLL, LLP
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,097A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MacKnight, Kamrin T.
 ; REGISTRATION NUMBER: 38,230
 ; REFERENCE/DOCKET NUMBER: FORS-02980
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 397-8338
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "DNA"
 US-08-934-097A-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 78;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19
 |||||
 Db 9 GCTGTGTGA 1

RESULT 156
 US-09-677-218B-51/c
 ; Sequence 51, Application US/09677218B
 ; Patent No. 6355437
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor I.
 ; APPLICANT: Brow, Mary Ann D.
 ; APPLICANT: Fors, Lance
 ; APPLICANT: Neri, Bruce P.
 ; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING

STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-677-218B-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19

Db 9 GCTGTCTGA 1

RESULT 157

US-09-677-192-51/c

Sequence 51, Application US/09677192

Patent No. 6358691

GENERAL INFORMATION:

APPLICANT: Lyamichiev, Victor I.

APPLICANT: Brow, Mary Ann D.

APPLICANT: Fors, Lance

APPLICANT: Neri, Bruce P.

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

TITLE OF INVENTION: OLIGONUCLEOTIDES

FILE REFERENCE: FORS-04708

CURRENT APPLICATION NUMBER: US/09/677,192

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/034,205

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 51

LENGTH: 10

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-677-192-51

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19

Db 9 GCTGTCTGA 1

RESULT 158

US-09-154-750A-14

Sequence 14, Application US/09154750A

Patent No. 6432640

GENERAL INFORMATION:

APPLICANT: Vogelstein, Bert

APPLICANT: Kinzler, Kenneth

APPLICANT: Polyak, Kornelia

TITLE OF INVENTION: p53-Induced Apoptosis

FILE REFERENCE: 1107.75357

CURRENT APPLICATION NUMBER: US/09/154,750A

CURRENT FILING DATE: 1998-09-17

PRIOR APPLICATION NUMBER: 60/059,153

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/079817

PRIOR FILING DATE: 1998-03-30

NUMBER OF SEQ ID NOS: 93

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 10

TYPE: DNA

ORGANISM: Homo sapiens

US-09-154-750A-14

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TGACCTGGT 25

Db 1 TGTCCTGGT 9

RESULT 159

US-09-229-007A-81/c

Sequence 81, Application US/09229007A

Patent No. 6453242

GENERAL INFORMATION:

APPLICANT: Eisenberg, Stephen P.

APPLICANT: Case, Casey C.

APPLICANT: Cox III, George N.

APPLICANT: Jamieson, Andrew

APPLICANT: Rebar, Edward J.

APPLICANT: Sangamo Biosciences, Inc.

TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger

TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins

TITLE OF INVENTION: To Bind to Preslected Sites

FILE REFERENCE: 019496-001800US

CURRENT APPLICATION NUMBER: US/09/229,007A

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 81

LENGTH: 10

TYPE: DNA

ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4

US-09-229-007A-81

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      2 CATCCACCT 10
Db      10 CTTCCACCT 2

RESULT 160
US-09-261-115-57
; Sequence 57, Application US/09261115
; Patent No. 6458584
; GENERAL INFORMATION:
; APPLICANT: MIRZABEKOV, ANDREI
; APPLICANT: GUSCHIN, DMITRY Y.
; APPLICANT: SHIK, VALENTINE
; APPLICANT: DROBYSHV, ALEKSEI
; APPLICANT: FOTIN, ALEXANDER
; APPLICANT: YERSHOV, GENNADIY
; APPLICANT: LYSOV, YU
; TITLE OF INVENTION: CUSTOMIZED OLIGONUCLEOTIDE MICROCHIPS THAT CONVERT
; TITLE OF INVENTION: MULTIPLE GENETIC INFORMATION TO SIMPLE PATTERNS, ARE
; TITLE OF INVENTION: PORTABLE AND REUSABLE
; FILE REFERENCE: 21416/90184
; CURRENT APPLICATION NUMBER: US/09/261,115
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 57
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Customized
; OTHER INFORMATION: oligonucleotide
US-09-261-115-57

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      16 GTGACCTGG 24
Db      2 GTGAACCTGG 10

RESULT 161
US-09-914-259-119/c
; Sequence 119, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
US-09-914-259-119

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 TGCTGTGTG 18
Db      10 TGCTGTGTG 18
```

```
Db      9 TCCTGTGTG 1

RESULT 162
US-09-914-259-120
; Sequence 120, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
US-09-914-259-120

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      14 GTGTGACCT 22
Db      1 GTGTGTCTC 9

RESULT 163
US-09-508-753B-67/c
; Sequence 67, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 67
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-67

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CATCCACCT 10
Db      10 CATTCACCT 2

RESULT 164
US-09-508-753B-78
; Sequence 78, Application US/09508753B
```


; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 78
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-78

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 TGCTGTGTG 18
|||||
Db 2 TGCTGAGTG 10

RESULT 165
US-09-508-753B-89/c
; Sequence 89, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 89
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-89

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 GCTGTGTGA 19
|||||
Db 10 GGTGTGTGA 2

RESULT 166
US-09-508-753B-164
; Sequence 164, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO

; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 164
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-164

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 17 TGACCTGGT 25
|||||
Db 1 TGAACCTGGT 9

RESULT 167
US-09-508-753B-188
; Sequence 188, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Ei-ji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 188
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-188

Query Match 25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CATCCACCT 10
|||||
Db 1 CATCCACCT 9

RESULT 168
US-09-811-286-16/c
; Sequence 16, Application US/09811286
; Patent No. 6586183
; GENERAL INFORMATION:
; APPLICANT: Drysdale, Connie M
; APPLICANT: Judson, Richard S
; APPLICANT: Liggett, Stephen B
; APPLICANT: Nandabalan, Krishnan

```
; APPLICANT: Stack, Catherine B.
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
; FILE REFERENCE: MMH-0303US1
; CURRENT APPLICATION NUMBER: US/09/811,286
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-811-286-16

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 GTGACCTGG 24
Db 9 GTGAGCTGG 1

RESULT 169
US-09-402-618B-51/c
; Sequence 51, Application US/09402618B
; Patent No. 6709815
; GENERAL INFORMATION:
; APPLICANT: Dong, Fang
; APPLICANT: Lyamichev, Victor
; APPLICANT: Prudent, James
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce
; APPLICANT: Brow, Mary Ann
; APPLICANT: Anderson, Todd
; APPLICANT: Dahlberg, James
; TITLE OF INVENTION: Target-Dependent Reactions Using Structure-Bridging Oligonucleotides
; FILE REFERENCE: FORS-04012
; CURRENT APPLICATION NUMBER: US/09/402,618B
; CURRENT FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: PCT/US98/03194
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-402-618B-51

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19
Db 9 GCTGTCTGA 1

RESULT 170
US-09-825-574-51/c
; Sequence 51, Application US/09825574
; Patent No. 6709819
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Brow, Mary Ann D.
; APPLICANT: Fors, Lance
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
; Structure Probing With Structure-Bridging
```

```
; Oligonucleotides.
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,574
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/934,097
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: FORS-02980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-825-574-51

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19
Db 9 GCTGTCTGA 1

RESULT 171
US-10-113-424-81/c
; Sequence 81, Application US/10113424
; Patent No. 6785613
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preslected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/10/113,424
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US/09/229,007A
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Glycine max
```

```
;
; FEATURE:
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4
US-10-113-424-81

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCT 10
Db      10 CTTCACCT 2

RESULT 172
US-09-821-694A-26
; Sequence 26, Application US/09821694A
; Patent No. 6949340
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
; TITLE OF INVENTION: HYBRIDIZATION
; FILE REFERENCE: 0450-0001
; CURRENT APPLICATION NUMBER: US/09/821,694A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder
; OTHER INFORMATION: binding sequence
US-09-821-694A-26

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCT 10
Db      2 CATCCATCT 10

RESULT 173
US-09-821-694A-30/c
; Sequence 30, Application US/09821694A
; Patent No. 6949340
; GENERAL INFORMATION:
; APPLICANT: HILLS, WILLIAM D.
; TITLE OF INVENTION: METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID
; TITLE OF INVENTION: HYBRIDIZATION
; FILE REFERENCE: 0450-0001
; CURRENT APPLICATION NUMBER: US/09/821,694A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Decoder probe
; OTHER INFORMATION: sequence
US-09-821-694A-30

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATCCACCT 10
Db      9 CATCCATCT 1
```

```
RESULT 174
US-10-053-883-70/c
; Sequence 70, Application US/10053883
; Patent No. 6958217
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Morten Lorentz
; TITLE OF INVENTION: ASSAY AND KIT FOR ANALYZING GENE EXPRESSION
; FILE REFERENCE: PEDERSEN-1A
; CURRENT APPLICATION NUMBER: US/10/053,883
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: PA 2001 00126
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/267,704
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-053-883-70

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTG 16
Db      9 CATGCTGTG 1

RESULT 175
PCT-US93-09634-2/c
; Sequence 2, Application PC/TUS9309634
; GENERAL INFORMATION:
; APPLICANT: Kingston, Robert E.
; TITLE OF INVENTION: Bunker, Christopher Alden
; TITLE OF INVENTION: Protein Partner Screening Assays and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1100 New York Avenue, N.W.; Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09634
; FILING DATE: (herewith)
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 0609.274PC03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```

```

; MOLECULE TYPE: DNA
PCT-US93-09634-2

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCAGCTGCT 1

RESULT 176
PCT-US94-08023-14
; Sequence 14, Application PC/TUS9408023
; GENERAL INFORMATION:
; APPLICANT: de Kloet, Siwo R.
; TITLE OF INVENTION: Sex-Specific DNA Probe For Parrots,
; TITLE OF INVENTION: Methods And Kits
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08023
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,198
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: FI20979-34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-08023-14

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 21 CTGTGAAT 29
Db 1 CTGTGAAT 9

RESULT 177
PCT-US95-05265-24
; Sequence 24, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; PCT-US95-05265-24

Query Match      25.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 78;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 2 CCATCTGCT 10

Search completed: May 15, 2006, 14:59:59
Job time : 1 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 15:06:04 ; Search time 0.001 Seconds
(without alignments)
96.860 Million cell updates/sec

Title: US-09-904-968A-3-COPY
Perfect score: 29
Sequence: 1 ccacccacgtgtgtgacctgtaaat 29

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5
Searched: 106 seqs, 1670 residues

Total number of hits satisfying chosen parameters: 212

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 106 summaries

Database : pubmaindb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	29	100.0	29	1	US-09-904-968A-3
2	17.8	61.4	25	1	US-10-719-956-622076
3	15.6	53.8	22	1	US-10-021-425-62
4	15.6	53.8	22	1	US-10-900-856-65
5	15.2	52.4	21	1	US-10-349-143-11421
6	14.8	51.0	20	1	US-10-349-143-9340
7	14.8	51.0	20	1	US-10-831-901A-19537
8	14.8	51.0	20	1	US-10-831-901A-19538
9	14.8	51.0	20	1	US-10-831-901A-19539
10	14.2	49.0	20	1	US-09-853-666-18
11	14.2	49.0	20	1	US-09-345-373-97
12	14.2	49.0	20	1	US-10-075-446-97
13	14.2	49.0	20	1	US-10-035-212-97
14	14.2	49.0	20	1	US-10-695-957-18
15	14.2	49.0	20	1	US-10-733-311-97
16	14.2	49.0	20	1	US-10-901-210-97
17	13.4	46.2	19	1	US-10-349-143-6482
18	13.2	45.5	18	1	US-10-084-839-3261
19	12.8	44.1	17	1	US-10-061-201-1638
20	12.8	44.1	17	1	US-10-061-201-1639
21	12.8	44.1	18	1	US-09-961-077-1205
22	12.8	44.1	18	1	US-09-809-920-34
23	12.4	42.8	15	1	US-10-672-866-142
24	12.4	42.8	17	1	US-09-866-108-2171
25	12.4	42.8	17	1	US-09-866-108-2172
26	12.4	42.8	17	1	US-09-866-108-2173
27	12.4	42.8	17	1	US-09-866-108-2174
28	12.4	42.8	17	1	US-10-723-361-2171
29	12.4	42.8	17	1	US-10-723-361-2172
30	12.4	42.8	17	1	US-10-723-361-2173
31	12.4	42.8	17	1	US-10-723-361-2174
32	12.2	42.1	17	1	US-09-864-785-1502
33	12.2	42.1	17	1	US-09-864-785-2052

1	US-10-060-830-780	17	1	Sequence 780, App
1	US-10-061-201-1640	17	1	Sequence 1640, Ap
1	US-10-061-201-1641	17	1	Sequence 1641, Ap
1	US-10-061-201-1642	17	1	Sequence 1642, Ap
1	US-10-084-839-3258	17	1	Sequence 2258, Ap
1	US-09-866-108-2169	17	1	Sequence 2169, Ap
1	US-10-723-361-2169	17	1	Sequence 2169, Ap
1	US-10-723-361-2170	17	1	Sequence 2170, Ap
1	US-10-257-017B-145361	13	1	Sequence 145361,
1	US-10-257-017B-145362	13	1	Sequence 145362,
1	US-10-160-358-48	15	1	Sequence 48, Appl
1	US-10-433-542A-31	15	1	Sequence 31, Appl
1	US-10-257-480A-17	15	1	Sequence 17, Appl
1	US-10-084-839-3252	16	1	Sequence 3252, Ap
1	US-10-276-775-32	16	1	Sequence 32, Appl
1	US-10-138-674-5660	16	1	Sequence 5660, Ap
1	US-10-287-949A-5660	16	1	Sequence 5660, Ap
1	US-10-776-934-512	16	1	Sequence 93, Appl
1	US-10-776-934-513	16	1	Sequence 512, App
1	US-10-776-934-514	16	1	Sequence 513, App
1	US-10-776-934-515	16	1	Sequence 514, App
1	US-10-010-802-40	15	1	Sequence 515, App
1	US-09-504-231A-107	15	1	Sequence 40, Appl
1	US-09-274-553D-107	15	1	Sequence 107, App
1	US-10-339-674-1871	15	1	Sequence 107, App
1	US-10-984-919-371	15	1	Sequence 1871, Ap
1	US-10-271-429A-17	13	1	Sequence 371, App
1	US-10-146-038-1	14	1	Sequence 17, Appl
1	US-10-356-625-17	14	1	Sequence 1, Appl
1	US-10-468-753-30	14	1	Sequence 17, Appl
1	US-10-984-919-1139	14	1	Sequence 30, Appl
1	US-09-942-310-56	11	1	Sequence 1139, Ap
1	US-09-942-310-63	11	1	Sequence 56, Appl
1	US-10-450-797-855	11	1	Sequence 63, Appl
1	US-10-257-017B-305438	12	1	Sequence 855, App
1	US-10-257-017B-343129	12	1	Sequence 50, Appl
1	US-10-091-281-243	13	1	Sequence 305438,
1	US-10-257-017B-14111	13	1	Sequence 343129,
1	US-10-257-017B-14112	13	1	Sequence 243, App
1	US-10-257-017B-14113	13	1	Sequence 14111, A
1	US-10-257-017B-14114	13	1	Sequence 14112, A
1	US-10-257-017B-35449	13	1	Sequence 14113, A
1	US-10-257-017B-35450	13	1	Sequence 14114, A
1	US-10-257-017B-112883	13	1	Sequence 35449, A
1	US-10-257-017B-112884	13	1	Sequence 35450, A
1	US-10-257-017B-201617	13	1	Sequence 112883,
1	US-10-257-017B-201618	13	1	Sequence 112884,
1	US-09-504-231A-1393	14	1	Sequence 201617,
1	US-09-274-553D-1393	14	1	Sequence 201618,
1	US-10-024-944-6	14	1	Sequence 1393, Ap
1	US-10-721-157-6	14	1	Sequence 1393, Ap
1	US-10-984-919-1309	14	1	Sequence 6, Appl
1	US-09-510-378-25	14	1	Sequence 3, Appl
1	US-09-798-260-83	13	1	Sequence 1309, Ap
1	US-10-043-875-397	13	1	Sequence 25, Appl
1	US-10-043-875-422	13	1	Sequence 81, Appl
1	US-10-311-645A-118	13	1	Sequence 397, App
1	US-10-257-017B-145363	13	1	Sequence 422, App
1	US-10-257-017B-145364	13	1	Sequence 118, App
1	US-09-771-933-166	14	1	Sequence 145363,
1	US-10-146-058-15	14	1	Sequence 145364,
1	US-10-043-875-394	14	1	Sequence 166, App
1	US-10-043-875-398	14	1	Sequence 15, Appl
1	US-10-043-875-412	14	1	Sequence 394, App
1	US-10-043-875-414	14	1	Sequence 398, App
1	US-10-043-875-417	14	1	Sequence 412, App
1	US-10-043-875-421	14	1	Sequence 414, App
1	US-10-984-919-367	14	1	Sequence 417, App
1	US-10-984-919-1153	14	1	Sequence 421, App
1	US-10-984-919-1469	14	1	Sequence 367, App
1		14	1	Sequence 1153, Ap
1		14	1	Sequence 1469, Ap

ALIGNMENTS

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RESULT 1
US-09-904-968A-3
; Sequence 3, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer BPF14
US-09-904-968A-3

Query Match      100.0%; Score 29; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
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Db 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29

RESULT 2
US-10-719-956-622076
; Sequence 622076, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 622076
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-622076

Query Match      61.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 8;
Matches 19; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTAAA 28
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Db 3 CCTGCTGGGTGACCTTGTAAA 23

RESULT 3
US-10-021-425-62
; Sequence 62, Application US/10021425
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; Publication No. US20030148420A1
; GENERAL INFORMATION:
; APPLICANT: Suzanne L. Bolten
; APPLICANT: Alan M. Easton
; APPLICANT: Leslie C. Engel
; APPLICANT: Dean M. Messing
; APPLICANT: John S. Ng
; APPLICANT: Beverly A. Reitz
; APPLICANT: Scott A. Vaccaro
; APPLICANT: Mark C. Walker
; APPLICANT: Ping T. Wang
; APPLICANT: Robin A. Weinberg
; TITLE OF INVENTION: Aspergillus ochraceus 11 alpha
; FILE REFERENCE: S03196-00-US
; CURRENT APPLICATION NUMBER: US/10/021,425
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: USSN 60/244,300
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 22
; TYPE: DNA
; ORGANISM: human oxidoreductase primer 2C
US-10-021-425-62

Query Match      53.8%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGACCTG 23
    |||||
Db 1 CATCGACCACTGTGTGAGCTG 22

RESULT 4
US-10-900-856-65
; Sequence 65, Application US/10900856
; Publication No. US20050003473A1
; GENERAL INFORMATION:
; APPLICANT: Bolten, Suzanne L
; APPLICANT: Leslie, Engel C
; APPLICANT: Dean, Messing M
; APPLICANT: John, Ng S
; APPLICANT: Beverly, Reitz A
; APPLICANT: Scott, Vaccaro A
; APPLICANT: Mark, Walker C
; APPLICANT: Ping, Wang T
; APPLICANT: Robin, Weinberg A
; TITLE OF INVENTION: Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase
; FILE REFERENCE: 3196
; CURRENT APPLICATION NUMBER: US/10/900,856
; CURRENT FILING DATE: 2004-07-28
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 65
; LENGTH: 22
; TYPE: DNA
; ORGANISM: homo sapiens oxidoreductase primer 2C
US-10-900-856-65

Query Match      53.8%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGACCTG 23
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Db 1 CATCGACCACTGTGTGAGCTG 22
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RESULT 5
US-10-349-143-11421/c
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; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19538
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-19538

Query Match      51.0%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CTGTGTGACCTGGTAAAT 29
Db      2 CTCTGTAACTGGTAAAT 19

RESULT 9
US-10-831-901A-19539
; Sequence 19539, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Ecker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian A.
; APPLICANT: Hoistadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: ISIS0083-100 (BIOL00008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19539
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Antisense compound
US-10-831-901A-19539

Query Match      51.0%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CTGTGTGACCTGGTAAAT 29
Db      3 CTCTGTAACTGGTAAAT 20

RESULT 10
US-09-853-666-18
; Sequence 18, Application US/09853666
; Patent No. US20020018295A1
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Kaushal, Parveen
; APPLICANT: Spitznagel, Thomas
; APPLICANT: Unsworth, Edward
; APPLICANT: Khan, Fazal
; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations
; FILE REFERENCE: 1488.1030001
; CURRENT APPLICATION NUMBER: US/09/853,666
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/218,444
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-853-666-18

Query Match      49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACCTGCAGGGTGAC 19

RESULT 11
US-09-345-373-97
; Sequence 97, Application US/09345373
; Publication No. US20030077695A1
; GENERAL INFORMATION:
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: JIMENEZ, PABLO
; APPLICANT: DUAN, D. ROXANNE
; APPLICANT: RAMPY, MARK A.
; APPLICANT: MENDRICK, DONNA
; APPLICANT: ZHANG, JUN
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL A.
; APPLICANT: COLEMAN, TIMOTHY A.
; APPLICANT: GRUBER, JOACHIM R.
; APPLICANT: DILLON, PATRICK J.
; APPLICANT: GENTZ, REINER L.
; TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,373
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-345-373-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACCACTGCAGGGTGAC 19

RESULT 12

US-10-075-446-97
Sequence 97, Application US/10075446
Publication No. US20030129687A1

GENERAL INFORMATION:

APPLICANT: RUBEN, STEVEN M.
JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
MOORE, PAUL A.
COLEMAN, TIMOTHY A.
GRUBER, JOACHIM R.

TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/075,446
FILING DATE: 15-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/023,082
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFEE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-075-446-97

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACCACTGCAGGGTGAC 19

RESULT 13

US-10-035-212-97

Sequence 97, Application US/10035212
Publication No. US20030186904A1

GENERAL INFORMATION:

APPLICANT: RUBEN, STEVEN M.
JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
MOORE, PAUL A.
COLEMAN, TIMOTHY A.
GRUBER, JOACHIM R.
DILLON, PATRICK J.

```
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.0360000
; CURRENT APPLICATION NUMBER: US/10/035,212
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/286,368
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/331,168
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-035-212-97

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACTGCAGGGTGAC 19
      || ||||| |||||
;
RESULT 14
US-10-695-957-18
; Sequence 18, Application US/10695957
; Publication No. US200400639A1
; GENERAL INFORMATION:
; APPLICANT: Gentz et al.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2 Formulations
; FILE REFERENCE: PF402C1D1
; CURRENT APPLICATION NUMBER: US/10/695,957
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 09/853,666
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/218,444
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/068,493
; PRIOR FILING DATE: 1997-12-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-695-957-18

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACTGCAGGGTGAC 19
      || ||||| |||||
;
RESULT 15
US-10-733-311-97
; Sequence 97, Application US/10733311
; Publication No. US20040224387A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; APPLICANT: Jimenez, Pablo
; APPLICANT: Duan, D. Roxanne
; APPLICANT: Rumpy, Mark A.
; APPLICANT: Mendrick, Donna
; APPLICANT: Zhang, Jun
; APPLICANT: Ni, Jian
; APPLICANT: Moore, Paul A.
; APPLICANT: Coleman, Timothy A.
; APPLICANT: Gruber, Joachim R.
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.0360000
; CURRENT APPLICATION NUMBER: US/10/733,311
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US/09/610,651
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: PCT/US95/01790
; PRIOR FILING DATE: 1995-02-14
; PRIOR APPLICATION NUMBER: 08/461,195
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/696,135
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 08/862,432
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/023,852
; PRIOR FILING DATE: 1996-08-13
; PRIOR APPLICATION NUMBER: 60/039,045
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: 60/055,561
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 08/910,875
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/023,082
; PRIOR FILING DATE: 1998-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-10-733-311-97

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTGTGTGAC 20
Db      1 CAACCACTGCAGGGTGAC 19
      || ||||| |||||
;
RESULT 16
US-10-901-210-97
; Sequence 97, Application US/10901210
; Publication No. US20050037966A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Keratinocyte Growth Factor-2
; FILE REFERENCE: PF155P2D1
; CURRENT APPLICATION NUMBER: US/10/901,210
; CURRENT FILING DATE: 2004-07-29
; PRIOR APPLICATION NUMBER: 10/035,212
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/359,853
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/286,368
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/331,168
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 97
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer for construction of codon-optimized KGF-2?33
US-10-901-210-97

Query Match          49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGAC 20
    ||||||| | |||||
Db 1 CAACACCTGCAGGTGAC 19

RESULT 17
US-10-349-143-6482/c
; Sequence 6482, Application US/10349143
; Publication No. US2004005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6482
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11745 for SEQ 2548,
US-10-349-143-6482

Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGGA 19
    ||||||| |||||
Db 19 CCGCCTGCTGTGGA 5

RESULT 18
US-10-849-839-3261/c
; Sequence 3261, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
```

```
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsatska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3261
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3261

Query Match          45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTG 18
    ||||||| ||||| |||
Db 18 CCATCCTTCTGCTGAGTG 1

RESULT 19
US-10-061-201-1638
; Sequence 1638, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1638
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1638
```

```

Query Match      44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTGTG 18
Db 2 ATCCACCTCTCTGTG 17

RESULT 20
US-10-061-201-1639
; Sequence 1639, Application US/10061201
; Publication No. US20030165229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1639
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1639

```

```

Query Match      44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTGTG 18
Db 1 ATCCACCTCTCTGTG 16

```

```

RESULT 21
US-09-961-077-1205
; Sequence 1205, Application US/09961077
; Publication No. US20030014775A1
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; Edington, Brent E.
; McSwiggen, James A.
; Merlo, Patricia Ann Owens
; Guo, Lining
; Skokut, Thomas A.
; Young, Scott A.
; Folkerts, Otto
; Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; MODULATION OF GENE EXPRESSION

```

```

IN PLANTS
NUMBER OF SEQUENCES: 1263
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/961,077
FILING DATE: 21-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,645
FILING DATE: July 12, 1996
APPLICATION NUMBER: 60/001,135
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300,726
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1205:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1205:
US-09-961-077-1205

```

```

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTGAC 20
Db 2 CCACCUAGUUGAC 17

```

```

RESULT 22
US-09-809-920-34/c
; Sequence 34, Application US/09809920
; Publication No. US20030139584A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
; EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
; THEREOF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/809,920
FILING DATE: 16-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/156,191
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51902
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-809-920-34

Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGAC 20
||| ||||| ||
Db 18 CCACATGCTGTGTAC 3

RESULT 23
US-10-672-866-142
Sequence 142, Application US/10672866
Publication No. US20050019915A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF SUPEROXIDE DISMUTASE 1,
TITLE OF INVENTION: SOLUBLE
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0242
CURRENT APPLICATION NUMBER: US/10/672,866
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/633,843
PRIOR FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: 09/888,360
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 339
SEQ ID NO 142
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-866-142

Query Match 42.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTT 15
|| ||||| ||
Db 1 CACCCACCTGCTT 14

RESULT 24
US-09-866-108-2171
Sequence 2171, Application US/09866108

Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFERENCE: AEOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 2171
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108-2171

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18
||| ||||| ||
Db 4 CCACCTGCTGTGAG 17

RESULT 25
US-09-866-108-2172
Sequence 2172, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2172

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18
|||||
DB 3 CCACCTGCTGTGAG 16
|||||

RESULT 26
US-09-866-108-2173
; Sequence 2173, Application US/09/866,108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2173
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2173

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18
|||||
DB 2 CCACCTGCTGTGAG 15
|||||

RESULT 27
US-09-866-108-2174
; Sequence 2174, Application US/09/866,108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2174
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108-2174

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
| | | | | | | | | | | | | | | | | |
Db 1 CCACCTGCTGTGTG 14

RESULT 28
US-10-723-361-2171
; Sequence 2171, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2171
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-723-361-2171

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
| | | | | | | | | | | | | | | | | |
Db 4 CCACCTGCTGTGTG 17

RESULT 29
US-10-723-361-2172
; Sequence 2172, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2172
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2172

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
| | | | | | | | | | | | | | | | | |
Db 3 CCACCTGCTGTGTG 16

RESULT 30
US-10-723-361-2173
; Sequence 2173, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.

```

; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2173
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2173

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 18
| | | | | | | | | | | | | | |
Db 2 CCACCTGCTGTG 15

RESULT 31
US-10-723-361-2174
; Sequence 2174, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 2174
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2174

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 18
| | | | | | | | | | | | | | |
Db 1 CCACCTGCTGTG 14

RESULT 32
US-09-864-785-1502
; Sequence 1502, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1502
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-1502

Query Match 42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 29;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGG 24
| | : | : | : | : | : |
Db 1 CCUACUGUGGACAAAG 17

RESULT 33
US-09-864-785-2052
; Sequence 2052, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: 400/022 (MBH00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785

```



```
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2052
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2052

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 29;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTGTA 19
   ||| ||| :|||:|
Db 1 AUCUCCUACUGUGUGA 17

RESULT 34
US-10-060-830-780/c
; Sequence 780, Application US/10060830
; Publication No. US20030032154A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN LCCL DOMAIN CONTAINING PROTEIN
; FILE REFERENCE: PB0169
; CURRENT APPLICATION NUMBER: US/10/060,830
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/325,062
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 1123
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 780
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-830-780

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTGGTAAA 28
   ||||| |||||
Db 17 CTGTGGCACCTGGTACA 1

RESULT 35
US-10-061-201-1640
; Sequence 1640, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
```

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; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1640
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1640

Query Match          42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGAC 20
   ||||| |||||
Db 1 TCCACCTCTCTGTGTC 17

RESULT 36
US-10-061-201-1641
; Sequence 1641, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1641
; LENGTH: 17
; TYPE: DNA
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```
; ORGANISM: Homo sapiens
US-10-061-201-1641

Query Match      42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTGACC 21
    ||||| || |||||
Db 1 CCACCTCCTCTGTGTCC 17

RESULT 37
US-10-061-201-1642
; Sequence 1642, Application US/10061201
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: HUMAN POSH-LIKE PROTEIN 1
; FILE REFERENCE: PB0178
; CURRENT APPLICATION NUMBER: US/10/061,201
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/328,205
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 4162
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 1642
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-061-201-1642

Query Match      42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CACCTGCTGTGTGACCT 22
    ||||| || |||||
Db 1 CACCTCCTCTGTGTCT 17

RESULT 38
US-10-084-839-3258/c
; Sequence 3258, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Arque, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
```

```
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lymaichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3258
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3258

Query Match      42.1%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17
    ||||| |||||
Db 17 CCATCCTCTCTGTGAGT 1

RESULT 39
US-09-866-108-2169
; Sequence 2169, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
```

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2169

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 16
|||||
Db 6 CCACCTGCTGTG 17

RESULT 40

US-09-866-108-2170
; Sequence 2170, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860

; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2170
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2170

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 16
|||||
Db 5 CCACCTGCTGTG 16

RESULT 41

US-10-723-361-2169
; Sequence 2169, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AND
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2169
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-2169

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 16
|||||
Db 6 CCACCTGCTGTG 17

RESULT 42

US-10-723-361-2170

Sequence 2170, Application US/10723361
Publication No. US20040137589A1

GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark

TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

FILE REFERENCE: PB0105
CURRENT APPLICATION NUMBER: US/10/723,361
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 09/866,108
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
SEQ ID NO 2170
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens

US-10-723-361-2170

Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTG 16
|||||
Db 5 CCACCTGCTGTG 16

RESULT 43
US-10-257-017B-145361/c
Sequence 145361, Application US/10257017B
Publication No. US20040241651A1

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin

TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosine
FILE REFERENCE: E01/1193/WO
CURRENT APPLICATION NUMBER: US/10/257,017B
CURRENT FILING DATE: 2002-10-07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 382046
SEQ ID NO 145361
LENGTH: 13
TYPE: DNA
ORGANISM: Artificial Sequence

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV m1Rz-247
US-10-257-480A-17

Query Match      39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 ACCTGCTGTGTGACC 21
Db      1 ACTTGCTGTGTAAVC 15

RESULT 46
US-10-433-542A-31/c
; Sequence 31, Application US/10433542A
; Publication No. US20040209263A1
; GENERAL INFORMATION:
; APPLICANT: Clawson, Gary A.
; TITLE OF INVENTION: SELECTION OF CATALYTIC NUCLEIC ACIDS
; TITLE OF INVENTION: TARGETED TO INFECTIOUS AGENTS
; FILE REFERENCE: 14017-007US1
; CURRENT APPLICATION NUMBER: US/10/433,542A
; CURRENT FILING DATE: 2003-06-04
; PRIOR APPLICATION NUMBER: PCT/US01/46178
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/251,810
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-433-542A-31

Query Match      39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TCACCTGCTGTG 16
Db      13 TCACCTGCTGCG 1

RESULT 47
US-10-257-480A-17/c
; Sequence 17, Application US/10257480A
; Publication No. US20040220123A1
; GENERAL INFORMATION:
; APPLICANT: Norris, James S.
; APPLICANT: Westwater, Caroline
; APPLICANT: Schofield, David A.
; APPLICANT: Schmidt, Michael G.
; APPLICANT: Hoel, Brian D.
; APPLICANT: Dolan, Joseph W.
; APPLICANT: Clawson, Gary A.
; APPLICANT: Pan, Wei-Hua
; TITLE OF INVENTION: TISSUE-SPECIFIC AND PATHOGEN-SPECIFIC TOXIC AGENTS,
; TITLE OF INVENTION: RIBOZYMES, DNAZYMES AND ANTISENSE OLIGONUCLEOTIDES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 14017-006US1 (PSU 99-2157)
; CURRENT APPLICATION NUMBER: US/10/257,480A
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: PCT/US01/12130
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/251,810
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/548,449
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 15
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV m1Rz-247
US-10-257-480A-17

Query Match      39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TCACCTGCTGTG 16
Db      13 TCACCTGCTGCG 1

RESULT 48
US-10-084-839-3252/c
; Sequence 3252, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamicheva, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsatska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3252
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3252

Query Match      38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTG 16
Db      16 CCATCCTCTCTGCTGAG 1

RESULT 49
US-10-276-775-32/c
; Sequence 32, Application US/10276775
; Publication No. US20040072170A1
; GENERAL INFORMATION:
; APPLICANT: Bunk, Daniela
; APPLICANT: Reuner, Birgit
```

; APPLICANT: Beck, Joachim
; APPLICANT: Henkel, Thomas
; TITLE OF INVENTION: Novel Target Genes For Diseases of the
; TITLE OF INVENTION: Heart
; FILE REFERENCE: 50290/004002
; CURRENT APPLICATION NUMBER: US/10/276,775
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: PCT/EP01/06165
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 60/207,400
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-276-775-32

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTGGT 25
|||:|:|:|:|:|:|:
Db 16 TGCTGTGTGAATGTT 1

RESULT 50

US-10-138-674-5660
; Sequence 5660, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5660

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTG 23
|||:|:|:|:|:|:|:
Db 1 CCUGCUGGCGGCUG 16

RESULT 51

US-10-287-949A-5660
; Sequence 5660, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5660
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5660

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 37;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTG 23
|||:|:|:|:|:|:|:
Db 1 CCUGCUGGCGGCUG 16

RESULT 52

US-10-776-934-93/c
; Sequence 93, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRU, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-93

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGTGTGTGA 19
|||:|:|:|:|:|:|:
Db 16 TGCCACTGTGTGTGA 1

RESULT 53

US-10-776-934-512/c
; Sequence 512, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRU, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372

; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 512
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
; US-10-776-934-512

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGA 19
| | | | | | | | | | | | | | | |
Db 16 TGCCACTGCTGTGTGA 1

RESULT 54
US-10-776-934-513/c
; Sequence 513, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 513
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(15)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
; US-10-776-934-513

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGA 19
| | | | | | | | | | | | | | | |
Db 16 TGCCACTGCTGTGTGA 1

RESULT 55
US-10-776-934-514/c
; Sequence 514, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 514
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(13)
; OTHER INFORMATION: phosphorothioate linkage
; US-10-776-934-514

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGA 19
| | | | | | | | | | | | | | | |
Db 16 TGCCACTGCTGTGTGA 1

RESULT 56
US-10-776-934-515/c
; Sequence 515, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THRUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10

```
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 515
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-515

Query Match      38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 37;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  TCACCTGCTGTGTGA 19
Db      16  TGCCACTGCTGTGTGA 1

RESULT 57
US-10-010-802-40
; Sequence 40, Application US/10010802
; Publication No. US20030078220A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Duda, Amy
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Windemuth, Andreas
; TITLE OF INVENTION: Drug Target Isogenes: Polymorphisms in the Interleukin
; FILE OF INVENTION: 4 Receptor Alpha Gene
; FILE REFERENCE: MMH-0002US2 IL4R alpha
; CURRENT APPLICATION NUMBER: US/10/010.802
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: PCT/US00/19094
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-802-40

Query Match      37.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  CACCTGTGTG 16
Db      1  CACCTGTGTG 11

RESULT 58
US-09-504-231A-107/c
; Sequence 107, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; APPLICANT: Macejak, Dennis
```

```
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: Ipi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-107

Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      16  GTGACCTGGTAAAT 29
Db      15  GTGACCTGATACAT 2

RESULT 59
US-09-274-553D-107/c
; Sequence 107, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED
; FILE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: Ipi 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-107

Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      16  GTGACCTGGTAAAT 29
Db      15  GTGACCTGATACAT 2
```

RESULT 60


```
US-10-339-674-1871
; TITLE OF INVENTION: Application US/10339674
; FILE REFERENCE: US20030204318A1
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Escherichia coli K-12 MG1655 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/339,674
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 3537
; SOFTWARE: Proprietary
; SEQ ID NO 1871
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Escherichia coli K-12 MG1655 complete genome.
; FEATURE:
; LOCATION: (2551260)...(2551274)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 2480
US-10-339-674-1871

Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTGGT 25
Db 1 CTGTTAAACCTGGT 14

RESULT 61
US-10-984-919-371
; Sequence 371, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 371
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-371

Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACTTGTG 14
Db 1 CCATCCACTTGTG 14

RESULT 62
US-10-271-429A-17/c
; Sequence 17, Application US/10271429A
; Publication No. US200400233A1
; GENERAL INFORMATION:
; APPLICANT: Atherogenics, Inc.
; TITLE OF INVENTION: Protection Against Oxidative Stress and Inflammation by a Cytopr
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; TITLE OF INVENTION: Response Element
; FILE REFERENCE: ATH118
; CURRENT APPLICATION NUMBER: US/10/271,429A
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/329,870
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/329,870
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 13
; TYPE: DNA
; ORGANISM: human
US-10-271-429A-17

Query Match 35.9%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGAC 20
Db 12 CTGCTGTGTGAC 1

RESULT 63
US-10-146-058-1/c
; Sequence 1, Application US/10146058
; Publication No. US20030040499A1
; GENERAL INFORMATION:
; APPLICANT: Schlengersiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlengersiepen, Karl-Hermann
; APPLICANT: Schlengersiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-1

Query Match          35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12
Db 13 CTATCCACCTGC 2

RESULT 64
US-10-356-625-17/c
; Sequence 17, Application US/10356625
; Publication No. US20030186290A1
; GENERAL INFORMATION:
; APPLICANT: Tournier-Lasserre, Elisabeth
; APPLICANT: Joutel, Anne
; APPLICANT: Bousser, Marie-Germaine
; APPLICANT: Bach, Jean-Francois
; TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
; TITLE OF INVENTION: THERAPEUTIC APPLICATION
; FILE REFERENCE: 03715.0048-00000
; CURRENT APPLICATION NUMBER: US/10/356,625
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/230,652
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: FR 96 09733
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: FR 97 04680
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: PCT/FR97/01433
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-356-625-17

Query Match          35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12
Db 14 CCACCCACCTGC 3

RESULT 65
US-10-468-753-30
; Sequence 30, Application US/10468753
; Publication No. US20040142337A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, Mikio
; APPLICANT: YAMAMOTO, Naoki
; APPLICANT: HIROSE, Kunitaka
; APPLICANT: SAKAI, Jun
; TITLE OF INVENTION: METHOD FOR PREPARATION OF CDNA TAGS FOR
; TITLE OF INVENTION: IDENTIFYING EXPRESSED GENES AND METHOD FOR ANALYSIS OF GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: TECH-005
; CURRENT APPLICATION NUMBER: US/10/468,753
; CURRENT FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/JP02/02338
```

```
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: JP 2001-73959
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-468-753-30

Query Match          35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGC 24
Db 2 TGTATGACCTGC 13

RESULT 66
US-10-984-919-1139/c
; Sequence 1139, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1139
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1139

Query Match          35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12
Db 13 CTATCCACCTGC 2

RESULT 67
US-09-942-310-56/c
; Sequence 56, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
; FILE REFERENCE: GG119.IUS
; CURRENT APPLICATION NUMBER: US/09/942,310
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 77
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-942-310-56

Query Match          34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      11 CCATCCACCT 2

RESULT 68
US-09-942-310-63
; Sequence 63, Application US/09942310
; Publication No. US20030044797A1
; GENERAL INFORMATION:
; APPLICANT: Risinger, Carl
; APPLICANT: Andersson, Maria K.
; APPLICANT: Lewander, Tommy
; APPLICANT: Olaisson, Erik
; TITLE OF INVENTION: Detection of CYP2D6 Polymorphisms
; FILE REFERENCE: G6119.1US
; CURRENT APPLICATION NUMBER: US/09/942,310
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: GB 0021286.0
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 11
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-942-310-63

Query Match          34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      1 CCATCCACCT 10

RESULT 69
US-10-450-797-855
; Sequence 855, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO
; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 855
; LENGTH: 11
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-10-450-797-855

Query Match          34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATCCACCTGC 12
Db      1 ATCCACCTGC 10

RESULT 70
US-10-219-446-50/c
; Sequence 50, Application US/10219446
; Publication No. US20040033497A1
; GENERAL INFORMATION:
; APPLICANT: Alarcon-Riquelme, Marta E.
; APPLICANT: Prokunina, Ludmila
; TITLE OF INVENTION: Polymorphisms of PD-1
; FILE REFERENCE: sthp-004
; CURRENT APPLICATION NUMBER: US/10/219,446
; CURRENT FILING DATE: 2002-08-13
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-219-446-50

Query Match          34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      12 CCATCCACCT 3

RESULT 71
US-10-257-017B-305438
; Sequence 305438, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 305438
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0021446
US-10-257-017B-305438

Query Match          34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCACCT 10
Db      2 CCATCCACCT 11
```

```
RESULT 72
US-10-257-017B-343129
; Sequence 343129, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 343129
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0042904
US-10-257-017B-343129

Query Match 34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 37; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 CCATCCACCT 10
Db 3 CCATCCACCT 12

RESULT 73
US-10-091-281-243
; Sequence 243, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 243
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AREB/AREB6.01 motif
US-10-091-281-243

Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 3 ATCCACCTGC 12
Db 2 ATCCACCTGC 11

RESULT 74
US-10-257-017B-14111/c
; Sequence 14111, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
```

```
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14111
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14111

Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 CCATCCACCT 10
Db 13 CCATCCACCT 4

RESULT 75
US-10-257-017B-14112
; Sequence 14112, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14112
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14112

Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 CCATCCACCT 10
Db 1 CCATCCACCT 10

RESULT 76
US-10-257-017B-14113/c
; Sequence 14113, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
```

```
; SEQ ID NO 14113
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14113

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 13 CCATCCACCT 4

RESULT 77
US-10-257-017B-14114
; Sequence 35449, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14114
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003223
US-10-257-017B-14114

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 1 CCATCCACCT 10

RESULT 78
US-10-257-017B-35449/c
; Sequence 35449, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 35449
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011230
US-10-257-017B-35449
```

```
Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 12 CCATCCACCT 3

RESULT 79
US-10-257-017B-35450
; Sequence 35450, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 35450
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0011230
US-10-257-017B-35450

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 2 CCATCCACCT 11

RESULT 80
US-10-257-017B-112883/c
; Sequence 112883, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112883
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028229
US-10-257-017B-112883

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 1 CCATCCACCT 11
```

```
Db      10 CCATCCACCT 1

RESULT 81
US-10-257-017B-112884
; Sequence 112884, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 112884
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0028229
US-10-257-017B-112884

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCCACCT 10
      |||||
Db      4 CCATCCACCT 13

RESULT 82
US-10-257-017B-201617/c
; Sequence 201617, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 201617
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0049588
US-10-257-017B-201617

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCCACCT 10
      |||||
Db      11 CCATCCACCT 2

RESULT 83
US-10-257-017B-201618
; Sequence 201618, Application US/10257017B
; Publication No. US20040241651A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 201618
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0049588
US-10-257-017B-201618

Query Match      34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCATCCACCT 10
      |||||
Db      3 CCATCCACCT 12

RESULT 84
US-09-504-231A-1393
; Sequence 1393, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: Ipi 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1393
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1393

Query Match      34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      9 CTGCTGTGTG 18
      |:|:|:|:|
Db      4 CUGCUGUGUG 13

RESULT 85
US-09-274-553D-1393
```

```
; Sequence 1393, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATED TO HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: Pti 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1393
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1393

Query Match      34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY  9 CTGCTGTGTG 18
Db  4 CUCGUGUG 13

RESULT 86
US-10-024-944-6
; Sequence 6, Application US/10024944
; Publication No. US20020123060A1
; GENERAL INFORMATION:
; APPLICANT: EXACT Science Corporation
; APPLICANT: Boles, T. Christian
; APPLICANT: Weir, Lawrence
; APPLICANT: Stone, Benjamin
; TITLE OF INVENTION: Detection of No. US20020123060A1-Viral Organisms With SRP RNA
; FILE REFERENCE: EXT-073
; CURRENT APPLICATION NUMBER: US/10/024,944
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 60/090,063
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 08/971,845
; PRIOR FILING DATE: 1997-08-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a short probe derived from the complementary sequence of E. coli 4.5S RNA region 44-65
US-10-024-944-6

Query Match      34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  17 TGACCTGGTA 26
Db  5 TGACCTGGTA 14

RESULT 87
US-10-721-157-6
; Sequence 6, Application US/10721157
; Publication No. US20040086932A1
; GENERAL INFORMATION:
; APPLICANT: Boles, T. Christian
; APPLICANT: Weir, Lawrence
; APPLICANT: Stone, Benjamin B
; TITLE OF INVENTION: Detection of Non-Viral Organisms with SRP RNA
; FILE REFERENCE: EXT-072C2
; CURRENT APPLICATION NUMBER: US/10/721,157
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US 60/090,063
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 10/024,944
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/336,609
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a short probe derived from the complementary sequence of E. coli 4.5S RNA region 44-65
US-10-721-157-6

Query Match      34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  17 TGACCTGGTA 26
Db  5 TGACCTGGTA 14

RESULT 88
US-10-984-919-1309/c
; Sequence 1309, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1309
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1309

Query Match      34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 ATCCACCTGC 12
```

Db 10 ATCCACCTGC 1

RESULT 89

US-09-510-378-25
; Sequence 25, Application US/09510378
; Publication No. US20030165823A1
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles G.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P. A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
; Detecting Cystic Fibrosis
; NUMBER OF SEQUENCES: 250
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/510,378
; FILING DATE: 22-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/544,381
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/510,521
; FILING DATE: 02-AUG-1995
; APPLICATION NUMBER: PCT/US94/12305
; FILING DATE: 26-OCT-1994
; APPLICATION NUMBER: US 08/284,064
; FILING DATE: 02-AUG-1994
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-510-378-25

Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGCCCT 13

RESULT 90

US-09-798-260-83
; Sequence 83, Application US/09798260
; Publication No. US20030165830A1
; GENERAL INFORMATION:
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Miyada, Charles G.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Chee, Mark
; APPLICANT: Fodor, Stephen P. A.
; APPLICANT: Huang, Xiaohua C.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: BIOTRANSFORMATION GENES
; FILE REFERENCE: 018547-015720US
; CURRENT APPLICATION NUMBER: US/09/798,260
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 08/778,794
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: US 08/544,381
; PRIOR FILING DATE: 1995-10-10
; PRIOR APPLICATION NUMBER: US 08/510,521
; PRIOR FILING DATE: 1995-08-02
; PRIOR APPLICATION NUMBER: WO PCT/US94/12305
; PRIOR FILING DATE: 1994-10-26
; PRIOR APPLICATION NUMBER: US 08/284,064
; PRIOR FILING DATE: 1994-08-02
; PRIOR APPLICATION NUMBER: US 08/143,312
; PRIOR FILING DATE: 1993-10-26
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe
US-09-798-260-83

Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGCCCT 13

RESULT 91

US-10-043-875-397/c
; Sequence 397, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; Transcriptionase Gene
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 018700005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1


```
; SEQ ID NO 397
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-397

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CATCCACTGCTG 14
    ||||| |||
Db  13 CATCCACGTACTG 1

RESULT 92
US-10-043-875-422/c
; Sequence 422, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043.875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 422
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-422

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CATCCACTGCTG 14
    ||||| |||
Db  13 CATCCACGTACTG 1

RESULT 93
US-10-311-645A-118
; Sequence 118, Application US/10311645A
; Publication No. US20040214302A1
; GENERAL INFORMATION:
; APPLICANT: Anthony, James
; APPLICANT: Lotincz, Attila
; APPLICANT: Williams, Inna
; APPLICANT: Troy, John
; APPLICANT: Tang, Yanglin
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS BY TYPE-SPECIFIC HYBRID CAPTURE METHOD
; FILE REFERENCE: 2629-4017US1
; CURRENT APPLICATION NUMBER: US/10/311.645A
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19353
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 09/594,839
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 13
; TYPE: DNA
```

```
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid probe: PZ-1
US-10-311-645A-118

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  5 CCACCTGCTGCTG 17
    ||||| |||
Db  1 CCACCTCCTGCGT 13

RESULT 94
US-10-257-017B-145363/c
; Sequence 145363, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145363
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145363

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 CCATCCACCTGCT 13
    ||||| |||
Db  13 CCATCCGCTACT 1

RESULT 95
US-10-257-017B-145364
; Sequence 145364, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 145364
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0036590
US-10-257-017B-145364

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 CCATCCACCTGCT 13
    ||||| |||
Db  13 CCATCCGCTACT 1
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Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCT 13
 ||||| ||| ||
 Db 1 CCATCCGCTACT 13

RESULT 96

US-09-771-933-166
 ; Sequence 166, Application US/09771933
 ; Publication No. US20030023387A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gill-Garrison, Rosalynn D
 ; APPLICANT: Martin, Christopher J
 ; APPLICANT: Sanchez-Felix, Manuel V
 ; TITLE OF INVENTION: Computer-assisted Means for Assessing Lifestyle Risk
 ; TITLE OF INVENTION: Factors
 ; FILE REFERENCE: 620-130
 ; CURRENT APPLICATION NUMBER: US/09/771,933
 ; CURRENT FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 205
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 166
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Probe
 US-09-771-933-166

Query Match 33.8%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 48;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTG 16
 ||||| ||| ||
 Db 2 TCCACCTCTGGG 14

RESULT 97

US-10-146-058-15
 ; Sequence 15, Application US/10146058
 ; Publication No. US2003004099A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlingensiepen, Georg-Ferdinand
 ; APPLICANT: Brysch, Wolfgang
 ; APPLICANT: Schlingensiepen, Karl-Hermann
 ; APPLICANT: Schlingensiepen, Reimar
 ; APPLICANT: Bogdahn, Ulrich
 ; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
 ; TITLE OF INVENTION: Immuno-suppressive effect of transforming-growth-factor beta
 ; NUMBER OF SEQUENCES: 137
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jacobson, Price, Holman & Stern
 ; STREET: 400 Seventh St. N.W.
 ; CITY: Washington D.C
 ; COUNTRY: U.S.A.
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/146.058
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/535,249
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 93 107 089.0
 ; FILING DATE: 30-APR-1993

;; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 93 107 849.7
 ; FILING DATE: 13-MAY-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Player, William E.
 ; REGISTRATION NUMBER: 31,409
 ; REFERENCE/DOCKET NUMBER: 10577/P58418
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)638-6666
 ; TELEFAX: (202) 393-5350
 ; TELEX: RCA 248593 IDEA UR
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; ANTI-SENSE: YES
 US-10-146-058-15

Query Match 33.8%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 48;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
 ||||| ||| ||
 Db 1 TGCTGTGTGACT 13

RESULT 98

US-10-043-875-394/c
 ; Sequence 394, Application US/10043875
 ; Publication No. US20030054339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stuyver, Koenraad
 ; APPLICANT: De Smet, Koenraad
 ; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
 ; TITLE OF INVENTION: Transcriptase Gene
 ; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
 ; CURRENT APPLICATION NUMBER: US/10/043,875
 ; CURRENT FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: 60/286,102
 ; PRIOR FILING DATE: 2001-04-24
 ; PRIOR APPLICATION NUMBER: EP 01870085.6
 ; PRIOR FILING DATE: 2001-04-20
 ; PRIOR APPLICATION NUMBER: EP 01870005.4
 ; PRIOR FILING DATE: 2001-01-11
 ; NUMBER OF SEQ ID NOS: 884
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 394
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Human immunodeficiency virus
 US-10-043-875-394

Query Match 33.8%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 48;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
 ||||| ||| ||
 Db 14 CATCCACGTACTG 2

RESULT 99

US-10-043-875-398/c
 ; Sequence 398, Application US/10043875
 ; Publication No. US20030054339A1
 ; GENERAL INFORMATION:
 ; APPLICANT: De Smet, Koenraad
 ; APPLICANT: Stuyver, Lieven
 ; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse

; TITLE OF INVENTION: Transcriptase Gene
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 398
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-398

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
| | | | | | | | | |
Db 14 CATCCACATAGT 2

RESULT 100
US-10-043-875-412/c
; Sequence 412, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-412

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
| | | | | | | | | |
Db 14 CATCCACATAGT 2

RESULT 101
US-10-043-875-414/c
; Sequence 414, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875

; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 414
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-414

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
| | | | | | | | | |
Db 14 CATCCACGTAAGT 2

RESULT 102
US-10-043-875-417/c
; Sequence 417, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 417
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-417

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
| | | | | | | | | |
Db 13 CATCCACATAGT 1

RESULT 103
US-10-043-875-421/c
; Sequence 421, Application US/10043875
; Publication No. US20030054339A1
; GENERAL INFORMATION:
; APPLICANT: De Smet, Koenraad
; APPLICANT: Stuyver, Lieven
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)
; CURRENT APPLICATION NUMBER: US/10/043,875
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/286,102
; PRIOR FILING DATE: 2001-04-24

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; PRIOR APPLICATION NUMBER: EP 01870085.6
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: EP 01870005.4
; PRIOR FILING DATE: 2001-01-11
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 421
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-421

Query Match          33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CATCCACCTGCTG 14
Db      13 CATCCAGTACTG 1
|||||

RESULT 104
US-10-984-919-367
; Sequence 367, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 367
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-367

Query Match          33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      11 GCTGTGTGACCTG 23
Db      1 GCTGTGTACCCAG 13
|||||

RESULT 105
US-10-984-919-1153
; Sequence 1153, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
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; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1153
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1153

Query Match          33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 TGCTGTGTGACCT 22
Db      1 TGCTGTGTGTACT 13
|||||

RESULT 106
US-10-984-919-1469/c
; Sequence 1469, Application US/10984919
; Publication No. US20050130927A1
; GENERAL INFORMATION:
; APPLICANT: Schlingensiepen, Karl-Hermann
; APPLICANT: Brysch, Wolfgang
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
; FILE REFERENCE: 10496/P63763USO
; CURRENT APPLICATION NUMBER: US/10/984,919
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US/09/341,700
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: PCT/EP98/00497
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: EP 97 101 531.8
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 1764
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1469
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: antisense oligonucleotide
US-10-984-919-1469

Query Match          33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.8%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 CTGTGTGACCTGG 24
Db      13 CTGTCTGACATGG 1
|||||

Search completed: May 15, 2006, 15:06:05
Job time : 1 secs
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 15:24:11 ; Search time 0.001 Seconds
(without alignments)
136.184 Million cell updates/sec

Title: US-09-904-968A-3-COPY
Perfect score: 29
Sequence: 1 ccattccactgtgtgtgacctgtaata 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5
Searched: 124 seqs, 2348 residues

Total number of hits satisfying chosen parameters: 248

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 124 summaries

Database : pubnewdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17.6	60.7	25	1	US-11-121-849-418301
2	16.8	57.9	20	1	US-10-310-914A-1382191
3	16.8	57.9	21	1	US-10-310-914A-289945
4	16.2	55.9	23	1	US-10-310-914A-739052
5	15.6	55.2	22	1	US-10-310-914A-738911
6	15.8	54.5	21	1	US-10-310-914A-1382178
7	15.4	53.1	19	1	US-11-101-244-1259291
8	15.4	53.1	19	1	US-11-083-784-1259291
9	15.1	51.7	19	1	US-10-310-914A-943748
10	15.1	51.7	20	1	US-10-310-914A-1142003
11	14.8	51.0	18	1	US-10-310-914A-1382190
12	14.8	51.0	19	1	US-11-101-244-561054
13	14.8	51.0	19	1	US-11-101-244-681930
14	14.8	51.0	19	1	US-11-101-244-807207
15	14.8	51.0	19	1	US-11-101-244-935230
16	14.8	51.0	19	1	US-11-101-244-1066344
17	14.8	51.0	19	1	US-11-101-244-1309698
18	14.8	51.0	19	1	US-11-083-784-561054
19	14.8	51.0	19	1	US-11-083-784-681930
20	14.8	51.0	19	1	US-11-083-784-807207
21	14.8	51.0	19	1	US-11-083-784-935230
22	14.8	51.0	19	1	US-11-083-784-1066344
23	14.8	51.0	19	1	US-11-083-784-1309698
24	14.8	51.0	21	1	US-10-310-914A-1382262
25	14.4	49.7	18	1	US-10-310-914A-753677
26	14.4	49.7	18	1	US-10-310-914A-776270
27	14.4	49.7	18	1	US-10-310-914A-846082
28	14.4	49.7	19	1	US-11-101-244-60143
29	14.4	49.7	19	1	US-11-101-244-732143
30	14.4	49.7	19	1	US-11-101-244-732234
31	14.4	49.7	19	1	US-11-101-244-1350412
32	14.4	49.7	19	1	US-11-101-244-1350424
33	14.4	49.7	19	1	US-11-083-784-60143

Sequence 732143,	19	1	US-11-083-784-732143	49.7	14.4	34
Sequence 732234,	19	1	US-11-083-784-732234	49.7	14.4	35
Sequence 1350412,	19	1	US-11-083-784-1350412	49.7	14.4	36
Sequence 1350424,	19	1	US-11-083-784-1350424	49.7	14.4	37
Sequence 1087566,	20	1	US-10-310-914A-1087566	49.7	14.4	38
Sequence 169031,	19	1	US-11-101-244-169031	49.0	14.2	39
Sequence 169132,	19	1	US-11-101-244-169132	49.0	14.2	40
Sequence 169222,	19	1	US-11-101-244-169222	49.0	14.2	41
Sequence 169323,	19	1	US-11-101-244-169323	49.0	14.2	42
Sequence 179633,	19	1	US-11-101-244-179633	49.0	14.2	43
Sequence 385863,	19	1	US-11-101-244-385863	49.0	14.2	44
Sequence 599457,	19	1	US-11-101-244-599457	49.0	14.2	45
Sequence 491187,	19	1	US-11-101-244-491187	49.0	14.2	46
Sequence 762299,	19	1	US-11-101-244-762299	49.0	14.2	47
Sequence 762404,	19	1	US-11-101-244-762404	49.0	14.2	48
Sequence 767248,	19	1	US-11-101-244-767248	49.0	14.2	49
Sequence 767320,	19	1	US-11-101-244-767320	49.0	14.2	50
Sequence 1316239,	19	1	US-11-101-244-1316239	49.0	14.2	51
Sequence 1338912,	19	1	US-11-101-244-1338912	49.0	14.2	52
Sequence 1559238,	19	1	US-11-101-244-1559238	49.0	14.2	53
Sequence 169031,	19	1	US-11-083-784-169031	49.0	14.2	54
Sequence 169132,	19	1	US-11-083-784-169132	49.0	14.2	55
Sequence 169222,	19	1	US-11-083-784-169222	49.0	14.2	56
Sequence 169323,	19	1	US-11-083-784-169323	49.0	14.2	57
Sequence 179633,	19	1	US-11-083-784-179633	49.0	14.2	58
Sequence 385863,	19	1	US-11-083-784-385863	49.0	14.2	59
Sequence 491187,	19	1	US-11-083-784-491187	49.0	14.2	60
Sequence 599457,	19	1	US-11-083-784-599457	49.0	14.2	61
Sequence 762299,	19	1	US-11-083-784-762299	49.0	14.2	62
Sequence 762404,	19	1	US-11-083-784-762404	49.0	14.2	63
Sequence 767248,	19	1	US-11-083-784-767248	49.0	14.2	64
Sequence 767320,	19	1	US-11-083-784-767320	49.0	14.2	65
Sequence 1316239,	19	1	US-11-083-784-1316239	49.0	14.2	66
Sequence 1338912,	19	1	US-11-083-784-1338912	49.0	14.2	67
Sequence 1559238,	19	1	US-11-083-784-1559238	49.0	14.2	68
Sequence 169031,	19	1	US-10-898-311-111	47.6	13.8	69
Sequence 169132,	19	1	US-10-898-311-111	47.6	13.8	70
Sequence 169222,	19	1	US-10-310-914A-161892	47.6	13.8	71
Sequence 169323,	19	1	US-10-310-914A-161893	47.6	13.8	72
Sequence 179633,	19	1	US-10-310-914A-1323233	47.6	13.8	73
Sequence 282638,	19	1	US-11-101-244-282638	47.6	13.8	74
Sequence 403263,	19	1	US-11-101-244-403263	47.6	13.8	75
Sequence 403331,	19	1	US-11-101-244-403331	47.6	13.8	76
Sequence 672456,	19	1	US-11-101-244-672456	47.6	13.8	77
Sequence 677906,	19	1	US-11-101-244-677906	47.6	13.8	78
Sequence 847054,	19	1	US-11-101-244-847054	47.6	13.8	79
Sequence 1035429,	19	1	US-11-101-244-1035429	47.6	13.8	80
Sequence 1436644,	19	1	US-11-101-244-1436644	47.6	13.8	81
Sequence 1467224,	19	1	US-11-101-244-1467224	47.6	13.8	82
Sequence 1568291,	19	1	US-11-101-244-1568291	47.6	13.8	83
Sequence 1568369,	19	1	US-11-101-244-1568369	47.6	13.8	84
Sequence 1568629,	19	1	US-11-083-784-1568629	47.6	13.8	85
Sequence 1568639,	19	1	US-11-083-784-1568639	47.6	13.8	86
Sequence 1568643,	19	1	US-11-083-784-1568643	47.6	13.8	87
Sequence 1436706,	19	1	US-11-083-784-1436706	47.6	13.8	88
Sequence 403263,	19	1	US-11-083-784-403263	47.6	13.8	89
Sequence 403331,	19	1	US-11-083-784-403331	47.6	13.8	90
Sequence 672456,	19	1	US-11-083-784-672456	47.6	13.8	91
Sequence 677906,	19	1	US-11-083-784-677906	47.6	13.8	92
Sequence 847054,	19	1	US-11-083-784-847054	47.6	13.8	93
Sequence 1035429,	19	1	US-11-083-784-1035429	47.6	13.8	94
Sequence 1436644,	19	1	US-11-083-784-1436644	47.6	13.8	95
Sequence 1467224,	19	1	US-11-083-784-1467224	47.6	13.8	96
Sequence 1568291,	19	1	US-11-083-784-1568291	47.6	13.8	97
Sequence 1568369,	19	1	US-11-083-784-1568369	47.6	13.8	98
Sequence 1568629,	19	1	US-11-083-784-1568629	47.6	13.8	99
Sequence 1568639,	19	1	US-10-310-914A-1317194	46.2	13.4	100
Sequence 1317194,	18	1	US-10-310-914A-1317194	46.2	13.4	101
Sequence 472976,	19	1	US-10-310-914A-472976	46.2	13.4	102
Sequence 549557,	19	1	US-10-310-914A-549557	46.2	13.4	103
Sequence 821390,	19	1	US-11-101-244-821390	46.2	13.4	104
Sequence 859101,	19	1	US-11-101-244-859101	46.2	13.4	105
Sequence 1260137,	19	1	US-11-101-244-1260137	46.2	13.4	106
Sequence 1260202,	19	1	US-11-101-244-1260202	46.2	13.4	107
Sequence 1318311,	19	1	US-11-101-244-1318311	46.2	13.4	108

Published Applications
NA New


```
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 738911
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-738911

Query Match          55.2%; Score 16; DB 1; Length 22;
Best Local Similarity 68.8%; Pred. No. 21;
Matches 11; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACCT 22
Db 5 ACCGCGUGUGACCU 20

RESULT 6
US-10-310-914A-1382178
; Sequence 1382178, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382178
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382178

Query Match          54.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 63.2%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTG 23
Db 3 CCCCUGUGUGGCCUG 21

RESULT 7
US-11-101-244-1259291/c
; Sequence 1259291, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
```

```
; SEQ ID NO 1259291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1259291

Query Match          53.1%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18
Db 18 CATCCACCTGCTGTGTG 2

RESULT 8
US-11-083-784-1259291/c
; Sequence 1259291, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1259291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1259291

Query Match          53.1%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTG 18
Db 18 CATCCACCTGCTGTGTG 2

RESULT 9
US-10-310-914A-943748
; Sequence 943748, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 943748
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-943748
```

```

Query Match          51.7%; Score 15; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGG 24
Db 1 UGCUGUGAGCCUGG 15

RESULT 10
US-10-310-914A-1142003
; Sequence 1142003, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1142003
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1142003

Query Match          51.7%; Score 15; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCTGG 24
Db 1 UGCUGUGAGCCUGG 15

RESULT 11
US-10-310-914A-1382190
; Sequence 1382190, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382190
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382190

Query Match          51.0%; Score 14.8; DB 1; Length 18;
Best Local Similarity 61.1%; Pred. No. 34;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCT 22
Db 1 CCCCUGUGAGCCUGG 18

RESULT 12
US-11-101-244-561054
; Sequence 561054, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

```

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; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 561054
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-561054

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGGA 19
Db 2 CAUCUACCCGUGUGUGA 19

RESULT 13
US-11-101-244-681930
; Sequence 681930, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681930
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-681930

Query Match          51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGACCTGGTA 26
Db 2 CUCCUAGUGAGCCUGGUA 19

RESULT 14
US-11-101-244-807207
; Sequence 807207, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

```



```
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 807207
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-807207
```

```
Query Match 51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGGTA 26
   |||: ||| |||: |||
Db 2 CUGCUAUGGCGCUGGUA 19
```

```
RESULT 15
US-11-101-244-935230
; Sequence 935230, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 935230
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-935230
```

```
Query Match 51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGTA 19
   ||| |||: |||: |||
Db 2 CCUCUACCGUGUGUGA 19
```

```
RESULT 16
US-11-101-244-1066344
; Sequence 1066344, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1066344
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1066344
```

```
Query Match 51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGGTA 26
   |||: ||| |||: |||
Db 2 CUGCUGUGAACUGGUA 19
```

```
RESULT 17
US-11-101-244-1309698
; Sequence 1309698, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1309698
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1309698
```

```
Query Match 51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGGTA 26
   |||: ||| |||: |||
Db 2 CUGCUGUGAGCUGGUA 19
```

```
RESULT 18
US-11-083-784-561054
; Sequence 561054, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```



```

; Publication No. US20050245475A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorovta, Anastasiya
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US
; CURRENT FILING DATE: 2005-03-
; PRIOR APPLICATION NUMBER: US/1
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/5
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/4
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1066344
;
; LENGTH: 19
;
; TYPE: RNA
;
; ORGANISM: Homo sapiens
US-11-083-784-1066344

```

Query Match 51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. NO. 32;
Matches 10; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGGTA 26
|:|:|:|:|:|:|:|:
Db 2 CUGCUGUCUGAACUGGUA 19

RESULT 23

```

US-11-083-784-1309698
/ Sequence 1309698, Application US/11083784
/ Publication NO. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scarsgill, Stephen
/ TITLE OF INVENTION: Functional and Hyper
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ CURRENT FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1309698
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1309698

```

Query Match 51.0%; Score 14.8; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 32;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTACCTGGTA 26
| : | : | : | : | : | :
Db 2 CUGCUGCGUGAGCUGGUA 19

RESULT 24

```

US-10-310-914A-1382262
; Sequence 1382262, Application US/10310914A
; Publication NO. US2006000332A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuizat
; TITLE OF INVENTION: Bioinformatically detected
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1382262
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382262

```

Query Match	51.0%	Score 14.8;	DB 1;	Length 21;
Best Local Similarity	61.1%	Pred. No. 29;		
Matches 11; Conservative	5;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 5 CCACCTGCTGTGTGACCT 22
|||:|:|:|:|:|:
Db 4 CCCCCUGUGUGGGCCU 21

RESULT 25

```

US-10-310-914A-753677
; Sequence 753677, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kvuzat
; TITLE OF INVENTION: Bioinformatically detected
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 753677
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-753677

```

Query Match	49.7%	Score 14.4'	DB 1	Length 18;
Best Local Similarity	75.0%	Pred. No. 37;		
Matches 12: Conservative	3;	Mismatches	1;	Indels
			0;	Gaps
			0;	

Qy 1 CCATCCACCTGCTGTG 16
||| |||||:|:|
Db 3 CCAGCCACCUCUG 18

RESULT 26

```

; RES: 28
; US-10-310-914A-776270
; Sequence 776270, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzaat
; TITLE OF INVENTION: Bioinformatically det
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 776270

```

```

; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-776270

Query Match          49.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 68.8%; Pred. No. 37;
Matches 11; Conservative 4; Mismatches 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTG 16
Db 3 CCAUCAACCGUGUG 18

RESULT 27
US-10-310-914A-846082
; Sequence 846082, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 846082
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-846082

Query Match          49.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTG 16
Db 3 CCAGCCACCGUGUG 18

RESULT 28
US-11-101-244-60143
; Sequence 60143, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 60143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-60143

Query Match          49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

;

```

```

Qy 7 ACCTGCTGTGTGACCT 22
Db 2 ACUUCUGUGUGACCU 17

RESULT 29
US-11-101-244-732143
; Sequence 732143, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 732143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-732143

Query Match          49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTG 23
Db 1 CCUACUGUGUGACCU 16

RESULT 30
US-11-101-244-732234
; Sequence 732234, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 732234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-732234

Query Match          49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

```

QY 8 CCTGCTGTGTGACCTG 23
||:|||||:|:|:|:
Db 1 CCUACUGUGUACCUG 16

RESULT 31
US-11-101-244-1350412
; Sequence 1350412, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350412
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1350412

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGT 17
||:|||||:|:|:|:
Db 4 CAUCCACCGUGUACCU 19

RESULT 32
US-11-101-244-1350424
; Sequence 1350424, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1350424

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGT 17

Db 2 CAUCCACCGUGUACCU 17
||:|||||:|:|:|:

RESULT 33
US-11-083-784-60143
; Sequence 60143, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 60143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-60143

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCTGCTGTGTGACCT 22
||:|||||:|:|:|:
Db 2 ACUUGCUGUGUACCU 17

RESULT 34
US-11-083-784-732143
; Sequence 732143, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 732143
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-732143

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;

Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CCTGCTGTGTGACCTG 23
||:|:|:|:|:|:
Db 1 CCUACUGUGAGCCG 16

RESULT 35
US-11-083-784-732234
; Sequence 732234, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 732234
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-732234

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTG 23
||:|:|:|:|:|:
Db 1 CCUACUGUGAGCCG 16

RESULT 36
US-11-083-784-1350412
; Sequence 1350412, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350412
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1350412

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CATCCACCTGCTGTGT 17
||:|:|:|:|:|:
Db 4 CAUCCACCUGUGUAU 19

RESULT 37
US-11-083-784-1350424
; Sequence 1350424, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1350424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1350424

Query Match 49.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 35;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGT 17
||:|:|:|:|:|:
Db 2 CAUCCACCUGUGUAU 17

RESULT 38
US-10-310-914A-1087566
; Sequence 1087566, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087566
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087566

Query Match 49.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTGTGTA 27

```
Db          3  CUGUGAGACCUGGUGA 18
|:|:|:|:|:|:|:|:|:|:|
RESULT 39
US-11-101-244-169031
; Sequence 169031, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169031
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-169031
Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| |||||:|:|:|:|:|

Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 40
US-11-101-244-169132
; Sequence 169132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-169132
Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| |||||:|:|:|:|:|

Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 41
US-11-101-244-169222
; Sequence 169222, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169222
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-169222
Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| |||||:|:|:|:|:|

Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 42
US-11-101-244-169323
; Sequence 169323, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169323
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-169323
Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| |||||:|:|:|:|:|

Db 1 CCACCCACCUGCAGAGUGA 19
```

```

RESULT 45
US-11-101-244-491187
; Sequence 491187, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491187
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-491187
Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTGA 19
    ||| ||| :||:|:|
Db 1 CCACCCUCAUGCUGUGUGA 19

RESULT 46
US-11-101-244-599457
; Sequence 599457, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 599457
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-599457
Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACTGTGTA 26
Db 1 CCUGGUGGUGACCGUGUA 19

```



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RESULT 47
US-11-101-244-762299
; Sequence 762299, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 762299
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-762299

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTGA 19
      |||: ||: ||: ||: ||: ||
Db      1 CCAUUAACUUGUGUGUGA 19

RESULT 48
US-11-101-244-762404
; Sequence 762404, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 762404
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-762404

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTGA 19
      |||: ||: ||: ||: ||: ||
Db      1 CCAUUAACUUGUGUGUGA 19

RESULT 49
US-11-101-244-762404
; Sequence 762404, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 762404
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-762404

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTGA 19
      |||: ||: ||: ||: ||: ||
Db      1 CCAUUAACUUGUGUGUGA 19

RESULT 50
US-11-101-244-767320
; Sequence 767320, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 767320
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-767320

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      8 CCTGCTGTGTGACCTGGTA 26
      |||: ||: ||: ||: ||: ||
Db      1 CCUGGUGUGGCCUGGAA 19

RESULT 51
US-11-101-244-1316239
```

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; Sequence 1316239, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1316239
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1316239

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      8 CCTGCTGTGTGACCTGGTA 26
      |||:|:|:|:|:|:|:|
Db      1 CCUGCUGGUGACUGGAA 19

RESULT 52
US-11-101-244-1338912
; Sequence 1338912, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1338912
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1338912

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTGA 19
      |||:|:|:|:|:|:|:|
Db      1 CCAUCCACCUAGACUGA 19

RESULT 53
US-11-101-244-1559238
; Sequence 1559238, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1559238
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1559238

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTGA 19
      |||:|:|:|:|:|:|:|
Db      1 CCACCCACCUAGACUGA 19

RESULT 54
US-11-083-784-169031
; Sequence 169031, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169031
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-169031

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CCATCCACCTGCTGTGTGA 19
      |||:|:|:|:|:|:|:|
Db      1 CCACCCACCUAGACUGA 19

RESULT 55
US-11-083-784-169132
```

; Sequence 169132, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-169132

Query Match 49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| ||||| ||| |||
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 56
US-11-083-784-169222
; Sequence 169222, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169222
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-169222

Query Match 49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| ||||| ||| |||
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 57
US-11-083-784-169323
; Sequence 169323, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 169323
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-169323

Query Match 49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 37;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
||| ||||| ||| |||
Db 1 CCACCCACCUGCAGAGUGA 19

RESULT 58
US-11-083-784-179633
; Sequence 179633, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 179633
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-179633

Query Match 49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 52.8%; Pred. No. 37;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGTGACCTGGTA 26

```
Db      1  CCUACUGUGGCCUGGUA 19
||: |:|:|:| ||:|:|
Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCATCCACCTGCTGTGTA 19
||||| |:|:|:|
Db      1  CCAUGGACCCACCGUGUGA 19

RESULT 59
US-11-083-784-385863
; Sequence 385863, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 385863
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-385863

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCATCCACCTGCTGTGTA 19
||||| |:|:|:|
Db      1  CCAUGGACCCACCGUGUGA 19

RESULT 60
US-11-083-784-491187
; Sequence 491187, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 491187
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-491187

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCATCCACCTGCTGTGTA 19
||||| |:|:|:|
Db      1  CCAUGGACCCACCGUGUGA 19

Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCATCCACCTGCTGTGTA 19
||||| |:|:|:|
Db      1  CCACCCUACUGGUGUGUGA 19

Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1  CCATCCACCTGCTGTGTA 19
||||| |:|:|:|
Db      1  CCACCCUACUGGUGUGUGA 19

RESULT 61
US-11-083-784-599457
; Sequence 599457, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 599457
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-599457

Query Match      49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      8  CTTGCTGTGTGACCTGTA 26
||:|:| |:|:|:|
Db      1  CCUGGUGGUGACCGUGGUA 19

RESULT 62
US-11-083-784-762299
; Sequence 762299, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 762299
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-762299
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-767248

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
    |||: ||: |||: |||: |||
Db 1 CCAUUAACUGGUGUGA 19

RESULT 63
US-11-083-784-762404
; Sequence 762404, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 762404
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-762404

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
    |||: ||: |||: |||: |||
Db 1 CCAUUAACUGGUGUGA 19

RESULT 64
US-11-083-784-767248
; Sequence 767248, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 767248
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-767248

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGTA 19
    |||: ||: |||: |||: |||
Db 1 CCAUUAACUGGUGUGA 19

RESULT 65
US-11-083-784-767320
; Sequence 767320, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 767320
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-767320

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCGCTGTGTGACCTGGTA 26
    |||: ||: |||: |||: |||
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 66
US-11-083-784-1316239
; Sequence 1316239, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1316239
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1316239

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCGCTGTGTGACCTGGTA 26
    |||: ||: |||: |||: |||
Db 1 CCUGGUGUGGCCUGGAA 19
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-767248

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCGCTGTGTGACCTGGTA 26
    |||: ||: |||: |||: |||
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 65
US-11-083-784-767320
; Sequence 767320, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 767320
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-767320

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCGCTGTGTGACCTGGTA 26
    |||: ||: |||: |||: |||
Db 1 CCUGGUGUGGCCUGGAA 19

RESULT 66
US-11-083-784-1316239
; Sequence 1316239, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1316239
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1316239

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 37;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 8 CCGCTGTGTGACCTGGTA 26
    |||: ||: |||: |||: |||
Db 1 CCUGGUGUGGCCUGGAA 19
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 1316239
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1316239

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CCTGCTGTGTGACCTGTGTA 26
Db      1 CCUGCUGGUGACGUGAA 19

RESULT 67
US-11-083-784-1338912
; Sequence 1338912, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1338912
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1338912

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTGTA 19
Db      1 CCAUCCACGACGACUGUGA 19

RESULT 68
US-11-083-784-1559238
; Sequence 1559238, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2003-09-10

; SOFTWARE: Proprietary
; SEQ ID NO 1559238
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1559238

Query Match          49.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 52.6%; Pred. No. 37;
Matches 10; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      8 CCTGCTGTGTGACCTGTGTA 26
Db      1 CCUGCUGUGACUGUGUA 19

RESULT 69
US-10-898-311-111
; Sequence 111, Application US/10898311
; Publication No. US2005027608A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Guerdiolini, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vitamin D Receptor Gene
; FILE REFERENCE: 400/200 (MBH04-586)
; CURRENT APPLICATION NUMBER: US/10/898,311
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 10/757,803
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/306,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 111
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-898-311-111

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 40;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      5 CCACCTGCTGTGTGACC 21
Db      1 CCACCUGCUGAGAGACC 17

RESULT 70
```



```
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 282638
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-282638

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17
Db 1 CCAUCCUGCUGUGUCU 17

RESULT 75
US-11-101-244-403263
; Sequence 403263, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-403263

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17
Db 1 CCAUCCUGCUGUGUCU 17

RESULT 76
US-11-101-244-403331
; Sequence 403331, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403331
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-403331

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17
Db 1 CCAUCCUGCUGUGUCU 17

RESULT 77
US-11-101-244-672456
; Sequence 672456, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 672456
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-672456

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGTTAAAT 29
Db 1 UGUGUGAGCUGGGAAAU 17

RESULT 78
US-11-101-244-677906
; Sequence 677906, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```



```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 677906
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-677906
```

```
Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 52.9%; Pred. No. 40;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 13 TGTGTGACCTGCTGAAT 29
Db 1 UGUGUGUCCUUGUAAU 17
```

```
RESULT 79
US-11-101-244-847054/c
; Sequence 847054, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 847054
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-847054
```

```
Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 CATCCACCTGCTGTGTG 18
Db 18 CATCTCTCTCTGTGTG 2
```

```
RESULT 80
US-11-101-244-1035429/c
; Sequence 1035429, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1035429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1035429
```

```
Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 ATCCACCTGCTGTGTGA 19
Db 17 ATCCACCTGCAATGTGA 1
```

```
RESULT 81
US-11-101-244-1436644/c
; Sequence 1436644, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1436644
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1436644
```

```
Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 CATCCACCTGCTGTGTG 18
Db 18 CATCCACCTGCTCTTGT 2
```

```
RESULT 82
US-11-101-244-1436706/c
; Sequence 1436706, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1436706
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1436706

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  CATCCACCTGCTGTG 18
Db  17 CATCCACCTGCTCTTG 1

RESULT 83
US-11-101-244-1467224
; Sequence 1467224, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1467224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1467224

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy  7  ACCTGCTGTGTGACCTG 23
Db  3  ACCUGUGUGUCACUUG 19

RESULT 84
US-11-101-244-1568291
; Sequence 1568291, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1568291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1568291

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 40;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy  1  CCATCCACCTGCTGTGT 17
Db  3  CCAGCCACCUCUGUGU 19

RESULT 85
US-11-101-244-1568369
; Sequence 1568369, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1568369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1568369

Query Match      47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 40;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy  1  CCATCCACCTGCTGTGT 17
Db  1  CCAGCCACCUCUGUGU 17

RESULT 86
US-11-083-784-282638
; Sequence 282638, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 282638
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-282638

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGT 17
   |||:| | | | | | | | | | | | | | | | |
Db 1 CCAUCCUGCUGUGUCU 17

RESULT 87
US-11-083-784-403263
; Sequence 403263, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-403263

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGT 17
   |||:| | | | | | | | | | | | | | | | |
Db 1 CCAUCCUGCUGUGUCU 17

RESULT 88
US-11-083-784-403331
; Sequence 403331, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 403331
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-403331

Query Match          47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGCTGAAT 29
   :|:|:| | | | | | | | | | | | | | | |
Db 1 UGUGUGAGCUGGGAU 17

RESULT 90
US-11-083-784-677906
; Sequence 677906, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```


US-11-083-784-1436706/c
; Sequence 1436706, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1436706
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1436706

Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGTGG 18
Db 17 CATCCACCTGCTCTTTG 1

RESULT 95

US-11-083-784-1467224
; Sequence 1467224, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1467224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1467224

Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 40;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTGACCTG 23
Db 3 ACCGCGUGUCACUUG 19

RESULT 96

US-11-083-784-1568291
; Sequence 1568291, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1568291
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1568291

Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 40;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCTGTGT 17
Db 1 CCAGCCACCCUCCUGUGU 17

RESULT 97

US-11-083-784-1568369
; Sequence 1568369, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1568369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1568369

Query Match 47.6%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 40;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 CCATCCACCTGCTGT 17
    ||| |||||:|:|:|:
Db 3 CCAGCCACCCUGUGU 19
    ||| |||||:|:|:|:

RESULT 98
US-10-914A-606643/c
; Sequence 606643, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 606643
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-606643
```

```
Query Match 46.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 14 GTGTGACCTGGTAAA 28
    ||||| ||||| |||||
Db 15 GAGTGACCTGGTAAA 1
```

```
RESULT 99
US-10-310-914A-1317194
; Sequence 1317194, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1317194
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1317194
```

```
Query Match 46.2%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 47;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 CACCTGCTGTGTGAC 20
    |||||:|:|:|:
Db 1 CACCUGCUGGUGAC 15
```

```
RESULT 100
US-10-310-914A-472976
; Sequence 472976, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
```

```
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 472976
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-472976
```

```
Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 10 TGCTGTGTGACCTGG 24
    :||:|:|:|:|:|
Db 1 UGCUCUGAGACGUG 15
```

```
RESULT 101
US-10-310-914A-549957
; Sequence 549957, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 549957
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-549957
```

```
Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 10 TGCTGTGTGACCTGG 24
    :||:|:|:|:|:|
Db 4 UGCUCUGAGACGUG 18
```

```
RESULT 102
US-11-101-244-821390
; Sequence 821390, Application US/1101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 821390
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
```

US-11-101-244-821390

Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 15 TGTGACCTGGTAAAT 29
|:||||:|:|:|:
Db 3 UGUGACCUUGUAAAU 17

RESULT 103

US-11-101-244-859101
; Sequence 859101, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 859101
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-859101

Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTGCTGTGTGACCTG 23
|:||||:|:|:|:
Db 2 CUGCUGUCUGACCUG 16

RESULT 104

US-11-101-244-1260137
; Sequence 1260137, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260137
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1260137

Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 14 GTGTGACCTGGTAAA 28
|:||||:|:|:|:
Db 2 GAGUGACCUUGUAAA 16

RESULT 105

US-11-101-244-1260202
; Sequence 1260202, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1260202

Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 14 GTGTGACCTGGTAAA 28
|:||||:|:|:|:
Db 3 GAGUGACCUUGUAAA 17

RESULT 106

US-11-101-244-1318311/c
; Sequence 1318311, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1318311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1318311

```
Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 TCCACCTGCTGTGG 18
Db      18 TCCACCTGCTGTGG 4

RESULT 107
US-11-101-244-1544345/c
; Sequence 1544345, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1544345
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1544345

Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CCTGCTGTGTGACCT 22
Db      16 CCTGCTGTGTAACT 2

RESULT 108
US-11-083-784-821390
; Sequence 821390, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 821390
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-821390

Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CCTGCTGTGTGACCT 22
Db      16 CCTGCTGTGTAACT 2

RESULT 109
US-11-083-784-859101
; Sequence 859101, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 859101
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-859101

Query Match          46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTGCTGTGTGACCTG 23
Db      2 CUGCUGUCUGACCTG 16

RESULT 110
US-11-083-784-1260137
; Sequence 1260137, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260137
; LENGTH: 19
```



```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1260137

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGGTAAA 28
   |:|:|:|:|:|:|:|:|:|
Db 2 GAGUGACCGUGUAAA 16

RESULT 111
US-11-083-784-1260202
; Sequence 1260202, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1260202
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1260202

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 44;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGGTAAA 28
   |:|:|:|:|:|:|:|:|:|
Db 3 GAGUGACCGUGUAAA 17

RESULT 112
US-11-083-784-1318311/c
; Sequence 1318311, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 1318311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1318311

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTG 18
   |:|:|:|:|:|:|:|:|:|
Db 18 TCCACCTGCTGTGTG 4

RESULT 113
US-11-083-784-1544345/c
; Sequence 1544345, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1544345
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1544345

Query Match      46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGTGACCT 22
   |:|:|:|:|:|:|:|:|:|
Db 16 CCTGCTGTGTACCT 2

RESULT 114
US-10-310-914A-623917
; Sequence 623917, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 623917
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-623917
```

```

Query Match      45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CACCTGCTGTGTGACCTG 23
   |||:::|::|::|::|
Db 1 CAGCUGCUCUGGUGCCUG 18

RESULT 115
US-10-310-914A-784062
; Sequence 784062, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 784062
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-784062

Query Match      45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTGTGAC 20
   |::|::|::|::|::|
Db 1 AUGAACUUGCUGUGUGAC 18

RESULT 116
US-10-310-914A-1081549
; Sequence 1081549, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1081549
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1081549

Query Match      45.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTGTGAC 20
   |::|::|::|::|::|
Db 1 AUGAACUUGCUGUGUGAC 18

RESULT 117
US-10-310-914A-608562/c
; Sequence 608562, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 183276
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-183276

```

```

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 608562
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-608562

Query Match      44.8%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTGCTGTGTG 18
   |||::|::|::|::|
Db 17 CACCTGCTGTGTG 5

RESULT 118
US-10-310-914A-730768
; Sequence 730768, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730768
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-730768

Query Match      44.8%; Score 13; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 51;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTGG 24
   |::|::|::|::|::|
Db 3 CUGUGUGACCCUG 15

RESULT 119
US-10-310-914A-183276/c
; Sequence 183276, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 183276
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-183276

```

```
Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACTGCTGTGT 17
Db 16 CCTCCACTGCTGGT 1
      |||||
      |||||
      |||||
      |||||
      |||||

RESULT 120
US-10-310-914A-481748/c
; Sequence 481748, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 481748
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-481748

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGG 24
Db 17 CTGCTGTGTGACCCAG 2
      |||||
      |||||
      |||||
      |||||
      |||||

RESULT 121
US-10-310-914A-954247/c
; Sequence 954247, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 954247
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-954247

Query Match      44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 53;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGG 24
Db 18 CAGCTGTGTGACCCGG 3
      |||||
      |||||
      |||||
      |||||
      |||||

RESULT 122
US-10-880-315-224
; Sequence 224, Application US/10880315
; Publication No. US2005028849A1
; GENERAL INFORMATION:
; APPLICANT: Hwang, Yuchi
```

```
; APPLICANT: Chen, Kuang-Den
; APPLICANT: Chang, Chingwei
; APPLICANT: Chen, Jui-Lin
; APPLICANT: Chen, Ding-Shinn
; APPLICANT: Chen, Pei-Jer
; APPLICANT: Lai, Ming-Yang
; TITLE OF INVENTION: RESPONSIVENESS TO THERAPY FOR LIVER
; FILE REFERENCE: 14720-004001
; CURRENT APPLICATION NUMBER: US/10/880,315
; CURRENT FILING DATE: 2004-06-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 224
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-880-315-224

Query Match      37.2%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTG 23
Db 1 TGGTGTGTGTCCTG 14
      |||||
      |||||
      |||||
      |||||
      |||||

RESULT 123
US-11-269-003-81/c
; Sequence 81, Application US/11269003
; Publication No. US20060051809A1
; GENERAL INFORMATION:
; APPLICANT: Nazarenko, Irina
; APPLICANT: Lorincz, Attila
; APPLICANT: Eder, Paul
; APPLICANT: Lowe, Brian
; APPLICANT: Mallonee, Richard
; APPLICANT: Thai, Ha
; TITLE OF INVENTION: DETECTION OF NUCLEIC ACIDS BY TARGET-SPECIFIC HYBRID CAPTURE
; FILE REFERENCE: 2629-4066
; CURRENT APPLICATION NUMBER: US/11/269,003
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: US 11/005,617
; PRIOR FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 10/971,251
; PRIOR FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: US 09/594,839
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 13
; TYPE: DNA
; ORGANISM: HPV
US-11-269-003-81

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGTGTGTGT 17
Db 13 CCACCTCTCTGCGT 1
      |||||
      |||||
      |||||
      |||||
      |||||

RESULT 124
US-11-176-026A-24/c
; Sequence 24, Application US/11176026A
; Publication No. US20060069074A1
```

Mon May 15 15:24:56 2006

```
; GENERAL INFORMATION:
; APPLICANT: Lemanske, Robert
; APPLICANT: Sorkness, Christine
; APPLICANT: Chinchilli, Vernon
; APPLICANT: Liu, Wenlei
; APPLICANT: Phillips, Brenda
; APPLICANT: Zeiger, Robert
; APPLICANT: Heldt, Gregory
; APPLICANT: Martinez, Fernando
; APPLICANT: Klimecki, Walter
; APPLICANT: Guilbert, Theresa
; APPLICANT: Morgan, Wayne
; APPLICANT: Szefer, Stanley
; APPLICANT: Larsen, Gary
; APPLICANT: Taussig, Lynn
; APPLICANT: Spahn, Joseph
; APPLICANT: Strunk, Robert
; APPLICANT: Bacharier, Leonard
; APPLICANT: Bloomberg, Gordon
; TITLE OF INVENTION: GENETIC PREDICTOR OF EFFICACY OF ANTI-ASTHMATIC AGENT FOR
; FILE OF INVENTION: IMPROVING PULMONARY FUNCTION
; FILE REFERENCE: 960296.00195
; CURRENT APPLICATION NUMBER: US/11/176,026A
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: US 60/585,872
; PRIOR FILING DATE: 2004-07-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA FAM probe sequence for -47 SNP.
US-11-176-026A-24

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4  TCCACCTGCTGTG 16
      ||| |||||
Db      14  TCCGCTGCTGAG 2

Search completed: May 15, 2006, 15:24:12
Job time : 1 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 15:03:38 ; Search time 0.001 Seconds
(without alignments)
322.538 Million cell updates/sec

Title: US-09-904-968A-3-COPY

Perfect score: 29

Sequence: 1 ccacccacctgtgtgtaactggtgtaaat 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 446 seqs, 5561 residues

Total number of hits satisfying chosen parameters: 892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 448 summaries

Database : ngsdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	29	100.0	29	1 AAD30229	BP14 PCR primer, Oxred 2C primer us
2	15.6	53.8	22	1 AAD42395	Human biallelic ma
3	15.2	52.4	21	1 AAZ77065	Human biallelic ma
4	14.8	51.0	20	1 AAZ74984	SARS coronavirus a
5	14.8	51.0	20	1 ADY78981	Primer used to cod
6	14.2	49.0	20	1 AAX85859	PCR primer for E.c
7	14.2	49.0	20	1 AAZ11144	Human KGF-2 mutant
8	14.2	49.0	20	1 AAA71269	PCR primer #10 for
9	14.2	49.0	20	1 AAF31967	Codon-optimised KG
10	14.2	49.0	20	1 AAC92946	KGF-2 delta-33s co
11	14.2	49.0	20	1 ABQ83060	E. coli keratinocy
12	14.2	49.0	20	1 ADA95533	Extend primer 48 u
13	14.2	49.0	20	1 ADD66206	Codon optimised KG
14	14.2	49.0	20	1 ADO50763	Human peroxiredoxi
15	14.2	49.0	20	1 ADT98004	Human keratinocyte
16	13.8	47.6	17	1 ADP09253	Extend primer 48 u
17	13.4	46.2	18	1 ADZ20529	Mouse G alpha-15 t
18	13.4	46.2	19	1 AAZ72126	Human biallelic ma
19	13.4	46.2	19	1 ADV60526	sRNA-9 used to in
20	13.2	45.5	18	1 AAZ44771	Human FADD primer
21	13	44.8	15	1 AAS99971	Human NPR1 gene al
22	12.8	44.1	17	1 AAT80089	Primer #1 for 4-co
23	12.8	44.1	17	1 ABV90926	Human POSHL1 scann
24	12.8	44.1	17	1 ABV90925	Human POSHL1 scann
25	12.8	44.1	18	1 AAT96932	Human pRb2/p130 tu
26	12.8	44.1	18	1 AAX63330	Delta-9 desaturase
27	12.4	42.8	15	1 ADW64053	Human superoxide d
28	12.4	42.8	17	1 ABN02182	Human GMPLP-1 17-m
29	12.4	42.8	17	1 ABN02180	Human GMPLP-1 17-m
30	12.4	42.8	17	1 ABN02179	Human GMPLP-1 17-m
31	12.4	42.8	17	1 ABN02181	Human GMPLP-1 17-m
32	12.4	42.8	17	1 ABT39421	Tumour suppression
33	12.4	42.8	17	1 ABT39428	Tumour suppression

34	12.4	42.8	17	1 ADI51118	Human tumour suppr
35	12.4	42.8	17	1 ACN65269	Human GMPLP-1 prob
36	12.4	42.8	17	1 ACN65270	Human GMPLP-1 prob
37	12.4	42.8	17	1 ACN65272	Human GMPLP-1 prob
38	12.4	42.8	17	1 ACN65271	Human GMPLP-1 prob
39	12.2	42.1	17	1 ABV90927	Human POSHL1 scann
40	12.2	42.1	17	1 ABV90928	Human POSHL1 scann
41	12.2	42.1	17	1 ABV90929	Human POSHL1 scann
42	12.2	42.1	17	1 ACN03462	WNK Zinkzyme substr
43	12.2	42.1	17	1 ACN07683	NFKB sub-unit modu
44	12.2	42.1	17	1 ACN08233	Necrosis factor ka
45	12	41.4	17	1 ABN02177	Human GMPLP-1 17-m
46	12	41.4	17	1 ABN02178	Human GMPLP-1 17-m
47	12	41.4	17	1 ADB41885	Tumour suppression
48	12	41.4	17	1 ACC51536	Human tumour suppr
49	12	41.4	17	1 ACN65268	Human GMPLP-1 prob
50	12	41.4	17	1 ACN65267	Human GMPLP-1 prob
51	11.8	40.7	15	1 ADV35523	Human anti-HER2 NC
52	11.8	40.7	15	1 ADV35886	Human anti-HER2 NC
53	11.4	39.3	13	1 ABF45364	Oligonucleotide SE
54	11.4	39.3	13	1 ABP45365	Oligonucleotide SE
55	11.4	39.3	15	1 ABA02592	HBV targeted riboz
56	11.4	39.3	15	1 ABS64208	Tachykinin recepto
57	11.2	38.6	16	1 AAD27264	PCR primer for pro
58	11.2	38.6	16	1 AAD27231	M13 universal reve
59	11.2	38.6	16	1 ABZ75913	M13 universal reve
60	11.2	38.6	16	1 ADZ70024	Human survivin gen
61	11.2	38.6	16	1 ADW09556	Human survivin ant
62	11.2	38.6	16	1 ADW09954	Human survivin ant
63	11.2	38.6	16	1 ADW09955	Human survivin ant
64	11.2	38.6	16	1 ADW09535	Human survivin ant
65	11.2	38.6	16	1 ADW09957	Human survivin ant
66	11	37.9	12	1 AAZ48742	PCR primer for hum
67	11	37.9	12	1 AAQ04007	Primer used in det
68	11	37.9	15	1 AAF69397	Human l4Ralpha ge
69	11	37.9	15	1 ABA99295	Human EDG5 allele
70	11	37.9	15	1 ABL45833	Human EDG5 allele
71	11	37.9	15	1 AAS16726	Human APOA4 allele
72	11	37.9	15	1 AAL39723	SMOH polymorphism
73	11	37.9	15	1 ACF57574	Human ALDOB gene a
74	11	37.9	15	1 ADQ30419	Human VRI exon id
75	10.8	37.2	14	1 AAV92814	Human A-raf target
76	10.8	37.2	15	1 AAV48782	ErbB-2 gene antise
77	10.8	37.2	15	1 AAZ62474	Substrate for HH r
78	10.8	37.2	15	1 AAH18890	UCP3 polymorphism
79	10.8	37.2	15	1 AAF52803	IGF-1 oligonucleot
80	10.8	37.2	15	1 AAF45867	IGFBP2 oligonucleo
81	10.8	37.2	15	1 AAF52804	IGF-1 oligonucleot
82	10.8	37.2	15	1 AAF45868	IGFBP2 oligonucleo
83	10.8	37.2	15	1 ADV35524	Human anti-HER2 NC
84	10.8	37.2	15	1 ABX00325	Human anti-HER2 NC
85	10.8	37.2	15	1 ABX00325	Hepatitis C virus
86	10.8	37.2	15	1 AEB74235	Cytoprotective res
87	10.6	36.6	15	1 ABL88273	Hepatitis C virus
88	10.6	36.6	15	1 ABK12178	Human Tachykinin R
89	10.4	35.9	13	1 ACC70394	CDNA tag for gene
90	10.4	35.9	13	1 ADL72846	Antisense oligonuc
91	10.4	35.9	14	1 AAQ78352	Human Notch3 gene
92	10.4	35.9	14	1 AAV57016	Human A-raf target
93	10.4	35.9	14	1 AAV92815	Human A-raf target
94	10.4	35.9	14	1 ABQ83257	Expressed gene ide
95	10	34.5	10	1 AAZ86497	Metastatic breast
96	10	34.5	10	1 AAZ86497	Primer #22 for det
97	10	34.5	10	1 AAZ86497	Mouse Et gene 5' s
98	10	34.5	10	1 ADD71273	Human Et gene 5' s
99	10	34.5	11	1 ABQ87100	Human skin stress/
100	10	34.5	11	1 ABV66313	Human skin EST 409
101	10	34.5	11	1 ABV65203	Human skin EST 298
102	10	34.5	11	1 ABV63737	Human skin EST 152
103	10	34.5	11	1 ABV71158	Human skin EST 894
104	10	34.5	11	1 AAD34268	Human CYP2D6 gene
105	10	34.5	11	1 ABT39421	Human VRI exon id
106	10	34.5	12	1 ABT39428	Oligonucleotide pr

N-Geneseg

107	10	34.5	12	1	ABI05465	Oligonucleotide pr
c 108	10	34.5	12	1	ADQ30383	Human VRI exon 1d
c 109	10	34.5	12	1	ADQ30420	Human VRI exon 1d
c 110	10	34.5	13	1	ABC35433	Oligonucleotide SE
c 111	10	34.5	13	1	ABF12886	Oligonucleotide SE
c 112	10	34.5	13	1	ABC14106	Oligonucleotide SE
c 113	10	34.5	13	1	ABC14104	Oligonucleotide SE
c 114	10	34.5	13	1	ABH01641	Oligonucleotide SE
c 115	10	34.5	13	1	ABC14107	Oligonucleotide SE
c 116	10	34.5	13	1	ABC35432	Oligonucleotide SE
c 117	10	34.5	13	1	ABF12887	Oligonucleotide SE
c 118	10	34.5	13	1	ABH01640	Oligonucleotide SE
c 119	10	34.5	13	1	ABC14105	Oligonucleotide SE
c 120	10	34.5	13	1	ADE14132	Optineurin promote
c 121	10	34.5	14	1	AAV92770	Human A-raf target
c 122	10	34.5	14	1	AAZ64774	Substrate for hair
c 123	10	34.5	14	1	AAZ37042	Probe targeted to
c 124	10	34.5	14	1	ABX01611	Hepatitis C virus
c 125	10	34.5	14	1	ABE76535	Hepatitis C virus
c 126	9.8	33.8	13	1	AAA06015	CFTR gene analysis
c 127	9.8	33.8	13	1	ABF45366	Oligonucleotide SE
c 128	9.8	33.8	13	1	ABF45367	Oligonucleotide SE
c 129	9.8	33.8	13	1	ABK28875	HPV blocker probe
c 130	9.8	33.8	13	1	ABZ34180	HIV-1 reverse tran
c 131	9.8	33.8	13	1	ABZ34155	HIV-1 reverse tran
c 132	9.8	33.8	13	1	ADF48833	DNA array associat
c 133	9.8	33.8	14	1	AAQ78366	Antisense oligonuc
c 134	9.8	33.8	14	1	AAV48778	ErbB-2 gene antis
c 135	9.8	33.8	14	1	ABZ34156	HIV-1 reverse tran
c 136	9.8	33.8	14	1	ABZ34175	HIV-1 reverse tran
c 137	9.8	33.8	14	1	ABZ34152	HIV-1 reverse tran
c 138	9.8	33.8	14	1	ABZ34170	HIV-1 reverse tran
c 139	9.8	33.8	14	1	ABZ34179	HIV-1 reverse tran
c 140	9.8	33.8	14	1	ABZ34172	HIV-1 reverse tran
c 141	9.8	33.8	14	1	AEA60845	Blood fluke Sjpp 5
c 142	9.4	32.4	11	1	AAZ18959	Murine MRL SAGE ta
c 143	9.4	32.4	11	1	AAZ18744	Murine C57BL/6 SAG
c 144	9.4	32.4	11	1	AAA96508	Consensus sequence
c 145	9.4	32.4	11	1	ABQ86330	Human skin stress/
c 146	9.4	32.4	11	1	ABV64871	Human skin EST 265
c 147	9.4	32.4	11	1	ABV66455	Human skin EST 424
c 148	9.4	32.4	11	1	ABV67092	Human skin EST 487
c 149	9.4	32.4	11	1	ABV70439	Human skin EST 822
c 150	9.4	32.4	11	1	ABV63018	Human skin EST 804
c 151	9.4	32.4	11	1	ABV65196	Human skin EST 298
c 152	9.4	32.4	11	1	ABV67859	Human skin EST 564
c 153	9.4	32.4	11	1	ADQ34760	Human facial skin-
c 154	9.4	32.4	11	1	ADQ33707	Human facial skin-
c 155	9.4	32.4	12	1	AAZ48741	PCR primer for hum
c 156	9.4	32.4	12	1	AAQ04006	Primer used in det
c 157	9.4	32.4	12	1	AAV40900	Primer CBFMYHA:10
c 158	9.4	32.4	12	1	AAA06782	VEGF derived short
c 159	9.4	32.4	12	1	AAA06783	VEGF derived short
c 160	9.4	32.4	12	1	ABH86901	Oligonucleotide pr
c 161	9.4	32.4	12	1	AAD54083	HNF1-131-1 gene SN
c 162	9.4	32.4	12	1	AAZ51397	Human polyamine ox
c 163	9.4	32.4	13	1	AAA54184	5' exon-intron jun
c 164	9.4	32.4	13	1	ABC87602	Oligonucleotide SE
c 165	9.4	32.4	13	1	ABC87603	Oligonucleotide SE
c 166	9.4	32.4	13	1	ACC70395	Cytoprotective res
c 167	9	31.0	10	1	AAZ79202	Human dendritic ce
c 168	9	31.0	10	1	AAZ78009	Human dendritic ce
c 169	9	31.0	10	1	AAZ78129	Human dendritic ce
c 170	9	31.0	10	1	AAZ85467	Metastatic breast
c 171	9	31.0	10	1	AAZ86332	Metastatic breast
c 172	9	31.0	10	1	AAZ81042	Metastatic breast
c 173	9	31.0	10	1	AAZ82620	Metastatic breast
c 174	9	31.0	10	1	AAH63185	Human colon epithe
c 175	9	31.0	10	1	AAZ57316	Human CHNB2 allel
c 176	9	31.0	10	1	AAH32728	LPS activated huma
c 177	9	31.0	10	1	ABA81652	Human phospholipid
c 178	9	31.0	10	1	AAF35559	Yeast NORF gene SA
c 179	9	31.0	10	1	AAF34581	Yeast NORF Gene SA

c 180	9	31.0	10	1	AAF37646	Yeast NORF gene SA
c 181	9	31.0	10	1	ABU52170	Human PER1 preferr
c 182	9	31.0	10	1	AAZ94664	Human PTP gene al
c 183	9	31.0	10	1	AAZ39779	SMOH polymorphism
c 184	9	31.0	10	1	ADZ14133	Optineurin promote
c 185	9	31.0	10	1	ADQ30369	Human VRI exon 1d
c 186	9	31.0	11	1	AAZ19836	Transcription fact
c 187	9	31.0	11	1	AAZ16595	Human MN gene 5' d
c 188	9	31.0	11	1	AAZ52514	Human MN gene intr
c 189	9	31.0	11	1	ABQ86329	Human skin stress/
c 190	9	31.0	11	1	ABQ62312	Human skin EST 98
c 191	9	31.0	11	1	ABV69491	Human skin EST 727
c 192	9	31.0	11	1	ABV69733	Human skin EST 751
c 193	9	31.0	11	1	ABU91944	Human Pan-Endothel
c 194	9	31.0	11	1	ABX71869	DNA tag used to id
c 195	9	31.0	11	1	ADK41823	Human MN gene intr
c 196	9	31.0	12	1	ABH83073	Oligonucleotide pr
c 197	9	31.0	12	1	ABH66469	Oligonucleotide pr
c 198	9	31.0	12	1	ABH17481	Oligonucleotide pr
c 199	9	31.0	12	1	ABH77789	Oligonucleotide pr
c 200	9	31.0	12	1	ABH74143	Oligonucleotide pr
c 201	9	31.0	12	1	ABH17480	Oligonucleotide pr
c 202	9	31.0	12	1	ABH73202	Oligonucleotide pr
c 203	9	31.0	12	1	ABH56716	Oligonucleotide pr
c 204	9	31.0	12	1	AAZ44624	Muscle creatine ki
c 205	9	31.0	12	1	ADF78489	Chromosomal abnorm
c 206	9	31.0	12	1	ADQ08498	Human papillomavir
c 207	9	31.0	12	1	ADQ98085	Human SNP TSC21610
c 208	9	31.0	12	1	ADQ80752	Human DNA PCR prim
c 209	8.8	30.3	12	1	AAQ86030	IT10C3 coding regi
c 210	8.8	30.3	12	1	AAQ88466	Human mitochondria
c 211	8.8	30.3	12	1	AAZ59759	Bacteriophage M13m
c 212	8.8	30.3	12	1	ABH24861	Oligonucleotide pr
c 213	8.8	30.3	12	1	ABH11597	Oligonucleotide pr
c 214	8.8	30.3	12	1	ABH10363	Oligonucleotide pr
c 215	8.8	30.3	12	1	ABH52832	Oligonucleotide pr
c 216	8.8	30.3	12	1	ABH39693	Oligonucleotide pr
c 217	8.8	30.3	12	1	ABH80092	Oligonucleotide pr
c 218	8.8	30.3	12	1	ABH77417	Oligonucleotide pr
c 219	8.8	30.3	12	1	ABH83668	Oligonucleotide pr
c 220	8.8	30.3	12	1	ABH87588	Oligonucleotide pr
c 221	8.8	30.3	12	1	ABH40468	Oligonucleotide pr
c 222	8.8	30.3	12	1	ABH60766	Oligonucleotide pr
c 223	8.8	30.3	12	1	ABH62806	Oligonucleotide pr
c 224	8.8	30.3	12	1	ABH17729	Oligonucleotide pr
c 225	8.8	30.3	12	1	ABH94984	Oligonucleotide pr
c 226	8.8	30.3	12	1	ABH26645	Oligonucleotide pr
c 227	8.8	30.3	12	1	ABH39600	Oligonucleotide pr
c 228	8.8	30.3	12	1	ABH59140	Oligonucleotide pr
c 229	8.8	30.3	12	1	ABH60733	Oligonucleotide pr
c 230	8.8	30.3	12	1	ABH26571	Oligonucleotide pr
c 231	8.8	30.3	12	1	ABH77044	Oligonucleotide pr
c 232	8.8	30.3	12	1	ABH84669	Oligonucleotide pr
c 233	8.8	30.3	12	1	ACD28673	Human acid sphingo
c 234	8.8	30.3	12	1	ABH13943	Optineurin promote
c 235	8.8	30.3	12	1	ABZ77024	Bovine DGAT exon-i
c 236	8.8	30.3	12	1	ADZ24155	Human SNP detectio
c 237	8.8	30.3	12	1	ADZ77727	Breast cancer dete
c 238	8.6	29.7	11	1	ADZ77874	Breast cancer dete
c 239	8.6	29.7	11	1	ADZ77394	Breast cancer dete
c 240	8.6	29.7	11	1	AAZ44125	PCR primer #6 desi
c 241	8.6	29.7	12	1	AAZ97150	HIV-1 NL4-3 LTR nu
c 242	8.4	29.0	10	1	AAQ96785	HIV-1 NL4-3 nef ge
c 243	8.4	29.0	10	1	AAQ97151	HIV-1 NL4-3 LTR nu
c 244	8.4	29.0	10	1	AAQ96482	HIV-1 NL4-3 nef ge
c 245	8.4	29.0	10	1	AAQ97149	HIV-1 NL4-3 LTR nu
c 246	8.4	29.0	10	1	AAV34960	Synthetic Agaricus
c 247	8.4	29.0	10	1	AAV03254	Homo sapiens mutan
c 248	8.4	29.0	10	1	AAZ18637	p53 serial analysi
c 249	8.4	29.0	10	1	AAZ11274	Splice donor site
c 250	8.4	29.0	10	1	AAZ78697	Human dendritic ce
c 251	8.4	29.0	10	1	AAZ77846	Human dendritic ce
c 252	8.4	29.0	10	1	AAZ77846	Human dendritic ce

253	8.4	29.0	10	1	AAZ79150	Human dendritic ce	326	8.4	29.0	11	1	ABV68983	Human skin EST 676
254	8.4	29.0	10	1	AAZ84055	Metastatic breast	C 327	8.4	29.0	11	1	ABV67130	Human skin EST 491
255	8.4	29.0	10	1	AAZ81988	Metastatic breast	C 328	8.4	29.0	11	1	ABV67225	Human skin EST 501
C 256	8.4	29.0	10	1	AAZ83343	Metastatic breast	C 329	8.4	29.0	11	1	ABV67773	Human skin EST 555
C 257	8.4	29.0	10	1	AAZ83792	Metastatic breast	C 330	8.4	29.0	11	1	ABV62764	Human skin EST 550
258	8.4	29.0	10	1	AAZ86544	Metastatic breast	C 331	8.4	29.0	11	1	ABV62815	Human skin EST 601
259	8.4	29.0	10	1	AAZ81303	Metastatic breast	C 332	8.4	29.0	11	1	ABV69214	Human skin EST 700
260	8.4	29.0	10	1	AAZ74087	Human dendritic ce	C 333	8.4	29.0	11	1	ABV70185	Human skin EST 797
C 261	8.4	29.0	10	1	AAZ73981	Human dendritic ce	C 334	8.4	29.0	11	1	ABV70837	Human skin EST 862
C 262	8.4	29.0	10	1	AAZ56364	Human macrophage g	C 335	8.4	29.0	11	1	ABV65404	Human skin EST 319
C 263	8.4	29.0	10	1	AAZ591928	PCR primer for mur	C 336	8.4	29.0	11	1	ABV66252	Human skin EST 403
264	8.4	29.0	10	1	AAH189978	UCP3 polymorphism	C 337	8.4	29.0	11	1	ABV67008	Human skin EST 479
265	8.4	29.0	10	1	AAH19943	Mouse Treg immunor	C 338	8.4	29.0	11	1	ABV69518	Human skin EST 730
266	8.4	29.0	10	1	AAI67394	Human FKBP8 gene p	C 339	8.4	29.0	11	1	ABV70736	Human skin EST 852
267	8.4	29.0	10	1	AAH63201	Human colon epithe	C 340	8.4	29.0	11	1	ABV66438	Human skin EST 422
268	8.4	29.0	10	1	AAH631192	Human colon epithe	C 341	8.4	29.0	11	1	ABV67400	Human skin EST 518
269	8.4	29.0	10	1	AAH63266	Human colon epithe	C 342	8.4	29.0	11	1	ABV67423	Human skin EST 520
270	8.4	29.0	10	1	AAH63751	Human ubiquitously	C 343	8.4	29.0	11	1	ABV70236	Human skin EST 802
271	8.4	29.0	10	1	AAH32787	LPS activated huma	C 344	8.4	29.0	11	1	ABV63416	Human skin EST 120
272	8.4	29.0	10	1	AAH41694	Anti-PEP gene cons	C 345	8.4	29.0	11	1	ABV64243	Human skin EST 202
C 273	8.4	29.0	10	1	ABA06109	Human normal hepat	C 346	8.4	29.0	11	1	ABV67475	Human skin EST 526
C 274	8.4	29.0	10	1	NAF69625	Human IL4Ralpha ge	C 347	8.4	29.0	11	1	ABV71564	Human skin EST 945
C 275	8.4	29.0	10	1	NAF341164	Yeast NORF gene SA	C 348	8.4	29.0	11	1	ABV67586	Human skin EST 537
C 276	8.4	29.0	10	1	NAF35667	Yeast NORF gene SA	C 349	8.4	29.0	11	1	ABV68554	Human skin EST 634
C 277	8.4	29.0	10	1	AAF35804	Yeast NORF gene SA	C 350	8.4	29.0	11	1	AD40434	Bovine DGAT1 gene
C 278	8.4	29.0	10	1	AAF44017	Yeast NORF gene SA	C 351	8.4	29.0	11	1	ABV78654	RXR binding site f
C 279	8.4	29.0	10	1	AAF43467	Yeast NORF gene SA	C 352	8.4	29.0	11	1	ADG13657	Human EGFR Amberzy
280	8.4	29.0	10	1	NAF34829	Yeast NORF gene SA	C 353	8.4	29.0	11	1	ADR41836	Human MN gene intr
C 281	8.4	29.0	10	1	AAF35820	Yeast NORF gene SA	C 354	8.4	29.0	11	1	ADQ35801	Human hair-bearing
C 282	8.4	29.0	10	1	AAF35485	Yeast NORF gene SA	C 355	8.4	29.0	11	1	ADQ35910	Human hair-bearing
283	8.4	29.0	10	1	ABL42879	Human maturation/a	C 356	8.4	29.0	11	1	ADQ35843	Human hair-bearing
284	8.4	29.0	10	1	ABL42726	Human maturation/a	C 357	8.4	29.0	11	1	ADQ33204	Human facial skin-
285	8.4	29.0	10	1	ABL42777	Human maturation/a	C 358	8.4	29.0	11	1	ADQ33521	Human facial skin-
286	8.4	29.0	10	1	ABL42899	Human maturation/a	C 359	8.4	29.0	11	1	ADQ33860	Human facial skin-
C 287	8.4	29.0	10	1	ABL39528	Human ETRF primer-	C 360	8.4	29.0	11	1	ADQ33652	Human facial skin-
C 288	8.4	29.0	10	1	ABV84850	Human mitochondria	C 361	8.4	29.0	11	1	ADQ34937	Human facial skin-
C 289	8.4	29.0	10	1	ABK09446	Human NPR1 gene al	C 362	8.4	29.0	11	1	ADQ32556	Human facial skin-
C 290	8.4	29.0	10	1	ABK09921	P2RY1 gene allele-	C 363	8.4	29.0	11	1	ADQ33878	Human facial skin-
C 291	8.4	29.0	10	1	ABK09919	P2RY1 gene allele-	C 364	8.4	29.0	11	1	ADQ32289	Human facial skin-
C 292	8.4	29.0	10	1	ABS64284	Tachykinin recepto	C 365	8.4	29.0	11	1	ADQ32869	Human facial skin-
C 293	8.4	29.0	10	1	ABS64271	Tachykinin recepto	C 366	8.4	29.0	11	1	ADQ34474	Human facial skin-
294	8.4	29.0	10	1	AAZ99384	Aldehyde dehydroge	C 367	8.4	29.0	12	1	AAQ52115	Breast cancer spec
295	8.4	29.0	10	1	AAD47793	Human GNB3 gene po	C 368	8.4	29.0	12	1	AAV32307	Random primed reve
C 296	8.4	29.0	10	1	ACC69006	AMP protocol Hpall	C 369	8.4	29.0	12	1	AAV32258	Random primed reve
C 297	8.4	29.0	10	1	ABT14241	Nucleic acid PCR a	C 370	8.4	29.0	12	1	AAV32253	Random primed reve
C 298	8.4	29.0	10	1	ADE141194	Optineurin promote	C 371	8.4	29.0	12	1	AAZ41830	Organic material d
C 299	8.4	29.0	10	1	AAZ51289	SAGE transcript ta	C 372	8.4	29.0	12	1	AAZ41780	Microbe detection
C 300	8.4	29.0	10	1	ADL96345	CD15+ myeloid cell	C 373	8.4	29.0	12	1	AAZ41564	Microbe detection
C 301	8.4	29.0	10	1	ADG13687	Human EGFR Ambery	C 374	8.4	29.0	12	1	AAZ41614	Human smoothelin v
302	8.4	29.0	10	1	ADH14437	Human retinoblasto	C 375	8.4	29.0	12	1	AAF74730	Human smoothelin v
C 303	8.4	29.0	10	1	ADK12825	Human glioma endot	C 376	8.4	29.0	12	1	AAZ501805	Human smoothelin g
C 304	8.4	29.0	10	1	ADR27999	Murine VE-statin e	C 377	8.4	29.0	12	1	AAZ97965	Primer used to ill
C 305	8.4	29.0	10	1	ADS78008	Breast cancer dete	C 378	8.4	29.0	12	1	AAZ97915	Primer used to ill
C 306	8.4	29.0	10	1	ADS76235	Breast cancer dete	C 379	8.4	29.0	12	1	AB129917	Oligonucleotide pr
307	8.4	29.0	10	1	ADS76988	Breast cancer dete	C 380	8.4	29.0	12	1	ABH85587	Oligonucleotide pr
C 308	8.4	29.0	10	1	ADS77286	Breast cancer dete	C 381	8.4	29.0	12	1	ABH59162	Oligonucleotide pr
309	8.4	29.0	10	1	ADS76987	Breast cancer dete	C 382	8.4	29.0	12	1	ABH74750	Oligonucleotide pr
C 310	8.4	29.0	10	1	ADU19159	Hypoxia-related tu	C 383	8.4	29.0	12	1	ABH75922	Oligonucleotide pr
C 311	8.4	29.0	10	1	ADU19427	Hypoxia-related tu	C 384	8.4	29.0	12	1	ABH75922	Oligonucleotide pr
312	8.4	29.0	11	1	AAZ55915	CYP1B1 gene exon I	C 385	8.4	29.0	12	1	AB153560	Oligonucleotide pr
313	8.4	29.0	11	1	AAZ18975	Murine MRL SAGE ta	C 386	8.4	29.0	12	1	AB159024	Oligonucleotide pr
314	8.4	29.0	11	1	AAZ18803	Murine C57BL/6 SAG	C 387	8.4	29.0	12	1	AB160693	Oligonucleotide pr
C 315	8.4	29.0	11	1	AAZ16608	Human MN gene 3' a	C 388	8.4	29.0	12	1	AB118817	Oligonucleotide pr
C 316	8.4	29.0	11	1	AAZ52527	Human MN gene intr	C 389	8.4	29.0	12	1	ABH71861	Oligonucleotide pr
317	8.4	29.0	11	1	AAZ75228	Human RXR binding	C 390	8.4	29.0	12	1	ABH77312	Oligonucleotide pr
C 318	8.4	29.0	11	1	ABQ86838	Human skin stress/	C 391	8.4	29.0	12	1	AB118206	Oligonucleotide pr
C 319	8.4	29.0	11	1	ABQ86763	Human skin stress/	C 392	8.4	29.0	12	1	AB143158	Oligonucleotide pr
320	8.4	29.0	11	1	ABQ86990	Human skin stress/	C 393	8.4	29.0	12	1	AB169159	Oligonucleotide pr
C 321	8.4	29.0	11	1	ABQ87167	Human skin stress/	C 394	8.4	29.0	12	1	ABH81976	Oligonucleotide pr
322	8.4	29.0	11	1	ABQ87430	Human skin stress/	C 395	8.4	29.0	12	1	AB169157	Oligonucleotide pr
323	8.4	29.0	11	1	ABQ86674	Human skin stress/	C 396	8.4	29.0	12	1	AB180903	Oligonucleotide pr
324	8.4	29.0	11	1	ABV63315	Human skin EST 110	C 397	8.4	29.0	12	1	ABH97813	Oligonucleotide pr
C 325	8.4	29.0	11	1	ABV66003	Human skin EST 378	C 398	8.4	29.0	12	1	ABH93473	Oligonucleotide pr

399	8.4	29.0	12	1	ABI43157	oligonucleotide pr
400	8.4	29.0	12	1	ABI72787	oligonucleotide pr
401	8.4	29.0	12	1	ABI05466	oligonucleotide pr
402	8.4	29.0	12	1	ABI13967	oligonucleotide pr
c 403	8.4	29.0	12	1	ABI16340	oligonucleotide pr
404	8.4	29.0	12	1	ABH69681	oligonucleotide pr
405	8.4	29.0	12	1	ABI137541	oligonucleotide pr
c 406	8.4	29.0	12	1	ABH77664	oligonucleotide pr
407	8.4	29.0	12	1	ABH86388	oligonucleotide pr
c 408	8.4	29.0	12	1	ABH74692	oligonucleotide pr
409	8.4	29.0	12	1	ABI02272	oligonucleotide pr
c 410	8.4	29.0	12	1	ABI177388	oligonucleotide pr
411	8.4	29.0	12	1	ABH97611	oligonucleotide pr
412	8.4	29.0	12	1	ABH84024	oligonucleotide pr
c 413	8.4	29.0	12	1	ABH85692	oligonucleotide pr
c 414	8.4	29.0	12	1	ABI53806	oligonucleotide pr
415	8.4	29.0	12	1	ABI19386	oligonucleotide pr
416	8.4	29.0	12	1	ABH69682	oligonucleotide pr
417	8.4	29.0	12	1	ABI29310	oligonucleotide pr
418	8.4	29.0	12	1	ABH84793	oligonucleotide pr
c 419	8.4	29.0	12	1	ABI73341	oligonucleotide pr
c 420	8.4	29.0	12	1	ABI59818	oligonucleotide pr
421	8.4	29.0	12	1	ABK72569	Human OPAL gene, e
422	8.4	29.0	12	1	ABK72535	Human OPAL gene, e
c 423	8.4	29.0	12	1	AAAL42695	Rice seed bZIP tra
c 424	8.4	29.0	12	1	AAAL42645	Rice seed bZIP tra
425	8.4	29.0	12	1	ABK29928	Beta-lactamase pro
426	8.4	29.0	12	1	ABK30092	Beta-lactamase pro
427	8.4	29.0	12	1	ABA91368	DNA encoding neuro
428	8.4	29.0	12	1	ADE85925	Immunostimulatory
c 429	8.4	29.0	12	1	ADF78662	Chromosomal abnorm
c 430	8.4	29.0	12	1	ADF78486	Chromosomal abnorm
431	8.4	29.0	12	1	ABZ72938	Rod opsin hammehe
432	8.4	29.0	12	1	ADM56049	Antibacterial pept
c 433	8.4	29.0	12	1	ADM56293	Mouse SLC26A6 anio
434	8.4	29.0	12	1	AE880299	Organic waste trea
c 435	8.4	29.0	12	1	ADM76195	NEPHA gene transcr
c 436	8.4	29.0	12	1	ADQ30184	Marine VR1 exon 1d
c 437	8.4	29.0	12	1	ADQ30185	Marine VR1 exon 1d
c 438	8.4	29.0	12	1	ADQ30343	Human VR1 exon 1d
c 439	8.4	29.0	12	1	ADR32504	Human nicking agen
c 440	8.4	29.0	12	1	ADR98238	Human chromosome 2
c 441	8.4	29.0	12	1	ADR98062	Human SNP TSC04700
c 442	8.4	29.0	12	1	ADS08925	Human DNA PCR prim
c 443	8.4	29.0	12	1	ADS08749	Human DNA PCR prim
444	8.4	29.0	12	1	ADZ15183	PCR primer used to
445	8.4	29.0	12	1	ADZ24372	Human SNP detectio
446	8.4	29.0	12	1	AEA50022	Construct Pc-pcDNA
447	7.4	25.5	10	1	ABK09921	P2RY1 gene allele-
c 448	7.4	25.5	10	1	ADU19159	Hypoxia-related tu

ALIGNMENTS

RESULT 1	
AAD30229	
ID	AAD30229 standard; DNA; 29 BP.
XX	
AC	AAD30229;
XX	
DT	17-MAY-2002 (first entry)
XX	
DE	BPF14 PCR primer, to generate human PKD1 gene long range templates.
XX	
KW	Human; PKD1 gene; autosomal dominant polycystic kidney disease; ADPKD;
KW	acquired cystic disease; transgenic animal; PCR primer; ss.
XX	
OS	Homo sapiens.
XX	
FN	WO200206529-A2.
XX	
XX	24-JAN-2002.
PA	(PHAA) PHARMACIA CORP.
XX	
PF	26-OCT-2001; 2001WO-US051070.
XX	
XX	30-OCT-2000; 2000US-0244300P.
XX	
PD	13-JUN-2002.
XX	
PN	WO200246386-A2.
XX	
OS	Homo sapiens.
XX	
DE	Oxred 2C primer used to sequence human cytochrome p450 reductase DNA.
XX	
KW	11 alpha hydroxylase; enzyme; sitosterol; eplerenone; cell therapy;
KW	steroid bioconversion; antiinflammatory; antiarthritic; cytostatic;
KW	cardiant; human; cytochrome p450 reductase; primer; ss.
XX	
DT	04-NOV-2002 (first entry)
XX	
AC	AAD42395;
XX	
ID	AAD42395 standard; DNA; 22 BP.
XX	
DT	
XX	
DE	
XX	
KW	
KW	
KW	
XX	
OS	
XX	
PN	
XX	
PD	
XX	
PF	
XX	
XX	
XX	
PA	

XX	13-JUL-2001; 2001WO-US022035.
PF	
XX	
PR	13-JUL-2000; 2000US-0218261P.
XX	13-APR-2001; 2001US-0283691P.
XX	(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA	
XX	
PI	Germino GG, Watnick TJ, Phakdeekitcharoen B;
XX	WPI; 2002-179805/23.
DR	
XX	
PT	Novel primer for diagnosing polycystic kidney disease-associated
PT	disorder, comprises regions having sequence that selectively hybridizes
PT	to polycystic kidney disease gene sequence.
XX	
PS	Claim 6; Page 98; 192pp; English.
XX	
CC	The present invention relates to compositions and methods useful for the
CC	identification and detection of polycystic kidney disease (PKD1) gene
CC	mutations. The invention also relates to primers comprising a 5' region
CC	having a sequence that selectively hybridizes to a PKD1 gene sequence and
CC	optionally, to a PKD1 homologue sequence and an adjacent 3' region having
CC	a sequence that selectively hybridizes to a PKD1 gene sequence and not to
CC	a PKD1 homologue sequence. Primer pairs of the invention are useful for
CC	detecting the presence or absence of a mutation in a PKD1 polynucleotide
CC	in a sample, for identifying a subject at risk for a PKD1-associated
CC	disorder such as autosomal dominant polycystic kidney disease (ADPKD) or
CC	acquired cystic disease and for diagnosing a PKD1- associated disorder in
CC	a subject. They are useful for selectively amplifying a region of a PKD1
CC	gene. PKD1 DNA fragments are useful detecting the presence of a mutant
CC	PKD1 polynucleotide in a sample, as a probe for an amplification
CC	reaction, in hybridization or amplification assays of biological samples
CC	to detect abnormalities of PKD1 expression and for engineering transgenic
CC	animals. The present sequence is a PCR primer used to generate human PKD1
CC	gene long range templates (exon 1-34)
XX	
SQ	Sequence 29 BP; 6 A; 9 C; 6 G; 8 T; 0 U; 0 Other;

Query Match	100.0%;	Score 29;	DB 1;	Length 29;
Best Local Similarity	100.0%;	Pred. No. 0.047;		
Matches	29;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	1	CCATCCACCTGCTGTGTGACCTGGTAAAT	29
Db	1	CCATCCACCTGCTGTGTGACCTGGTAAAT	29

RESULT 2
AAD42395


```

PA (BOLT/) BOLTON S.
PA (CLAY/) CLAYTON R.
PA (EAST/) EASTON A.
PA (ENGE/) ENGEL L.
PA (MESS/) MESSING D.
XX
XX Bolton S, Clayton R, Easton A, Engel L, Messing D;
XX
XX WPI; 2002-547772/58.
XX
XX New isolated Aspergillus ochraceus 11 alpha-hydroxylase or
PT oxidoreductase, for bioconversion of steroid substances to their 11 alpha
PT hydroxy counterparts in heterologous cells.
XX
XX Example 12; Page 178; 181pp; English.
XX
XX The present invention relates to novel cytochrome P450-like enzyme
CC (Aspergillus ochraceus 11 alpha hydroxylase protein), oxidoreductases and
CC polynucleotides encoding such proteins. Host cells comprising the
CC sequences of the invention are useful for making one or more enzymes from
CC the metabolic pathway for the synthesis of sitosterol to eplerenone. They
CC are useful for selective oxidation of a compound to an hydroxylated
CC product. Compositions of the invention are useful for producing spores
CC from A. ochraceus, A. niger, A. nidulans, Rhizopus oryzae, R. stolonifer,
CC R. arrhizus Trichothecium roseum, Fusarium oxysporum and M. olivaceum
CC etc, preferably to produce spores from A. ochraceus. Sequences of the
CC invention are useful in bioconversion of steroid substances to their 11
CC alpha-hydroxy counterparts. They are also used in cell therapy. The
CC present sequence is a primer used to sequence human cytochrome p450
CC reductase DNA. This sequence is used in the exemplification of the
CC invention
XX
XX Sequence 22 BP; 4 A; 7 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 53.8%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGACCTG 23
DB ||||| ||||| ||||| |||||
1 CATGACCACCTGTGTGACTG 22

RESULT 3
AAZ77065/C
ID AAZ77065 standard; DNA; 21 BP.
XX
XX AAZ77065;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:11421.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954500-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-IB000822.
PF
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX
XX 23-NOV-1998; 98US-0109732P.
PR
XX
XX (GEST ) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI
WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 2222; 2745pp; English.
XX

```

```

XX
XX WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 9; Page 2665; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
XX Sequence 21 BP; 7 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 52.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGACC 21
DB ||||| ||||| ||||| |||||
21 CATTGACTTGTGTGTGACC 2

RESULT 4
AAZ74984
ID AAZ74984 standard; DNA; 20 BP.
XX
XX AAZ74984;
AC
XX
XX 10-SEP-2001 (first entry)
DT
XX
XX Human biallelic marker downstream amplification primer SEQ ID NO:9340.
DE
XX
XX Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954500-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 21-APR-1999; 99WO-IB000822.
PF
XX
XX 21-APR-1998; 98US-0082614P.
PR
XX
XX 23-NOV-1998; 98US-0109732P.
PR
XX
XX (GEST ) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI
WPI; 2000-013267/01.
XX
XX Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
XX Claim 8; Page 2222; 2745pp; English.
XX

```

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention

XX SQ Sequence 20 BP; 2 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 51.0%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGACC 21
| | | | | | | | | | | | | | | | | | | | | |
Db 3 TGCACCTGCTGTGTGACC 20

RESULT 5

ID ADV78981
ADV78981 standard; DNA; 20 BP.

XX AC ADV78981;

XX DT 02-JUN-2005 (first entry)

XX KW SARS coronavirus antisense primer SEQ ID NO 19539.

XX KW Severe acute respiratory syndrome; SARS coronavirus infection;

XX KW phosphorothioate; antisense; antisense oligonucleotide;

XX KW antisense therapy; diagnostic; virucide; gene therapy; ss; primer.

XX OS SARS coronavirus.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..15

FT /*tag= a

FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyl (2-MOE) wing, Internucleoside

FT linkages are phosphorothioate and all cytidine

FT nucleotides are 5-methylcytidine."

FT modified_base 6..15

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-O-methoxyethyl (2-MOE) wing, Internucleoside

FT linkages are phosphorothioate and all cytidine

FT nucleotides are 5-methylcytidine."

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone. All cytidine

FT nucleotides are 5methylcytidine"

XX PN WO2005023083-A2.

XX PD 17-MAR-2005.

XX PF 27-APR-2004; 2004WO-US013050.

XX XX 28-APR-2003; 2003US-0466426P.

XX PR 30-APR-2003; 2003US-0467770P.

XX PR 06-MAY-2003; 2003US-0468562P.

XX PR 06-MAY-2003; 2003US-0468627P.

PR 10-JUN-2003; 2003US-0477637P.
PR 27-JUN-2003; 2003US-0483579P.
PR 28-APR-2004; 51US-00483579.

XX (ISIS-) ISIS PHARM INC.

XX Crooke ST, Ecker DJ, Sampath R, Freier SM, Massire C;
PI Hofstadler SA, Lowery KS, Swayze EE, Baker BF, Bennett FC;
XX WPI; 2005-223236/23.

XX New oligomeric compound comprising 8-80 nucleobases targeted to a nucleic
PT acid molecule encoding severe acute respiratory syndrome (SARS) virus,
PT useful for treating a disease or condition associated with a SARS virus.

XX Example 18; SEQ ID NO 19539; 130pp; English.

XX This invention describes a novel oligomeric compound comprising 8-80
CC nucleobases targeted to a nucleic acid molecule encoding severe acute
CC respiratory syndrome (SARS) virus, where the compound hybridizes with the
CC nucleic acid molecule encoding SARS virus and reduces the expression of
CC SARS virus by at least 50%. The invention also describes 1) a method for
CC reducing the expression of a SARS virus in cells or tissues; 2) a method
CC for screening for a modulator of a SARS virus; 3) a diagnostic method for
CC identifying a disease state; 4) a kit or assay device; 5) modulating the
CC frameshift efficiency of a coronavirus; 6) screening for a modulator of a
CC frameshift site; 7) a ribosomal frameshift reporting plasmid comprising a
CC viral sequence containing a ribosomal frameshift site and a luciferase
CC reporter gene and 8) characterization of a previously uncharacterized
CC frameshift site in a coronavirus RNA. The compound is a 15-30 nucleobases
CC antisense chimeric oligonucleotide. At least a portion of the compound
CC hybridizes with RNA to form an oligonucleotide-RNA duplex. It has at
CC least one modified internucleoside linkage, modified sugar moiety, or
CC modified nucleobase, specifically, phosphorothioate internucleoside
CC linkage, 2'-O-methoxyethyl sugar moiety, or 5-methylcytosine.

CC Specifically, the compound is targeted to a frameshift site of viral RNA,
CC where the compound specifically hybridizes with the frameshift site and
CC modulates the process of ribosomal frameshift of the viral RNA. The
CC modulator of SARS virus expression comprises an oligonucleotide, an
CC antisense oligonucleotide, a DNA oligonucleotide, an RNA oligonucleotide,
CC a chimeric oligonucleotide, or an RNA oligonucleotide having at least a
CC portion that is hybridizable with RNA to form an oligonucleotide-RNA
CC duplex. Characterizing a previously uncharacterized frameshift site in a
CC coronavirus RNA comprises obtaining RNA sequences of known coronaviruses
CC with known frameshift sites, obtaining an RNA sequence of a coronavirus
CC with an uncharacterized frameshift site and performing covariance
CC analysis on multiple sequence alignments of the RNA sequences of known
CC coronaviruses and the RNA sequence of the coronavirus with an
CC uncharacterized frameshift site. The compound is useful for treating an
CC animal having a disease or condition associated with a SARS virus so that
CC expression of SARS virus is reduced, where the disease or condition is a
CC viral infection. The compound is also useful for treating an individual
CC having a disease or condition associated with a coronavirus so that the
CC propagation of the coronavirus is inhibited as a result of modulation of
CC the frameshift site of the coronavirus. The compounds are useful for
CC diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC Oligonucleotides were synthesized via solid phase P(III) phosphoramidite
CC chemistry on an automated synthesizer. Phosphodiester internucleoside
CC linkages were afforded by oxidation with aqueous iodine. Phosphorothioate
CC internucleoside linkages were generated by sulfuration utilizing 3,H-
CC 1,2-benzodithiole-3-one 1,1 dioxide in anhydrous acetonitrile. This
CC sequence represents a chimeric phosphorothioate oligonucleotide targeted
CC to SARS coronavirus.

XX SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 51.0%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTGGTAAAT 29

| | | | | | | | | | | | | | | | | | | | | |

Db 3 CTCTGTAACCTGGTAAAT 20


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RESULT 8
ID AAA71269 standard; DNA; 20 BP.
XX
AC AAA71269;
XX
DT 20-NOV-2000 (first entry)
XX
DE Human KGF-2 mutant KGFdelta33 codon optimised primer SEQ ID NO: 97.
XX
KW Human; keratinocyte growth factor; KGF-2; antiulcer; antidiabetic;
KW antiinflammatory; cytoprotective; dermatological; gastrointestinal;
KW hepatic; respiratory; renal; cerebroprotective; mucositis; treatment;
KW epithelial cell proliferation; inflammatory bowel disease; lung damage;
KW liver disorder; diabetes; oral injury; gastrointestinal injury;
KW gut toxicity; gastric; duodenal; epidermolysis bullosa; skin graft;
KW skin disorder; renal failure; brain injury; intestinal fibrosis;
KW proctitis; female reproductive tract disorder; pulmonary fibrosis;
KW pneumonitis; pleural retraction; hemopoietic syndrome; myelotoxicity;
KW mutant; primer; ss.
XX
OS Homo sapiens.
XX
PN US6077692-A.
XX
PD 20-JUN-2000.
XX
PF 13-FEB-1998; 98US-00023082.
XX
PR 14-FEB-1995; 95WO-US001790.
PR 05-JUN-1995; 95US-00461195.
PR 13-AUG-1996; 96US-0023852P.
PR 28-FEB-1997; 97US-0039045P.
PR 23-MAY-1997; 97US-00862432.
PR 13-AUG-1997; 97US-0055561P.
PR 13-AUG-1997; 97US-00910875.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Mendrick D, Duan DR, Ni J, Jimenez P, Coleman TA, Gruber JR;
PI Dillon PJ, Gentz RL, Ruben SM, Zhang J, Moore PA, Rampy MA;
XX
XX WPI; 2000-441307/38.
XX
PT Novel keratinocyte growth factor useful for promoting and accelerating
PT wound healing, comprising at least 10 contiguous amino acids from a
PT specific amino acid sequence.
XX
PS Example 16; Col 187-188; 190pp; English.
XX
CC This invention describes a novel human keratinocyte growth factor, KGF-2
CC (I), which has antiulcer, antidiabetic, antiinflammatory, cytoprotective,
CC dermatological, gastrointestinal, hepatic, respiratory, renal and
CC cerebroprotective activity. (I) is useful for stimulating epithelial cell
CC proliferation in patients suffering from wound, mucositis, ulcer such as
CC venous stasis ulcer, diabetic ulcer and cubitus ulcer. (I) is also useful
CC for treating inflammatory bowel disease, liver disorder, lung damage,
CC diabetes, oral injury, gastrointestinal injury, gut toxicity, gastric
CC ulcer, duodenal ulcer, epidermolysis bullosa, skin graft, skin disorder,
CC renal failure, brain injury, breast tissue injury, urothelial damage,
CC female reproductive tract disorder, intestinal fibrosis, proctitis,
CC pulmonary fibrosis, pneumonitis, pleural retraction, hemopoietic syndrome
CC and myelotoxicity. (I) is also useful for increasing the adherence of
CC skin grafts to wound beds and to stimulate re-epithelialization from the
CC wound beds, to produce changes in hepatocyte proliferation, to reduce the
CC side effects of gut toxicity, to regenerate skin in full and partial
CC thickness skin defects, and to prevent and heal damage to lungs. KGF-2
CC shows enhanced activity, increased stability, higher yield and better
CC solubility. This sequence represents a human KGF-2 mutant protein primer
CC described in the method of the invention
XX
Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTGTGTGAC 20
   |||||||
Db 1 CAACCACTGCAGGGTGAC 19

RESULT 9
AAF31967
ID AAF31967 standard; DNA; 20 BP.
XX
AC AAF31967;
XX
DT 10-APR-2001 (first entry)
XX
DE PCR primer #10 for mutant KGF-2 construct.
XX
KW Keratinocyte growth factor; KGF-2; epithelial cell proliferation; wound;
KW mucositis; ulcer; inflammatory bowel disease; liver disorder;
KW lung damage; diabetes; oral injury; gastrointestinal injury;
KW epidermolysis bullosa; renal failure; brain injury; proctitis;
KW pulmonary fibrosis; haemopoietic syndrome; ovary injury; infertility;
KW liver fibrosis; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200102433-A1.
XX
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-US018328.
XX
PR 02-JUL-1999; 99US-0142343P.
PR 14-JUL-1999; 99US-0143648P.
PR 15-JUL-1999; 99US-0144024P.
PR 12-AUG-1999; 99US-0148628P.
PR 19-AUG-1999; 99US-0149935P.
PR 03-NOV-1999; 99US-0163375P.
PR 22-DEC-1999; 99US-0171677P.
PR 19-APR-2000; 2000US-0198322P.
PR 19-MAY-2000; 2000US-0205417P.
PR 30-JUN-2000; 2000US-00142343.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
XX
XX WPI; 2001-071578/08.
XX
PT A polynucleotide encoding the human keratinocyte growth factor useful for
PT stimulating epithelial cell proliferation in a patients that has e.g a
PT wound.
XX
PS Example 16; Page 337; 591pp; English.
XX
CC The present invention relates to human keratinocyte growth factor (KGF-2;
CC see AAF31901 and AAB61657). The present sequence is a PCR primer for KGF-
CC 2. KGF-2 can be used to stimulate epithelial cell proliferation in a
CC patient, where the patient has a wound, mucositis, an ulcer, inflammatory
CC bowel disease, liver disorder, lung damage, diabetes, oral injury,
CC gastrointestinal injury, gut toxicity, epidermolysis bullosa, skin graft,
CC skin disorder, renal failure, brain injury, breast tissue injury,
CC urothelial damage, female reproductive tract disorder, intestinal
CC fibrosis, proctitis, pulmonary fibrosis, pneumonitis, plural
CC retraction, haemopoietic syndrome, and myelotoxicity. In addition, KGF-2
CC can be used in the treatment or prevention of ovary injury, infertility,
CC or fibrosis of the liver. KGF-2 also promotes internal healing, donor
CC site healing, internal surgical wound healing or healing of incisional
CC wounds made during cosmetic surgery in a patient

```

XX SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CATCCACCTGCTGTGTGAC 20
|| |||||
Db 1 CAACCACTGCAGGTGAC 19
RESULT 10
ID AAC92946
XX AAC92946 standard; DNA; 20 BP.
AC AAC92946;
XX 27-MAR-2001 (first entry)
XX Codon-optimised KGF-2 delta-33 PCR primer PM05, SEQ ID NO:18.
XX Human, keratinocyte growth factor-2; KGF-2; wound healing; vulnery;
KW epithelial cell proliferation; epidermal keratinocyte proliferation;
KW soft tissue growth; ischaemic injury; skin disorder;
KW skin graft adherence; deletion mutant; Escherichia coli;
KW codon optimisation; PCR primer; ss.
XX Homo sapiens.
OS Synthetic.
XX WO200072872-A1.
XX 07-DEC-2000.
XX 02-JUN-2000; 2000WO-US015186.
XX 02-JUN-1999; 99US-0137448P.
PR 22-OCT-1999; 99US-0160913P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA (GENTZ) GENTZ R L.
PA (CHOP) CHOPRA A.
PA (KAUS) KAUSHAL P.
PA (SPIT) SPITZNAGEL T.
PA (UNSW) UNSWORTH E.
PA (KHAN) KHAN F.
XX Gentz RL, Chopra A, Kaushal P, Spitznagel T, Unsworth E, Khan F;
XX WPI; 2001-041105/05.
XX Pharmaceutical composition useful for stimulating epithelial cell
PT proliferation and basal keratinocytes for wound healing comprises
PT keratinocyte growth factor-2, in liquid or lyophilized forms.
XX Disclosure; Page 54; 101pp; English.
XX The invention relates to a pharmaceutical composition comprising 0.02-40
CC mg/ml (w/v) keratinocyte growth factor-2 (KGF-2) protein; a buffer having
CC buffering capacity of pH 5-8 at 5-50 mM; a diluent to bring the
CC composition to a designated volume; and a preservative such as m-cresol,
CC chlorobutanol, or a mixture of methyl paraben and propyl paraben or their
CC reaction products. The KGF-2 used in the composition of the invention is
CC preferably a novel mutant selected from the KGF-2 deletion mutants
CC AAB60202 and AAB60204-B60214, and particularly the deletion mutant KGF-2
CC delta-33 (AAB60202). KGF-2 stimulates the proliferation of epithelial
CC cells and epidermal keratinocytes but not mesenchymal cells such as
CC fibroblasts. The compositions of the invention may therefore be used for
CC promoting or accelerating soft tissue growth or wound healing, or for
CC treating mucocystis or inflammatory bowel disease. The compositions may be
CC used to promote the healing of both superficial and deep wounds,
CC including those which involve damage of the dermis, and is effective both

CC in individuals with normal wound healing capacity, and in those in whom
CC healing is impaired (e.g., those with conditions such as diabetes,
CC infection, immunosuppression, malnutrition, and ischaemic blockage or
CC injury). The compositions may also be used to stimulate the healing of
CC eye tissue wounds, dental tissue wounds, oral cavity wounds, vascular and
CC dermal ulcers, burns, wounds associated with ischaemic injury, and skin
CC disorders such as psoriasis and epidermolysis bullosa. The KGF-2
CC compositions may additionally be used to increase the adherence of skin
CC grafts to a wound bed, to stimulate re-epithelialisation from the wound
CC bed, and to reduce the side effects of gut toxicity that result from
CC radiation, chemotherapy treatments or viral infections. The compositions
CC of the invention are stable over prolonged periods of storage, have
CC increased KGF-2 pharmacological activity and/or facilitate the
CC application or administration of KGF-2 in therapeutic regimens. The
CC present sequence represents a PCR primer used in the generation of
CC Escherichia coli codon-optimised DNA encoding the KGF-2 deletion mutant,
CC KGF-2 delta-33
XX
SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 CATCCACCTGCTGTGTGAC 20
|| |||||
Db 1 CAACCACTGCAGGTGAC 19
RESULT 11
ABQ83060
ID ABQ83060 standard; DNA; 20 BP.
XX ABQ83060;
AC ABQ83060;
XX 16-JAN-2003 (first entry)
XX KGF-2 delta-33s codon optimised PCR primer SEQ ID NO:97.
DE DE
XX Keratinocyte growth factor 2; KGF-2; fibroblast growth factor 12; FGF-12;
KW KGF-2 Delta28; inflammation; vulnery; dermatological;
KW pulmonary epithelial cell; mucositis; epidermolysis bullosa;
KW wound healing; PCR primer; ss.
XX Homo sapiens.
OS Synthetic.
XX WO200277155-A2.
PN 03-OCT-2002.
XX 04-JAN-2002; 2002WO-US000101.
PF 08-JAN-2001; 2001US-0259853P.
PR 26-APR-2001; 2001US-0286368P.
PR 09-NOV-2001; 2001US-0331168P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PU, Gentz RL;
XX WPI; 2003-018897/01.
XX Treating inflammation comprises administering Keratinocyte Growth Factor
PT -2delta28 to a patient.
XX Example 16; Page 356; 583pp; English.
XX The present invention describes a method for treating inflammation. The
CC method comprises administering keratinocyte growth factor 2 (KGF-2)
CC delta28 to a patient. Also described: (1) a method for stimulating the
CC growth of pulmonary epithelial cells; or (2) a method of preventing

CC mucositis, KGF-2 Delta28 has vulnerary and dermatological activities, and
 CC can be used in gene therapy. KGF-2 Delta28 is useful for treating
 CC inflammation, stimulating the growth of pulmonary epithelial cells or
 CC preventing mucositis. It can also be used for treating epidermolysis
 CC bullosa and for promoting wound healing. ABQ82994 to ABQ83130 and
 CC ABP54273 to ABP54311 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 49.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 27;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 CATCCACCTGCTGTGTGAC 20
 || ||||| |||||
 Db 1 CAACACCTGCAGGTGAC 19
 || ||||| |||||
 RESULT 12
 ADA95533
 ID ADA95533 standard; DNA; 20 BP.
 XX
 AC ADA95533;
 DT 20-NOV-2003 (first entry)
 XX
 DE E. coli keratinocyte growth factor 2 (KGF-2) mutant PCR primer #6.
 XX
 KW PCR; primer; ss; keratinocyte growth factor 2; KGF-2; epidermal cell;
 KW keratinocyte; wrinkle; aged skin; skin strength; epidermal thickening;
 KW scarring reduction; cosmetic surgery; epithelial cell; liver; pancreas;
 KW kidney; prostate; bladder; lung; oesophagus; wound healing; diabetes;
 KW ischaemic blockage; ischaemic injury; steroid; uraemia; malnutrition;
 KW vitamin deficiency; obesity; immunosuppression; radiation therapy;
 KW chemotherapy; anastomosis; ulcer; burn; mucositis;
 KW inflammatory bowel disease; inflammation; radiation-induced condition;
 KW viral hepatitis; liver failure; pancreatitis; lung damaging condition;
 KW renal failure.
 XX
 OS Escherichia coli.
 XX
 PN US2003077695-A1.
 XX
 XX 24-APR-2003.
 XX
 XX 01-JUL-1999; 99US-00345373.
 XX
 PR 14-FEB-1995; 95WO-US001790.
 PR 13-AUG-1996; 96US-0023852P.
 PR 28-FEB-1997; 97US-0039405P.
 PR 23-MAY-1997; 97US-00862432.
 PR 13-AUG-1997; 97US-0055561P.
 PR 13-AUG-1997; 97US-00910875.
 PR 13-FEB-1998; 98US-00023082.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
 PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
 XX
 XX WPI; 2003-596836/56.
 DR
 XX
 XX New Keratinocyte Growth Factor (KGF-2) polypeptides and polynucleotides,
 PT useful for treating or preventing mucositis or Crohn's disease, reducing
 PT scarring, or improving wound healing or skin strength.
 PT
 XX
 XX Example 16; Page 44; 195pp; English.
 PS
 XX The invention relates to Keratinocyte Growth Factor 2 (KGF-2)
 CC polypeptides and the polynucleotides encoding them. The KGF-2
 CC polypeptides are useful for stimulating the proliferation of epidermal
 CC cells (e.g. keratinocytes) to prevent or improve the appearance of

CC wrinkles or aged skin, improve skin strength, promote epidermal
 CC thickening, reduce scarring or improve healing after cosmetic surgery.
 CC The KGF-2 polypeptide is also useful for stimulating epithelial cells
 CC (e.g. epithelial cells of the liver, pancreas, kidney, prostate, bladder,
 CC lung or oesophagus) or promoting wound healing in a wound healing
 CC impaired individual (due to diabetes, ischaemic blockage or injury,
 CC steroids, non-steroid compounds, uraemia, malnutrition, vitamin
 CC deficiencies, obesity, infection, immunosuppression, radiation therapy or
 CC chemotherapy). The wound may be caused by surgery (e.g. colonic or
 CC gastrointestinal surgical procedures such as anastomosis), ulcers, burns,
 CC etc. The KGF-2 polypeptide is also useful for treating or preventing
 CC mucositis (e.g. oral, oesophageal, gastric or rectal), inflammatory bowel
 CC disease (e.g. ulcerative colitis or Crohn's disease), inflammation (e.g.
 CC psoriasis, eczema, dermatitis or arthritis), a radiation-induced
 CC condition (e.g. oral injury, pulmonary fibrosis, myelotoxicity), viral
 CC hepatitis, liver failure (caused by e.g. hepatitis, cirrhosis), lung
 CC pancreatitis, lung damaging conditions (e.g. emphysema, lung cancer,
 CC asthma), or renal failure. The polypeptide is further useful for
 CC promoting hair growth, treating tissue exposed to radiation (e.g.
 CC radiation for treating malignancy) or protecting tissue to be exposed to
 CC radiation, or promoting tissue growth or repair. This sequence represents
 CC a PCR primer used to amplify DNA encoding a KGF-2 polypeptide of the
 CC invention.
 XX
 XX Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 49.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 27;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 CATCCACCTGCTGTGTGAC 20
 || ||||| |||||
 Db 1 CAACACCTGCAGGTGAC 19
 || ||||| |||||
 RESULT 13
 ADD66206
 ID ADD66206 standard; DNA; 20 BP.
 XX
 AC ADD66206;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Codon optimised KGF-2delta33 PCR primer #1.
 XX
 KW Human; keratinocyte growth factor-2; KGF-2; ss; PCR;
 KW epidermal cell proliferation; epithelial cell proliferation;
 KW wound healing; colonic surgery; gastrointestinal surgery; mucositis;
 KW inflammatory bowel disease; inflammation; hair growth; radiation damage;
 KW tissue growth; female genital tract repair; urothelial healing;
 KW viral hepatitis; liver failure; pancreatitis; lung damaging condition;
 KW renal failure; primer; codon optimisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US2003129687-A1.
 XX
 XX 10-JUL-2003.
 PD
 XX
 XX 15-FEB-2002; 2002US-00075446.
 PF
 XX
 XX 14-FEB-1995; 95WO-US001790.
 PR 05-JUN-1995; 95US-00461195.
 PR 13-AUG-1996; 96US-0023852P.
 PR 28-FEB-1997; 97US-0039405P.
 PR 13-AUG-1997; 97US-0055561P.
 PR 13-AUG-1997; 97US-00910875.
 PR 13-FEB-1998; 98US-00023082.
 PR 01-JUL-1999; 99US-00345373.
 XX
 XX (RUBE/) RUBEN S M.
 PA (JIME/) JIMENEZ P.

PA (DUAN//) DUAN D R.
 PA (RAMP//) RAMPY M A.
 PA (MEND//) MENDRICK D.
 PA (ZHAN//) ZHANG J.
 PA (NIJJ//) NI J.
 PA (MOOR//) MOORE P A.
 PA (COLE//) COLEMAN T A.
 PA (GRUB//) GRUBER J R.
 PA (DILL//) DILLON P J.
 PA (GENT//) GENTZ R L.
 XX
 XX Ruben SM, Jimenez P, Duan DR, Rampy MA, Mendrick D, Zhang J;
 PI Ni J, Moore PA, Coleman TA, Gruber JR, Dillon PJ, Gentz RL;
 XX WPI; 2003-829563/77.
 XX
 XX New Keratinocyte Growth Factor-2 (KGF-2) polypeptide, useful for
 PT preparing a composition for reducing inflammation, promoting wound
 PT healing, hair growth, or treating or preventing liver or renal failure or
 PT pancreatitis.
 XX
 XX Example 16; SEQ ID NO 97; 183pp; English.
 XX
 XX The invention relates to an isolated polypeptide comprising a sequence
 CC having 95% identity with amino acid residues 138(Gly)-208(Ser), 123(Val)-
 CC 208(Ser), 104(Glu)-208(Ser), 77(Val)-208(Ser), 69(Ser)-208(Ser), 63(Ala)-
 CC 208(Ser), 37(Cys)-208(Ser), 36(Thr)-208(Ser), 2(Trp)-208(Ser), 63(Ala)-
 CC 153(Lys), 36(Thr)-153(Lys) or 138(Gly)-208(Ser) of human keratin growth
 CC factor-2 (KGF-2) appearing as ADB6111. Also included are an isolated
 CC polynucleotide encoding the polypeptide, a method of making a recombinant
 CC vector, a method of making a recombinant host cell, a recombinant host
 CC cell, a recombinant vector, a method of producing the polypeptide, a
 CC method of stimulating proliferation of epidermal cells, a method of
 CC stimulating proliferation of epithelial cells, a method of promoting
 CC wound healing, a method of treating wounds caused by a colonic or
 CC gastrointestinal surgical procedure, a method of treating or preventing
 CC mucositis, a method of treating inflammatory bowel disease, a method of
 CC reducing inflammation, a method of promoting hair growth, a method of
 CC treating tissue exposed to radiation or protecting tissue to be exposed
 CC to radiation, a method of promoting tissue growth or repair in the female
 CC genital tract, a method of promoting uterine healing, a method of
 CC treating or preventing viral hepatitis, liver failure, pancreatitis, lung
 CC damaging condition or renal failure. The polypeptide is useful for
 CC preparing a composition for reducing inflammation, promoting wound or
 CC uterine healing, hair growth, tissue growth or repair in the female
 CC genital tract, treating tissue exposed to radiation or protecting tissue
 CC to be exposed to radiation, or treating or preventing viral hepatitis,
 CC liver or renal failure, pancreatitis or lung damaging condition. The
 CC present sequence is a PCR primer used for creating a codon optimised and
 CC deleted (and also mutated) version of a KGF-2 coding sequence, for
 CC expression in E. coli.
 XX
 XX Seq Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 49.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 27;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 CATCCACCTGCTGTGTGAC 20
 Db 1 CAACCACTGCAGGTGAC 19
 RESULT 14
 ADO50763/c
 ID ADO50763 standard; DNA; 20 BP.
 XX
 XX ADO50763;
 XX
 XX 15-JUL-2004 (first entry)
 DT
 XX Human peroxiredoxin II (Prx II) antisense oligonucleotide SeqID10.
 DE
 XX

KW peroxiredoxin II; Prx II; antisense sequence; cancer chemotherapy;
 XX anti-oxidase; anticancer agent; cancer cell; ss; human.
 XX Homo sapiens.
 OS
 XX KR2002069392-A.
 PN
 XX 04-SEP-2002.
 PD
 XX 26-FEB-2001; 2001KR-00009637.
 PF
 XX 26-FEB-2001; 2001KR-00009637.
 PR
 XX (PHAR-) PHARMGENIA CO LTD.
 PA
 XX Kim HJ, Park JG;
 PI
 XX WPI; 2003-338914/32.
 DR
 XX Human peroxiredoxin ii antisense sequence and the use thereof.
 PT
 XX
 XX Claim 3; SEQ ID NO 10; 1pp; Korean.
 PS
 XX This invention relates to the novel use of a human peroxiredoxin II (Prx
 CC II) antisense sequence and its use for cancer chemotherapy. The human
 CC peroxiredoxin II has anti-oxidase activity. The human Prx II antisense
 CC sequence or its mutant contains complementary nucleotide sequence to Prx
 CC II coding gene and suppresses the expression of Prx II. It increases the
 CC sensitivity of an anticancer agent to cancer cells, therefore it can be
 CC used as a cancer chemotherapy agent to promote an anticancer agent to
 CC kill cancer cells more effectively. The present sequence is that of an
 CC antisense oligonucleotide which was targeted to the human peroxiredoxin
 CC II (Prx II) gene and which was used in the method of the invention.
 XX
 XX Seq Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 49.0%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 27;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 CATCCACCTGCTGTGTGAC 20
 Db 19 CATCCCCCTGCTGTGTGAC 1
 RESULT 15
 ADT98004
 ID ADT98004 standard; DNA; 20 BP.
 XX
 XX ADT98004;
 AC
 XX 16-DEC-2004 (first entry)
 DT
 XX Human keratinocyte growth factor-related oligonucleotide SeqID94.
 DE
 XX lung epithelial cell; cell proliferation stimulation; hyperkeratosis;
 KW buccal mucosa; tongue; oesophagus; keratinocyte growth factor; KGF-2;
 KW keratolytic; respiratory-Gen; lung disease; lung damage; emphysema;
 KW inhalation injury; hyaline membrane disease;
 KW infant respiratory distress syndrome; bronchiopulmonary dysplasia;
 KW lung fibrosis; ss; human.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 OS
 XX AU2003236478-A1.
 PN
 XX 18-SEP-2003.
 PD
 XX 26-AUG-2003; 2003AU-00236478.
 PF
 XX 26-AUG-2003; 2003AU-00236478.
 PR
 XX

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PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rumpy M, Jimenez P, Louie A, Russell D, Mendrick D;
XX WPI; 2004-662619/65.
XX
XX Stimulating (M1) proliferation of lung epithelial cells, or inducing
XX hyperkeratosis of the buccal mucosa, tongue and esophagus, by
XX administering to individual polypeptide having specific amino acid
XX residues of keratinocyte growth factor.
XX
XX Example 14; SEQ ID NO 97; 330pp; English.
XX
XX This invention relates to a novel method of stimulating proliferation of
XX lung epithelial cells, or inducing hyperkeratosis of the buccal mucosa,
XX tongue and esophagus. The method involves administering to an individual
XX a polypeptide comprising an amino acid sequence having amino acid
XX residues Arg(80)-Ser(208), Val(77)-Ser(208), Cys(37)-Ser(208), Thr(36)-
XX Ser(208) or Met(1)-Ser(208) of fully defined sequence of keratinocyte
XX growth factor (KGF-2) having 208 amino acids as given in specification.
XX The invention may be useful for the production of compounds with a
XX keratolytic or respiratory-gen activity. The method is useful for
XX stimulating proliferation of lung epithelial cells, or inducing
XX hyperkeratosis of the buccal mucosa, tongue and esophagus, where the
XX polypeptide is administered to treat or prevent lung diseases or lung
XX damage. The lung disease is acute or chronic lung disease, emphysema,
XX inhalation injuries, hyaline membrane disease, infant respiratory
XX distress syndrome or bronchiopulmonary dysplasia. The lung damage is
XX caused by lung fibrosis. The method enables stimulation of proliferation
XX of lung epithelial cells, or induction of hyperkeratosis of the buccal
XX mucosa, tongue and esophagus. The present sequence is that of an
XX oligonucleotide which was used in the exemplification of the invention.
XX
XX Sequence 20 BP; 5 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 27;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACACCTGCAGGTGAC 19
RESULT 16
ADP09253
ID ADP09253 standard; DNA; 17 BP.
AC ADP09253;
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Extend primer 48 used to genotype human chromogranin B polymorphism.
DE
XX
XX breast cancer; cytostatic; gene therapy; human; chromogranin B; CHGB;
KW secretogranin 1; SCG1; chromosome 20pter-p12; ss; PCR; primer; SNP;
KW single nucleotide polymorphism.
OS
XX
XX Homo sapiens.
XX
XX WO2004047767-A2.
FN
XX
XX 10-JUN-2004.
PD
XX
XX 25-NOV-2003; 2003WO-US037966.
PF
XX
XX 25-NOV-2002; 2002US-0429136P.
PR
XX
XX 24-JUL-2003; 2003US-0490234P.
XX
XX (SEQU-) SEQUENOM INC.
PA
XX
XX Roth RB, Nelson MR, Braun A, Kammerer SM, Reneland R;
XX

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DR WPI; 2004-441082/41.
XX
XX Identifying a subject at risk of breast cancer by detecting the presence
XX or absence of one or more nucleotide polymorphic variations, useful for
XX diagnosing, preventing and/or treating breast cancer.
XX
XX Example 5; Page 102; 286pp; English.
XX
XX The invention relates to a novel method for identifying a subject at risk
XX of breast cancer which comprises detecting the presence or absence of one
XX or more polymorphic variations associated with breast cancer in a nucleic
XX acid sample from a subject. The method of the invention has cytostatic
XX applications and may be useful for identifying a risk of breast cancer,
XX as well as therapeutic and prophylactic treatments that specifically
XX target breast cancer, such as gene therapy. The current sequence is that
XX of an extend primer of the invention which was used to genotype single
XX nucleotide polymorphisms within human chromogranin B (CHGB;secretogranin
XX 1;SCG1) DNA which is located at chromosomal position 20pter-p12.
XX
XX Sequence 17 BP; 3 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 47.6%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CATCCACCTGCTGTGTG 18
Db 1 CATGCACCACTGTGTG 17
RESULT 17
ADZ20529
ID ADZ20529 standard; DNA; 18 BP.
XX
XX ADZ20529;
XX
XX 30-JUN-2005 (first entry)
DT
XX
XX Mouse G alpha-15 tail oligonucleotide SEQ ID NO:3.
DE
XX
XX guanine nucleotide binding protein alpha 15; G alpha-15 protein;
KW G protein coupled receptor modulator; ss.
KW Mus musculus.
XX
XX US2005085625-A1.
XX
XX 21-APR-2005.
PD
XX
XX 16-DEC-2002; 2002US-00319821.
PF
XX
XX 30-OCT-2000; 2000US-0243770P.
PR
XX
XX 29-OCT-2001; 2001US-00984292.
PR
XX
XX 21-NOV-2001; 2001US-00989497.
PR
XX
XX 14-DEC-2001; 2001US-0339466P.
XX
XX (SENO-) SENOMYX INC.
PA
XX
XX Li X, Xu H, Staszewski L, Adler JE;
XX
XX WPI; 2005-305201/31.
XX
XX New isolated chimeric G alpha 15 variant protein, useful for analyzing
XX and discovering modulators of G-protein coupled receptors.
XX
XX Example 1; SEQ ID NO 3; 15pp; English.
XX
XX The invention relates to an isolated variant of a guanine nucleotide
XX binding protein alpha 15 (G alpha-15) protein (I) that exhibits increased
XX coupling to a given G-protein coupled receptor (GPCR) relative to the
XX native G alpha-15 protein and/or which couples to a particular GPCR not
XX normally coupled by the native G alpha-15 protein. Specifically claimed
XX is an isolated G alpha-15 variant protein (I) that has greater than 95 %

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CC amino acid sequence identity to the 374 amino acid sequence of ADZ20528,
 CC where the 5 carboxy-terminal codons are identical to the 5 carboxy-
 CC terminal codons of another G protein, e.g. G alpha-11, G alpha-q, G
 CC alpha-s, G alpha-13, G alpha-z, G alpha-o, G alpha-13, or G alpha-
 CC 14. Also described: (1) an isolated nucleic acid sequence encoding (1)
 CC including a nucleic acid encoding a polypeptide with greater than 80%,
 CC 90%, or 95% amino acid sequence identity to ADZ20528, where the last six
 CC codons are contained in any of ADZ20530-ADZ20538; (2) an antibody that
 CC selectively binds to (1), but not to the native G alpha-15 alpha protein;
 CC (3) an expression vector encoding (1), the vector including the nucleic
 CC acid sequence of (1) operably linked to a promoter that functions in
 CC mammalian cells or Xenopus oocytes; (4) a method for identifying a
 CC compound that modulates GPCR signaling; and (5) a method for producing a
 CC functional umami taste receptor or sweet taste receptor including
 CC producing a cell expressing (1) and T1R1/T1R3. The variants and methods
 CC are useful for analyzing and discovering modulators of G-protein coupled
 CC receptors. The present sequence represents the wild type mouse G alpha-15
 CC tail nucleotide sequence, which is given in an example from the present
 CC invention for the construction of G 15 chimeras.
 XX
 SQ Sequence 18 BP; 5 A; 5 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 46.2%; Score 13.4; DB 1; Length 18;
 Best Local Similarity 93.3%; Pred. No. 34;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACTGCTGTG 16
 |||||
 DB 3 CATCACTGCTGTG 17

RESULT 18
 AAZ72126/c
 ID AAZ72126 standard; DNA; 19 BP.
 XX AAZ72126;
 AC
 XX 10-SEP-2001 (first entry)
 DT
 XX
 DE Human biallelic marker upstream amplification primer SEQ ID NO:6482.

XX Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.

XX Homo sapiens.
 XX WO9954500-A2.
 XX
 XX 28-OCT-1999.
 PD

XX 21-APR-1999; 99WO-IB000822.

XX 21-APR-1998; 98US-0082614P.

XX 23-NOV-1998; 98US-0109732P.

XX (GEST) GENSET.

XX Cohen D, Blumenfeld M, Chumakov I;

XX WPI; 2000-013267/01.

XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.

XX Claim 9; Page 1613; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ65654 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention

XX Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 46.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 37;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGA 19
 |||||
 DB 19 CCGCCTGCTGTGTGA 5

RESULT 19
 ADV60526
 ID ADV60526 standard; DNA; 19 BP.
 XX
 AC ADV60526;
 XX

DT 24-FEB-2005 (first entry)

XX siRNA-9 used to inhibit human BAMBI expression Seq 5.

XX ss; antibody engineering;
 KW bone morphogenetic protein and activin brave bound inhibitor; BAMBI;
 KW colon cancer; liver cancer; antisense therapy; cytostatic; siRNA;
 KW RNA interference; small interfering RNA.

XX Synthetic.

XX WO2004106515-A1.

XX 09-DEC-2004.

XX 27-MAY-2004; 2004WO-JP007677.

XX 28-MAY-2003; 2003JP-00151302.

XX (SCIM-) SCIMEDIA LTD.

XX (AKIY/) AKIYAMA T.

XX Akiyama T, Sekiya T, Ohwada S;

XX WPI; 2005-021288/02.

XX Novel anti-bone morphogenetic protein and activin brave bound inhibitor
 PT antibody, useful as colon cancer or liver cancer diagnostic agent and
 PT therapeutic agent.

XX Claim 12; SEQ ID NO 5; 52pp; Japanese.

XX This invention relates to a novel antibody, namely the anti-bone
 CC morphogenetic protein and activin brave bound inhibitor (BAMBI) antibody.
 CC Specifically, it refers to a preparation of a monoclonal antibody that
 CC can be used as a colon cancer or liver cancer diagnostic agent. The
 CC present invention describes a diagnostic containing a primer or a probe
 CC that can detect the BAMBI gene. Furthermore, it provides a remedy for
 CC colon or liver cancer that comprises transformation with a vector in
 CC order to introduce nucleic acids that can be used in antisense therapy
 CC and the formation of BAMBI dsRNA. As such, these compositions exhibit
 CC cytostatic activity. This oligonucleotide sequence is an siRNA sequence
 CC used to inhibit BAMBI expression, given in an exemplification of the
 CC invention.

XX SQ Sequence 19 BP; 2 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 46.2%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 37;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTG 23
 Db 1 CTGCTGTGTGACCTG 15

RESULT 20
 AAZ44771/c
 ID AAZ44771 standard; DNA; 18 BP.
 XX AC AAZ44771;
 XX AC (first entry)
 XX DE Human FADD primer ISIS #23871.
 XX FADD; human; antisense; inhibitor; Fas-associated death domain; primer;
 XX probe; ss.
 XX OS Homo sapiens.
 XX FN US6015712-A.
 XX PD 18-JAN-2000.
 XX PF 19-JUL-1999; 99US-00357072.
 XX PR 19-JUL-1999; 99US-00357072.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Monia BP, Cowser LM, Baker BF, Zhang H;
 XX WPI; 2000-126316/11.
 XX Antisense oligonucleotides, useful for inhibiting human Fas-associated
 PT death domain (FADD) expression are targeted to the 3' untranslated region
 PT of the FADD gene.
 XX Example 16; Col 53-54; 37pp; English.

XX This invention describes novel antisense oligonucleotides (OGNs) (I) 8-20
 CC nucleotides in length that specifically hybridize with and inhibit
 CC nucleic acids encoding human Fas-associated death domain (FADD), targeted
 CC to the 3' untranslated region (3'UTR). (I) can be used to treat animals,
 CC especially humans, suspected of having or being prone to a disease or
 CC condition associated with FADD expression. AAZ44746-244831 represent
 CC primers and probes used in the method of the invention

XX SQ Sequence 18 BP; 5 A; 7 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 45.5%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCTGGTA 26
 Db 18 CTGGTGGCTGACCTGGTA 1

RESULT 21
 AAS99971
 ID AAS99971 standard; DNA; 15 BP.
 XX AC AAS99971;
 XX 12-MAR-2002 (first entry)

XX DE Human NPR1 gene allele-specific oligonucleotide probe #13.
 XX Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
 KW atrionatriuretic peptide receptor A; haplotyping; cytostatic; genotyping;
 KW haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
 KW drug screening; hypertension; hypotensive; sequencing primer; probe.
 XX OS Homo sapiens.
 XX PN WO200179231-A2.
 XX PD 25-OCT-2001.
 XX PF 16-APR-2001; 2001WO-US012300.
 XX PR 14-APR-2000; 2000US-0197330P.
 XX PA (GENA-) GENAISANCE PHARM INC.
 XX PI Bentivegna SC, Choi JY, Kliem SE, Nandabalan K;
 XX WPI; 2002-066340/09.
 XX Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
 PT an individual, involves determining identity of nucleotide pair at
 PT specific polymorphic sites for two copies of the gene.
 XX Claim 15; Page 14; 96pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human natriuretic peptide receptor A/guanylate cyclase A
 CC (atrionatriuretic peptide receptor A) or NPR1 polypeptide. A method for
 CC haplotyping the NPR1 gene in an individual comprises identifying the
 CC nucleotide at one or more polymorphic sites and determining whether one
 CC of the copies of the gene is defined by one of the NPR1 haplotypes given
 CC in the specification or whether both copies are defined by a haplotype
 CC pair. This method is useful in genotyping, whereby all possible haplotype
 CC pairs can be assigned to specific genotypes. An association between a
 CC trait and a haplotype or haplotype pair of the NPR1 gene can be
 CC identified by comparing the frequency of the haplotype or haplotype pair
 CC in a population exhibiting the trait with the frequency of the haplotype
 CC or haplotype pair in a reference population, where a higher haplotype
 CC frequency in the trait population indicates the trait is associated with
 CC the haplotype or haplotype pair. NPR1 and its corresponding DNA are used
 CC for studying the expression and function of NPR1, for use in screening
 CC for candidate drugs to treat diseases related to NPR1 activity, such as
 CC hypertension. The sequences are also useful for studying the effect of
 CC variation on the biological activity of NPR1 as well as on the binding
 CC affinity of candidate drugs targeting NPR1. Sequences AAS99959-AAS99990
 CC and ABK09390-ABK09462 represent probes, sequencing primers and PCR
 CC primers used to detect NPR1 gene polymorphisms

XX SQ Sequence 15 BP; 2 A; 4 C; 3 G; 5 T; 0 U; 1 Other;

Query Match 44.8%; Score 13; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 34;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTGTGACC 21
 Db 1 ACTTGCTGTGTGACC 15

RESULT 22
 AAT80089/c
 ID AAT80089 standard; cDNA; 17 BP.
 XX AC AAT80089;
 XX 21-NOV-1997 (first entry)
 XX Primer #1 for 4-coumaric acid coenzyme A ligase gene.

XX	14-coumaric acid coenzyme A ligase; 4CL gene; tobacco; Nicotiana tabacum;	XX	(AEOM-) AEOMICA INC.
KW	lignin; polymerase chain reaction; primer; amplify; PCR; ss.	XX	Shannon M;
XX	Synthetic.	PI	
OS		XX	WPI; 2002-684061/74.
XX		DR	
PN	JP09173069-A.	XX	Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
XX		PT	-1, useful for treating disorders associated with decreased expression or
XX		PT	activity of human POSHL1.
XX		XX	Example 2; SEQ ID NO 1639; 60pp + Sequence Listing; English.
XX		PS	
XX		XX	The invention relates to an isolated SH3 domain (POSH)-like signalling
XX		CC	protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX		CC	acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
XX		CC	(S1) having 95% deviations, especially conservative substitutions or a
XX		CC	fragment of the sequences comprising at least 8 contiguous amino acids.
XX		CC	Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX		CC	adaptor protein that interacts with Rho family small GTPases as well as
XX		CC	downstream components of the signal transduction pathway. (I) is useful
XX		CC	for identifying a specific binding partner. (II) and nucleic acids (II)
XX		CC	encoding (I) are useful for diagnosing, monitoring disease and treating
XX		CC	caused by altered expression of human POSHL1 including diagnosing and
XX		CC	treating cancer, they useful in the development of vaccines and (II) is
XX		CC	useful in gene therapy. (II) is useful for constructing microarrays which
XX		CC	are useful for measuring and for surveying gene expression and creating
XX		CC	transgenic non-human animals capable of producing the proteins. The
XX		CC	present sequence is that of a scanning oligonucleotide useful in examples
XX		CC	of the invention. Note: The present sequence did not form part of the
XX		CC	printed specification, but is based on sequence information supplied to
XX		CC	Derwent by the European Patent Office
XX		XX	Sequence 17 BP; 2 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
SQ			
Query Match 44.1%; Score 12.8; DB 1; Length 17;			
Best Local Similarity 87.5%; Pred. No. 42;			
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
OY	1 CCATCCACCTGCTGTG 16	OY	3 ATCCACCTGCTGTG 18
Db	: : : : : :	Db	: : : :
	17 CCRTCNACVGTGTG 2		1 ATCCACCTGCTGTG 16
RESULT 23			
ABV90926		ABV90925	
ID	ABV90926 standard; DNA; 17 BP.	ID	ABV90925 standard; DNA; 17 BP.
XX		XX	
AC	ABV90926;	AC	ABV90925;
XX		XX	
DT	23-DEC-2002 (first entry)	DT	23-DEC-2002 (first entry)
XX		XX	
DE	Human POSHL1 scanning oligonucleotide SEQ ID NO 1639.	DE	Human POSHL1 scanning oligonucleotide SEQ ID NO 1638.
XX		XX	
KW	Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;	KW	Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW	Rho GTPase; signal transduction; Gene expression; cancer; vaccine;	KW	Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW	gene therapy; transgenic; ss.	KW	gene therapy; transgenic; ss.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
PN	EP1239051-A2.	PN	EP1239051-A2.
XX		XX	
PD	11-SEP-2002.	PD	11-SEP-2002.
XX		XX	
XX		XX	
PF	28-JAN-2002; 2002EP-00001165.	PF	28-JAN-2002; 2002EP-00001165.
XX		XX	
XX		XX	
PR	30-JAN-2001; 2001WO-US000663.	PR	30-JAN-2001; 2001WO-US000663.
PR	30-JAN-2001; 2001WO-US000664.	PR	30-JAN-2001; 2001WO-US000664.
PR	30-JAN-2001; 2001WO-US000665.	PR	30-JAN-2001; 2001WO-US000665.
PR	30-JAN-2001; 2001WO-US000666.	PR	30-JAN-2001; 2001WO-US000666.
PR	30-JAN-2001; 2001WO-US000667.	PR	30-JAN-2001; 2001WO-US000667.
PR	30-JAN-2001; 2001WO-US000668.	PR	30-JAN-2001; 2001WO-US000668.
PR	30-JAN-2001; 2001WO-US000669.	PR	30-JAN-2001; 2001WO-US000669.
PR	30-JAN-2001; 2001WO-US000670.	PR	30-JAN-2001; 2001WO-US000670.
PR	23-MAY-2001; 2001US-00864761.	PR	30-JAN-2001; 2001WO-US000669.
PR	10-OCT-2001; 2001US-0328205P.	PR	30-JAN-2001; 2001WO-US000669.

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PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX PI
XX XX
XX WPI; 2002-684061/74..
XX
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX
XX Example 2; SEQ ID NO 1638; 60pp + Sequence Listing; English.
XX
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (III) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX
XX SQ Sequence 17 BP; 2 A; 7 C; 2 G; 6 T; 0 U; 0 Other;
Query Match 44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ATCCACCTGCTGTGTG 18
Db 2 ATCCACCTCTCTGTG 17
RESULT 25
AAT96932/c
ID AAT96932 standard; DNA; 18 BP.
XX
XX AAT96932;
AC
XX
XX 27-APR-1998 (first entry)
DT
XX
XX Human pRB2/p130 tumour suppressor gene intron 17/exon 18 boundary.
XX
XX Retinoblastoma susceptibility gene; pRB2; p130; pRB2/130 gene;
KW cell cycle; tumour suppressor gene; cancer; molecular marker; diagnosis;
KW prognosis; predisposition; endometrial carcinoma; ovary cancer;
KW lung squamous cell carcinoma; lung adenocarcinoma; human; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH intron 1..9
FT /*tag= a
FT /note= "3", end of 1079 bp intron 17"
FT 10..18
FT /*tag= b
FT /note= "5", end of 72 bp exon 18"
XX
XX WO9738125-A1.
PN
```

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11-APR-1997.
XX
XX 03-APR-1997; 97WO-US005598.
XX
XX 05-APR-1996; 96US-0014943P.
PR 05-JUN-1996; 96US-0019172P.
PR 21-JUN-1996; 96US-0020196P.
PR 03-MAR-1997; 97US-0039532P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Giordano A, Baldi A;
XX
XX WPI; 1997-512731/47.
XX
XX Tumour suppressor pRB2/p130 gene intron and promoter sequences - used for
PT the diagnosis and prognosis of cancer and predicting pre-disposition to
PT cancer.
XX
XX Example 5; Page 64; 169pp; English.
XX
XX This DNA sequence comprises the boundary region between intron 17 and
CC exon 18 of the human pRB2/p130 tumour suppressor gene. The gene was
CC isolated from a human P1 genomic library by PCR amplification (see
CC AAT96897-98). It contains 22 exons and 21 introns. Exon/intron boundaries
CC (see AAT96899-940) were identified by comparison of the genomic DNA
CC sequence with a previously isolated cDNA sequence. The level of pRB2/p130
CC expression correlates with the presence of cancer, tumour grade, and
CC patient prognosis. Methods are provided for the diagnosis and prognosis
CC of cancer and for prediction of predisposition to cancer, particularly
CC of endometrial carcinoma, ovarian cancer, a squamous cell carcinoma of the
CC lung, or adenocarcinoma of the lung (see AAT96831-96)
XX
XX SQ Sequence 18 BP; 6 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 TGTGTGACCTGGTAAA 28
Db 17 TTGTGACCTGGCAA 2
RESULT 26
AAX63330
ID AAX63330 standard; RNA; 18 BP.
XX
XX AAX63330;
AC
XX
XX 16-JUL-1999 (first entry)
DT
XX
XX Delta-9 desaturase hairpin ribozyme substrate SEQ ID NO:1205.
XX
XX Maize; corn; Zea mays; delta-9 desaturase; CBSS; target; substrate;
KW granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
XX Zea mays.
OS
XX
XX WO9710328-A2.
PN
XX
XX 20-MAR-1997.
PD
XX
XX 12-JUL-1996; 96WO-US011689.
PF
XX
XX 13-JUL-1995; 95US-0001135P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX (DOWC ) DOWELANCO.
PA
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XX Zwick MG, Edington BE, Mcswiggen JA, Merlo PAO, Guo L, Skokut TA;
PI Young SA, Folkerts O, Merlo DJ;
XX WPI; 1997-202224/18.
XX Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX Claim 40; Page 94; 155pp; English.
XX The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene,
CC preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX SQ Sequence 18 BP; 3 A; 6 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 5 CCACCTGCTGTGTGAC 20
Db 2 CCACCGAUGUUGAC 17
RESULT 27
ADW64053
ID ADW64053 standard; DNA; 15 BP.
XX AC ADW64053;
XX 07-APR-2005 (first entry)
XX Human superoxide dismutase 1 gene antisense oligo #130.
XX antimicrobial; antiinflammatory; cytostatic; antisense therapy;
KW superoxide dismutase; superoxide dismutase modulator; infection;
KW inflammation; tumor; ss; gene expression; 2'-MOE; 2'-MOE wings;
KW 2'-methoxyethyl; phosphorothioate.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..15
FT /*tag= b
FT /mod_base= OTHER
FT /note= "all internucleotide linkages are phosphorothioate
FT linkages. All C bases are 5-methylcytidine bases"
XX US2005019915-A1.
XX 27-JAN-2005.
XX 26-SEP-2003; 2003US-00672866.
XX 21-JUN-2001; 2001US-00888360.
XX 04-AUG-2003; 2003US-00633843.
XX (BENW/) BENNETT C F.
PA (DOBI/) DOBIE K W.
XX Bennett CF, Dobie KW;
PI

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XX WPI; 2005-100832/11.
XX New antisense compound which specifically hybridizes with and inhibits
PT the expression of human superoxide dismutase 1, soluble, useful for
PT treating diseases associated with expression of superoxide dismutase 1,
PT soluble.
XX Example 15; SEQ ID NO 142; 116pp; English.
XX The invention relates to an antisense compound 8-50 nucleobases in length
CC targeted to nucleobases 96-523 of a coding region of a nucleic acid
CC molecule encoding human superoxide dismutase 1, soluble comprising 874 bp
CC fully defined in the specification, where the compound specifically
CC hybridizes with and inhibits the expression of human superoxide dismutase
CC 1, soluble. The compound is useful for modulating of superoxide dismutase
CC 1, soluble expression or for treating diseases associated with expression
CC of superoxide dismutase 1, soluble. It can also be used to prevent or
CC delay infection, inflammation, or tumor formation. This sequence
CC corresponds to an antisense oligonucleotide targeted to the human
CC superoxide dismutase 1 gene for inhibition of gene expression.
XX SQ Sequence 15 BP; 3 A; 7 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 42.8%; Score 12.4; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 44;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CATCCACCTGCTGT 15
Db 1 CACCCACCTGCTGT 14
RESULT 28
ABN02182
ID ABN02182 standard; DNA; 17 BP.
XX AC ABN02182;
XX 29-MAY-2002 (first entry)
XX Human GMMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2174.
XX Human; genome-derived myosin-like protein 1; GMMLP-1; hGDMMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
OS WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX

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PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 2174; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 42.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 50;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 5 CCACCTGCTGTGTG 18
 DB 1 CCACCTGCTGTGTG 14
 RESULT 29
 ABN02180
 ID ABN02180 standard; DNA; 17 BP.
 XX
 AC ABN02180;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2172.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI WPI; 2002-179446/23.
 XX
 DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 2172; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 42.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 50;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 5 CCACCTGCTGTGTG 18
 DB 3 CCACCTGCTGTGTG 16
 RESULT 30
 ABN02179
 ID ABN02179 standard; DNA; 17 BP.
 XX
 AC ABN02179;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2171.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200192524-A2.
 XX

PD	06-DEC-2001.	Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2173.	XX
XX	25-MAY-2001; 2001WO-US016981.	Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;	XX
XX	26-MAY-2000; 2000US-0207456P.	muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;	KW
PR	21-SEP-2000; 2000US-0234687P.	skeletal muscle disorder; amplicon; screening; ss.	KW
PR	27-SEP-2000; 2000US-0236359P.	Homo sapiens.	XX
PR	04-OCT-2000; 2000GB-00024263.		XX
PR	30-JAN-2001; 2001WO-US000661.		XX
PR	30-JAN-2001; 2001WO-US000662.		XX
PR	30-JAN-2001; 2001WO-US000663.		XX
PR	30-JAN-2001; 2001WO-US000664.		XX
PR	30-JAN-2001; 2001WO-US000665.		XX
PR	30-JAN-2001; 2001WO-US000666.		XX
PR	30-JAN-2001; 2001WO-US000667.		XX
PR	30-JAN-2001; 2001WO-US000668.		XX
PR	30-JAN-2001; 2001WO-US000669.		XX
PR	05-FEB-2001; 2001US-0266860P.		XX
XX	(AEOM-) AEOMICA INC.		XX
PA			PA
PI	Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;		XX
XX	WPI; 2002-179446/23.		XX
DR			DR
XX			XX
PT	New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,		PT
PT	or as specific biomolecule capture probes for surface-enhanced laser		PT
PT	desorption ionization, comprises human myosin-like protein hGDMPLP-1.		PT
XX			XX
PS	Disclosure; SEQ ID NO 2171; 214pp; English.		PS
XX			XX
CC	The present invention describes a human genome-derived myosin-like		CC
CC	protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-		CC
CC	1 can be used in gene therapy and vaccine production. The hGDMPLP-1		CC
CC	nucleic acids can be used as probes to detect, characterize and quantify		CC
CC	hGDMPLP-1 nucleic acids in samples, as amplification substrates, to		CC
CC	provide initial substrates for the recombinant engineering of hGDMPLP-1		CC
CC	protein variants having desired phenotypic improvements, and for		CC
CC	expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be		CC
CC	used as immunogens to raise antibodies that specifically recognise hGDMPLP		CC
CC	-1 proteins, as standards in assays used to determine the concentration		CC
CC	and/or amount specifically of hGDMPLP proteins, as specific biomolecule		CC
CC	capture probes for surface-enhanced laser desorption ionisation, as		CC
CC	therapeutic supplement in patients having specific deficiency in hGDMPLP-1		CC
CC	production, and in vaccines or for replacement therapy. The		CC
CC	polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a		CC
CC	disorder associated with the expression of hGDMPLP-1, in particular heart		CC
CC	and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.		CC
CC	The present sequence represents an oligomer used in the screening of the		CC
CC	hGDMPLP-1 sequence in the exemplification of the present invention. N.B.		CC
CC	The sequence data for this patent did not form part of the printed		CC
CC	specification, but was obtained in electronic format directly from WIPO		CC
CC	at ftp.wipo.int/pub/published_pct_sequence		CC
XX			XX
SQ	Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;		SQ
	Query Match 42.8%; Score 12.4; DB 1; Length 17;		
	Best Local Similarity 92.9%; Pred. No. 50;		
	Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	5 CCACCTGCTGTGTG 18		QY
Db	4 CCACCTGCTGTGTG 17		Db
RESULT 31			
ABN02181			
ID	ABN02181 standard; DNA; 17 BP.		ID
XX			XX
AC	ABN02181;		AC
XX			XX
DT	29-MAY-2002 (first entry)		DT

```

Db      2 CCACCTGCTGTGAG 15
|||||
RESULT 32
ABT39421
ID  ABT39421 standard; DNA; 17 BP.
XX  AC
XX  ABT39421;
XX  DT
XX  12-JUN-2003 (first entry)
XX  Tumour suppression related human fukutin oligo SEQ ID No 5058.
DE  XX
XX  Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX  antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW  schizophrénia; protein chip; gene therapy; tumour suppression;
KW  human fukutin; ds.
XX  OS
XX  Homo sapiens.
XX  PN
XX  WO2003025175-A2.
XX  PD
XX  27-MAR-2003.
XX  PF
XX  17-SEP-2002; 2002WO-IB004208.
XX  PR
XX  17-SEP-2001; 2001FR-00011978.
XX  PA
XX  (MOLE-) MOLECULAR ENGINES LAB.
XX  PI
XX  Telerman A, Amson R, Tuijnder M;
XX  WPI; 2003-313353/30.
XX  DR
XX  New isolated nucleic acid, useful for treating viral diseases associated
XX  with tumors and cell degeneration, also related polypeptides, antibodies
XX  and transfected cells.
XX  FS
XX  Disclosure; Page 625; 720pp; French.
XX  CC
XX  The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX  given in the specification, a sequence containing at least 15 consecutive
XX  nucleotides from the 17 mer sequence, a sequence with, after optimal
XX  alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX  hybridizes to them under highly stringent conditions, or the complement
XX  of any of them, or the corresponding RNA. The novel isolated nucleic
XX  acids of the invention are useful as probes and primers for detecting,
XX  identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX  component of a gene chip, in vitro as (anti)sense reagents, and for
XX  production of recombinant polypeptides. Any of the nucleic acids,
XX  polypeptides, vectors containing the nucleic acids, cells containing the
XX  vector or antibodies directed against the polypeptides are useful for
XX  preparation of pharmaceuticals for prevention and/or treatment of viral
XX  diseases that are characterised by development of tumours or cell
XX  degeneration, specifically cancer but also Alzheimer's disease and
XX  schizophrénia. Analysis of the expression of the 17 mer nucleic acids in
XX  patient samples is useful for diagnosis and/or prognosis of these
XX  diseases. The polypeptides can also be used to generate antibodies, and
XX  both the polypeptide and antibodies are useful as components of protein
XX  chips. The nucleic acid sequences of the invention can be used in gene
XX  therapy. This polynucleotide sequence represents a tumour suppression
XX  related human fukutin oligonucleotide of the invention
XX  SQ
XX  Sequence 17 BP; 2 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 50;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTGT 15
|||||
Db      4 CATCCTCTGCTGT 17
|||||
RESULT 33
ABT39428
ID  ABT39428 standard; DNA; 17 BP.
XX  AC
XX  ABT39428;
XX  DT
XX  12-JUN-2003 (first entry)
XX  Tumour suppression related human fukutin oligo SEQ ID No 5065.
DE  XX
XX  Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX  antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW  schizophrénia; protein chip; gene therapy; tumour suppression;
KW  human fukutin; ds.
XX  OS
XX  Homo sapiens.
XX  PN
XX  WO2003025175-A2.
XX  PD
XX  27-MAR-2003.
XX  PF
XX  17-SEP-2002; 2002WO-IB004208.
XX  PR
XX  17-SEP-2001; 2001FR-00011978.
XX  PA
XX  (MOLE-) MOLECULAR ENGINES LAB.
XX  PI
XX  Telerman A, Amson R, Tuijnder M;
XX  WPI; 2003-313353/30.
XX  DR
XX  New isolated nucleic acid, useful for treating viral diseases associated
XX  with tumors and cell degeneration, also related polypeptides, antibodies
XX  and transfected cells.
XX  FS
XX  Disclosure; Page 626; 720pp; French.
XX  CC
XX  The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX  given in the specification, a sequence containing at least 15 consecutive
XX  nucleotides from the 17 mer sequence, a sequence with, after optimal
XX  alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX  hybridizes to them under highly stringent conditions, or the complement
XX  of any of them, or the corresponding RNA. The novel isolated nucleic
XX  acids of the invention are useful as probes and primers for detecting,
XX  identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX  component of a gene chip, in vitro as (anti)sense reagents, and for
XX  production of recombinant polypeptides. Any of the nucleic acids,
XX  polypeptides, vectors containing the nucleic acids, cells containing the
XX  vector or antibodies directed against the polypeptides are useful for
XX  preparation of pharmaceuticals for prevention and/or treatment of viral
XX  diseases that are characterised by development of tumours or cell
XX  degeneration, specifically cancer but also Alzheimer's disease and
XX  schizophrénia. Analysis of the expression of the 17 mer nucleic acids in
XX  patient samples is useful for diagnosis and/or prognosis of these
XX  diseases. The polypeptides can also be used to generate antibodies, and
XX  both the polypeptide and antibodies are useful as components of protein
XX  chips. The nucleic acid sequences of the invention can be used in gene
XX  therapy. This polynucleotide sequence represents a tumour suppression
XX  related human fukutin oligonucleotide of the invention
XX  SQ
XX  Sequence 17 BP; 2 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 50;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ATCCACCTGCTGTG 16
|||||
Db      2 ATCCACCTGCTTTG 15
|||||

```


RESULT 34
AD151118
ID AD151118 standard; DNA; 17 BP.
XX AC AD151118;
XX DT 15-APR-2004 (first entry)
XX DE Human tumour suppression/reversion-related DNA sequence SeqID3621.
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; viricide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX OS Homo sapiens.
XX PN W02003025177-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004523.
XX PR 17-SEP-2001; 2001FR-00011980.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WI: 2003-313354/30.
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
PS Disclosure; SEQ ID NO 3621; 30pp; French.
XX
XX This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, viricide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, identifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 50;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 ATCCACCTGCTGTG 16
|||||
Db 2 ATCCACCTGCTGTG 15

RESULT 35
ACN65269
ID ACN65269 standard; DNA; 17 BP.
XX AC ACN65269;
XX DT 02-DEC-2004 (first entry)
XX

DE Human GDMPLP-1 probe SEQ ID NO:2171.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
XX Homo sapiens.
XX OS
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
PR 25-MAY-2001; 2001US-0086610P.
XX
XX (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANY/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
PI WPI; 2004-533378/51.
XX
XX Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
XX Disclosure; SEQ ID NO 2171; 0pp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 98% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 50;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 5 CCACCTGCTGTG 18
|||||
Db 4 CCACCTGCTGTG 17

```
RESULT 36
ACN65270
ID ACN65270 standard; DNA; 17 BP.
XX
AC ACN65270;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPLP-1 probe SEQ ID NO:2172.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000861.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 30-JAN-2001; 2001WO-US000670.
XX
PR 05-FEB-2001; 2001US-0266860P.
XX
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
GU Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 2172; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63102
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 42.8%; Score 12.4; DB 1; Length 17;
```

```
Best Local Similarity 92.9%; Pred. No. 50;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTG 18
   |||||
Db 3 CCACCTGCTGTGAG 16

RESULT 37
ACN65272
ID ACN65272 standard; DNA; 17 BP.
XX
AC ACN65272;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human GDMPLP-1 probe SEQ ID NO:2174.
XX
KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
KW skeletal muscle function.
XX
OS Homo sapiens.
XX
PN US2004137589-A1.
XX
PD 15-JUL-2004.
XX
PF 26-NOV-2003; 2003US-00723361.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 21-SEP-2000; 2000US-0234687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PR 30-JAN-2001; 2001WO-US000661.
XX
PR 30-JAN-2001; 2001WO-US000662.
XX
PR 30-JAN-2001; 2001WO-US000663.
XX
PR 30-JAN-2001; 2001WO-US000664.
XX
PR 30-JAN-2001; 2001WO-US000665.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 30-JAN-2001; 2001WO-US000667.
XX
PR 30-JAN-2001; 2001WO-US000668.
XX
PR 30-JAN-2001; 2001WO-US000669.
XX
PR 05-FEB-2001; 2001US-0266860P.
XX
PR 25-MAY-2001; 2001US-00866108.
XX
PA (GUY/) GU Y.
PA (JIY/) JI Y.
PA (PENN/) PENN S G.
PA (HANZ/) HANZEL D K.
PA (RANK/) RANK D.
PA (CHEN/) CHEN W.
PA (SHAN/) SHANNON M E.
XX
GU Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
WPI; 2004-533378/51.
XX
PT Novel myosin-like protein-1, useful for treating or preventing disorder
PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
PT function.
XX
PS Disclosure; SEQ ID NO 2174; Opp; English.
XX
CC The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
```

CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102

SQ Sequence 17 BP; 3 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 42.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 50;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
 |||||
 Db 1 CCACCTGCTGTGAG 14

RESULT 38
 ACN65271
 ID ACN65271 standard; DNA; 17 BP.

AC ACN65271;

DT 02-DEC-2004 (first entry)

XX Human GDMLP-1 probe SEQ ID NO:2173.

XX Human; ss; probe; myosin-like protein-1; hGDMLP-1;
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
 KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX 15-JUN-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 05-FEB-2001; 2001US-0266860P.

XX 25-MAY-2001; 2001US-00866108.

XX (GUY/) GU Y.

XX (JIVY/) JI Y.

XX (PENW/) PENN S G.

XX (HANK/) HANZEL D K.

XX (RANK/) RANK D.

XX (CHEN/) CHEN W.

XX (SHAN/) SHANNON M E.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder

XX associated with decreased expression or activity of human genome-derived

XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle

XX function.

XX Disclosure; SEQ ID NO 2173; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63102

XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 42.8%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 50;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
 |||||
 Db 2 CCACCTGCTGTGAG 15

RESULT 39

ABV90927

XX ID ABV90927 standard; DNA; 17 BP.

XX AC ABV90927;

XX DT 23-DEC-2002 (first entry)

XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1640.

XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;

XX Rho GTPase; signal transduction; gene expression; cancer; vaccine;

XX gene therapy; transgenic; ss.

XX Homo sapiens.

XX EP1239051-A2.

XX 11-SEP-2002.

XX 28-JAN-2002; 2002EP-00001165.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 23-MAY-2001; 2001US-00864761.

XX 10-OCT-2001; 2001US-0328205P.

XX (AEOM-) AEOMICA INC.

XX Shannon M;

XX WPI; 2002-684061/74.

XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL

XX -1, useful for treating disorders associated with decreased expression or

XX activity of human POSHL1.

XX Example 2; SEQ ID NO 1640; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

XX protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

XX acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),

XX (S1) having 95% deviations, especially conservative substitutions or a

fragment of the sequences comprising at least 8 contiguous amino acids.
 Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnosing and treating cancer, they are useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office

XX
 SQ Sequence 17 BP; 1 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 42.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 55;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTGTGAC 20
 ||||| |||||
 Db 1 TCCACCTCCTCTGTGTC 17

RESULT 40
 ABV90929
 ID ABV90929 standard; DNA; 17 BP.
 XX
 AC ABV90929;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1642.
 XX
 KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1239051-A2.
 XX
 PD 11-SEP-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001165.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.
 XX
 PA (AEOM-) ABOMICA INC.
 XX
 PI Shannon M;
 XX
 DR WPI; 2002-684061/74.
 XX
 KW Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.
 XX
 PS Example 2; SEQ ID NO 1642; 60pp + Sequence Listing; English.
 XX
 KW The invention relates to an isolated SH3 domain (POSH)-like signalling

protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino acids (SI, ABBS3999), a sequence having 65% sequence identity to (SI), (SI) having 95% deviations, especially conservative substitutions or a fragment of the sequences comprising at least 8 contiguous amino acids. Human POSHL 1 is a proto-oncogene/oncogene product that functions as an adaptor protein that interacts with Rho family small GTPases as well as downstream components of the signal transduction pathway. (I) is useful for identifying a specific binding partner. (I) and nucleic acids (II) encoding (I) are useful for diagnosing, monitoring disease and treating caused by altered expression of human POSHL1 including diagnosing and treating cancer, they are useful in the development of vaccines and (II) is useful in gene therapy. (II) is useful for constructing microarrays which are useful for measuring and for surveying gene expression and creating transgenic non-human animals capable of producing the proteins. The present sequence is that of a scanning oligonucleotide useful in examples of the invention. Note: The present sequence did not form part of the printed specification, but is based on sequence information supplied to Derwent by the European Patent Office

XX
 SQ Sequence 17 BP; 1 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
 Query Match 42.1%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 55;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CACCTGCTGTGTGACCT 22
 ||||| |||||
 Db 1 CACCTCTCTGTGTCT 17

RESULT 41
 ABV90928
 ID ABV90928 standard; DNA; 17 BP.
 XX
 AC ABV90928;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1641.
 XX
 KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 KW gene therapy; transgenic; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1239051-A2.
 XX
 PD 11-SEP-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001165.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 23-MAY-2001; 2001US-00864761.
 PR 10-OCT-2001; 2001US-0328205P.
 XX
 PA (AEOM-) ABOMICA INC.
 XX
 PI Shannon M;
 XX
 DR WPI; 2002-684061/74.
 XX
 KW Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 PT -1, useful for treating disorders associated with decreased expression or
 PT activity of human POSHL1.
 XX

PS Example 2; SEQ ID NO 1641; 60pp + Sequence Listing; English.

XX The invention relates to an isolated SH3 domain (POSH)-like signalling

CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino

CC acids (SI, ABB83999), a sequence having 65% sequence identity to (SI),

CC (SI) having 95% deviations, especially conservative substitutions or a

CC fragment of the sequences comprising at least 8 contiguous amino acids.

CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an

CC adaptor protein that interacts with Rho family small GTPases as well as

CC downstream components of the signal transduction pathway. (I) is useful

CC for identifying a specific binding partner. (I) and nucleic acids (II)

CC encoded (I) are useful for diagnosing, monitoring disease and treating

CC caused by altered expression of human POSHL1 including diagnosing and

CC treating cancer, they are useful in the development of vaccines and (II) is

CC useful in gene therapy. (II) is useful for constructing microarrays which

CC are useful for measuring and for surveying gene expression and creating

CC transgenic non-human animals capable of producing the proteins. The

CC present sequence is that of a scanning oligonucleotide useful in examples

CC of the invention. Note: The present sequence did not form part of the

CC printed specification, but is based on sequence information supplied to

CC Derwent by the European Patent Office

XX

SQ Sequence 17 BP; 1 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 42.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 55;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CCACCTCTCTGTGACC 21

DB 1 CCACCTCTCTGTGTC 17

RESULT 42

ACN03462

ID ACN03462 standard; RNA; 17 BP.

XX

AC ACN03462;

XX

DT 22-APR-2004 (first entry)

DE WNV Zinzyme substrate SEQ ID NO 3465.

XX

XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;

KW virucide; neuroprotective; antibacterial; replication; pancreatitis;

KW encephalitis; myocarditis; meningitis; infection; hepatitis;

KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;

KW Amberzyme; Zinzyme; ss.

XX

OS West Nile Virus.

XX

PN WO200268637-A2.

XX

PD 06-SEP-2002.

XX

PF 19-OCT-2001; 2001WO-US048350.

XX

PR 20-OCT-2000; 2000US-0242411P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

XX

PI Blatt L, Mcswiggen JA;

XX

DR WPI; 2002-706994/76.

XX

PT New nucleic acid molecule that modulates replication of West Nile Virus

XX (WNV), useful for treating a condition related to WNV infection e.g.

PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX

PS Claim 23; SEQ ID NO 3465; 495pp; English.

XX

CC The invention relates to nucleic acid molecules that modulate replication

CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for

CC treating a condition related to WNV infection e.g. pancreatitis,

CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,

CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of

CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at

CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at

CC least three of the 5' terminal nucleotides and a 3' end modification of a

CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080

CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given

CC in the specification. The present sequence is that of a nucleic acid

CC molecule of the invention

XX

SQ Sequence 17 BP; 5 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 42.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 58.8%; Pred. No. 55;

Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTGTAAA 28

DB 1 CUGUGUGAGCUGACAAA 17

RESULT 43

ACA07683

ID ACA07683 standard; RNA; 17 BP.

XX

AC ACA07683;

XX

DT 03-JUN-2003 (first entry)

DE NFKB sub-unit modulating zinzyme substrate #82.

XX

XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;

KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;

KW lung cancer; prostate cancer; colorectal cancer; brain cancer;

KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;

KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;

KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;

KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;

KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;

KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;

KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;

KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;

KW transplant/graft rejection; reperfusion injury; glomerulonephritis;

KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX

OS Homo sapiens.

XX

PN US2002177568-A1.

XX

PD 28-NOV-2002.

XX

PF 23-MAY-2001; 2001US-00864785.

XX

PR 07-DEC-1992; 92US-00987132.

PR 18-MAY-1994; 94US-00245466.

PR 15-AUG-1994; 94US-00291932.

PR 23-DEC-1996; 96US-00777916.

XX

PA (STIN/) STINCHCOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

XX

PI Stinchcomb DT, Mcswiggen J, Draper KG;

XX

DR WPI; 2003-340953/32.

XX

PT Novel enzymatic nucleic acid molecules which down regulates expression of

XX a sequence encoding a subunit of nuclear factor kappa B useful for

treating cancer, inflammatory disorders and autoimmune diseases.

Claim 4; Page 38; 72pp; English.

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFkB), where (I) is an inozyme, zinyzyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg²⁺. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents the substrate of a novel enzymatic nucleic acid molecule

Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

very Match 42.18; Score 12.2; DB 1; Length 17;

Model	1st Local Similarity	Pred. No. 55;	Indels	Gaps
Conservative	10;	4;	3;	0;
Mismatches	10;	4;	3;	0;
Mismatches	10;	4;	3;	0;

QY 8 CCTGCTGTGTGACCTGG 24

Db 1 CCUACUGUGACAAAGG 17

RESULT 44

RESOLUTION
ACA08233

XX ACA08233:

03-JUN-2003 (first entry)

XX
DE Necrosis factor kappa B (NFkB) sub-unit modulating DNase #2.

Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
G-clavate; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;
prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;
pallitaxol; docetaxel; cisplatin; methotrexate; cyclophosphamide;
doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;
radiation therapy; inflammatory disease; asthma; diabetes;
rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
transplant/grat rejection; reperfusion injury; glomerulonephritis;
allergic airway inflammation; inflammatory bowel disease; infection; ss.

OS Synthetic.

AA
PN
US2002177568-A1.

28-NOV-2002.

23-MAY-2001: 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

18-MAY-1994; 94US-00245466.

15-AUG-1994; 94US-00291932.

23-DEC-1996; 96US-00777916.

(STIN/) STINCHCOMB D T.

(MCSW/) MCSWIGGEN J.

(DRAP/) DRAPER K G.

Stinchcomb DT, Mcswiggen J, Draper KG;

WPI; 2003-340953/32.

Novel enzymatic nucleic acid molecules which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B useful for treating cancer, inflammatory disorders and autoimmune diseases.

Claim 3: Page 44: 72pp: English:

The invention describes an enzymatic nucleic acid molecule (I) which down regulates expression of a sequence encoding a subunit of nuclear factor kappa B (NFkB), where (I) is an inozyme, zinozyme, G-cleaver or amberzyme configuration. The enzymatic nucleic acid molecule is adapted to treat cancer and is useful for down-regulating REL-A activity in a cell, for treating a patient having a condition associated with the level of REL-A. (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in the presence of a divalent cation, especially Mg²⁺. The enzymatic and antisense nucleic acid molecules are useful for treating breast, lung, prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic, cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or multidrug resistant cancer. The method involves use of other drug therapies such as monoclonal antibodies, REL-A-specific inhibitors or chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine or radiation therapy. The enzymatic and antisense nucleic acid molecules are also useful for treating inflammatory disease such as rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes, obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft rejection, gene therapy applications, ischaemia/reperfusion injury (central nervous system (CNS) and myocardial), glomerulonephritis, sepsis, allergic airway inflammation, inflammatory bowel disease or infection. This sequence represents an enzymatic nucleic acid used to modulate the function of a necrosis factor kappa B sub-unit

Sequence 17 BP: 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;

every Match 42.1%; Score 12.2; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 55;

Matches	9;	Conservative	5;	Mismatches	3;	Indels	0;	Gaps	0;
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3 ATCCACCTGCTGTGTGA 19

LT 45

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THE UNIVERSITY OF CHICAGO

Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon screening; ss.

Homo sapiens.

WO200192524-A2.

06-DEC-2001.

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XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX XX WPI; 2002-179446/23.
XX DR
XX PT New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
XX PT or as specific biomolecule capture probes for surface-enhanced laser
XX PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX XX
XX PS Disclosure; SEQ ID NO 2169; 214pp; English.
XX CC
XX CC The present invention describes a human genome-derived myosin-like
XX CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
XX CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
XX CC nucleic acids can be used as probes to detect, characterise and quantify
XX CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
XX CC provide initial substrates for the recombinant engineering of hGDMLP-1
XX CC protein variants having desired phenotypic improvements, and for
XX CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
XX CC used as immunogens to raise antibodies that specifically recognise hGDMLP
XX CC -1 proteins, as standards in assays used to determine the concentration
XX CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
XX CC capture probes for surface-enhanced laser desorption ionisation, as
XX CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
XX CC production, and in vaccines or for replacement therapy. The
XX CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
XX CC disorder associated with the expression of hGDMLP-1, in particular heart
XX CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
XX CC The present sequence represents an oligomer used in the screening of the
XX CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequence
XX SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 41.4%; Score 12; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CCACCTGCTGTG 16
Db 6 CCACCTGCTGTG 17
|||||
RESULT 46
ABN02178
ID ABN02178 standard; DNA; 17 BP.
XX AC ABN02178;
XX DT 29-MAY-2002 (first entry)
XX

```

Human GDMLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:2170.

Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart; muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease; skeletal muscle disorder; amplicon; screening; ss.

Homo sapiens.

WO200192524-A2.

06-DEC-2001.

25-MAY-2001; 2001WO-US016981.

26-MAY-2000; 2000US-0207456P.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.

04-OCT-2000; 2000GB-00024263.

30-JAN-2001; 2001WO-US000661.

30-JAN-2001; 2001WO-US000662.

30-JAN-2001; 2001WO-US000663.

30-JAN-2001; 2001WO-US000664.

30-JAN-2001; 2001WO-US000665.

30-JAN-2001; 2001WO-US000666.

30-JAN-2001; 2001WO-US000667.

30-JAN-2001; 2001WO-US000668.

30-JAN-2001; 2001WO-US000669.

30-JAN-2001; 2001WO-US000670.

05-FEB-2001; 2001US-0266860P.

(AEOM-) AEOMICA INC.

Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

WPI; 2002-179446/23.

New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins, or as specific biomolecule capture probes for surface-enhanced laser desorption ionization, comprises human myosin-like protein hGDMLP-1.

Disclosure; SEQ ID NO 2170; 214pp; English.

The present invention describes a human genome-derived myosin-like protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1 can be used in gene therapy and vaccine production. The hGDMLP-1 nucleic acids can be used as probes to detect, characterise and quantify hGDMLP-1 nucleic acids in samples, as amplification substrates, to provide initial substrates for the recombinant engineering of hGDMLP-1 protein variants having desired phenotypic improvements, and for expressing the proteins. The hGDMLP-1 proteins or polypeptides may be used as immunogens to raise antibodies that specifically recognise hGDMLP -1 proteins, as standards in assays used to determine the concentration and/or amount specifically of hGDMLP proteins, as specific biomolecule capture probes for surface-enhanced laser desorption ionisation, as therapeutic supplement in patients having specific deficiency in hGDMLP-1 production, and in vaccines or for replacement therapy. The polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a disorder associated with the expression of hGDMLP-1, in particular heart and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22. The present sequence represents an oligomer used in the screening of the hGDMLP-1 sequence in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence

Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CCACCTGCTGTG 16

|||||

6 CCACCTGCTGTG 17

|||||

Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 41.4%; Score 12; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CCACCTGCTGTG 16

|||||

```
Db          5 CCACCTGCTGTG 16

RESULT 47
ADB41885
ID ADB41885 standard; DNA; 17 BP.
XX
AC ADB41885;
XX
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2208.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
XX WO2003040369-A2.
XX
XX 15-MAY-2003.
XX
XX 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX
XX (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX
XX WPI; 2003-441574/41.
XX
XX New nucleic acid encoding human prostate membrane-specific antigen,
XX useful e.g. for treatment of tumors and viral infection, also related
XX polypeptide and antibodies.
XX
XX Disclosure; Page 290; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences,
XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX sequence having at least 80% identity, after optimal alignment, with the
XX nucleotides, a sequence that hybridizes under stringent conditions with
XX the nucleotides, or the complement, or corresponding RNA, of the
XX nucleotides. The nucleotides are used as probes or primers for detecting,
XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX sense and antisense sequences, of nucleotides involved in tumour
XX suppression or reversion, apoptosis and or viral resistance, to produce
XX recombinant polypeptides, and to prepare transgenic animals, as
XX experimental models. The nucleotides (also vectors containing them and
XX cells containing the vectors), the encoded polypeptides and antibodies
XX (Ab) against the polypeptide are useful for prevention and/or treatment
XX of viral infections or diseases characterized by development of tumours
XX or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX Analysis of the expression of the nucleotides can be used for diagnosis
XX and/or prognosis of these diseases. The nucleotides and polypeptides can
XX also be used to screen for their specific interactive molecules,
XX potentially useful for treating diseases associated with abnormal
XX expression of the nucleotides.
XX
XX Sequence 17 BP; 3 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CCATCCACCTGC 12
Db          4 CCATCCACCTGC 15

RESULT 48
ACCS1536
ID ACCS1536 standard; DNA; 17 BP.
XX
AC ACCS1536;
XX
XX 27-JUN-2003 (first entry)
DT
XX
DE Human tumour suppressor sequence #303.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
XX tumour regression; apoptosis; virus resistance; diagnosis;
XX cellular degeneration.
XX
XX Homo sapiens.
XX
XX FR2826373-A1.
XX
XX 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX
XX Tuijnder M, Telerman A, Amson R;
XX
XX WPI; 2003-250498/25.
XX
XX New nucleic acid sequences associated with tumor suppression, regression,
XX apoptosis or virus resistance are useful to diagnose and treat viral
XX disease, development of tumor cells and cell degeneration.
XX
XX Claim 1; Page 110; 798pp; French.
XX
XX This sequence represents an isolated nucleic acid sequence associated
XX with tumour suppression or regression, apoptosis or virus resistance. The
XX invention relates to these sequences or sequences having at least 80%
XX identity to them, and polypeptides encoded by the sequences or
XX polypeptides having 80% identity to the polypeptide sequences. The
XX invention is used to diagnose or treat viral disease or disease
XX characterized by development of tumour cells or cellular degeneration
XX
XX Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
XX
Query Match 41.4%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CCATCCACCTGC 12
Db          6 CCATCCACCTGC 17

RESULT 49
ACN65268
ID ACN65268 standard; DNA; 17 BP.
XX
XX ACN65268;
XX
XX 02-DEC-2004 (first entry)
DT
XX
DE Human GDMPLP-1 probe SEQ ID NO:2170.
XX
XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
XX hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
XX skeletal muscle function.
XX
XX Homo sapiens.
XX
XX US2004137589-A1.
XX
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PD 15-JUL-2004.
XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
PF KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 05-FEB-2001; 2001WO-US000670.
XX PR 25-MAY-2001; 2001US-0266860P.
XX PR 25-MAY-2001; 2001US-00866108.
XX PA (GUY/) GU Y.
XX PA (JIY/) JI Y.
XX PA (PENN/) PENN S G.
XX PA (HANZ/) HANZEL D K.
XX PA (RANK/) RANK D.
XX PA (CHEN/) CHEN W.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX PT Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX PS Disclosure; SEQ ID NO 2170; Opp; English.
XX CC The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63102
XX SQ Sequence 17 BP; 5 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
XX Query Match 41.4%; Score 12; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 5 CCACCTGCTGTG 16
XX Db 5 CCACCTGCTGTG 16
XX RESULT 50
XX ACN65267
XX ID ACN65267 standard; DNA; 17 BP.
XX AC ACN65267;
XX AC ACN65267;
XX DT 02-DEC-2004 (first entry)
XX DE Human GDMPLP-1 probe SEQ ID NO:2169.
XX XX

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KW KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
KW KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
XX KW skeletal muscle function.
XX OS Homo sapiens.
XX PN US2004137589-A1.
XX PD 15-JUL-2004.
XX PF 26-NOV-2003; 2003US-00723361.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 05-FEB-2001; 2001WO-US000670.
XX PR 25-MAY-2001; 2001US-0266860P.
XX PR 25-MAY-2001; 2001US-00866108.
XX PA (GUY/) GU Y.
XX PA (JIY/) JI Y.
XX PA (PENN/) PENN S G.
XX PA (HANZ/) HANZEL D K.
XX PA (RANK/) RANK D.
XX PA (CHEN/) CHEN W.
XX PA (SHAN/) SHANNON M E.
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
XX WPI; 2004-533378/51.
XX PT Novel myosin-like protein-1, useful for treating or preventing disorder
XX associated with decreased expression or activity of human genome-derived
XX myosin-like protein-1 such as disorder of heart and/or skeletal muscle
XX function.
XX PS Disclosure; SEQ ID NO 2169; Opp; English.
XX CC The invention relates to a novel polypeptide (I) comprising a sequence
XX (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
XX defined in the specification, a fragment of at least 8 amino acids of
XX (S1), 95% deviation from (S1) which are conservative substitutions, and
XX 65% identity to (S1). A polypeptide of the invention acts as an agonist or
XX antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
XX pharmaceutical composition of the invention is useful for treating or
XX preventing a disorder associated with decreased expression or activity of
XX hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
XX The present sequence represents a 17-mer nucleotide, used in the
XX invention for scanning the sequence represented in ACN63102
XX SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
XX Query Match 41.4%; Score 12; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 60;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 5 CCACCTGCTGTG 16
XX Db 6 CCACCTGCTGTG 17
XX RESULT 51
XX ADV35523/c

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ID ADV35523 standard; RNA; 15 BP.
XX
AC ADV35523;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human anti-HER2 NCH ribozyme substrate sequence #154.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX Homo sapiens.
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcsvigen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 7; Page 474; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,
XX zinzyme, and/or DNazyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present

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CC sequence represents a substrate/target sequence for an anti-HER2 NCH
CC ribozyme used in the examples of the present invention. Note: Some SEQ ID
CC Nos are repeated more than once in the specification, but these have
CC different sequences associated with them.
XX
SQ Sequence 15 BP; 3 A; 6 C; 4 G; 0 T; 2 U; 0 Other;
Query Match 40.7%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 57;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 CTGCTGTGTGACCTG 23
| | | | | | | | | |
Db 15 CTGCAGTGGGACCTG 1
RESULT 52
ADV35886
ID ADV35886 standard; RNA; 15 BP.
XX
AC ADV35886;
XX
XX 10-FEB-2005 (first entry)
XX
XX Human anti-HER2 NCH ribozyme substrate sequence #329.
XX
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
XX protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX ss.
XX Homo sapiens.
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX 27-SEP-1999; 99US-00406643.
XX 27-SEP-1999; 99US-0156236P.
XX 27-SEP-1999; 99US-0156467P.
XX 08-NOV-1999; 99US-00436430.
XX 06-DEC-1999; 99US-0169100P.
XX 29-DEC-1999; 99US-00474432.
XX 29-DEC-1999; 99US-0173612P.
XX 30-DEC-1999; 99US-00476387.
XX 04-FEB-2000; 2000US-00498824.
XX 20-MAR-2000; 2000US-00531025.
XX 14-APR-2000; 2000US-0197769P.
XX 23-MAY-2000; 2000US-00578223.
XX 09-AUG-2000; 2000US-00636385.
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcsvigen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpelsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 7; Page 478; 717pp; English.

```


Best Local Similarity 92.3%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCT 13
Db 1 CCATCCACCTACT 13

RESULT 55

ABA02592/c
ID ABA02592 standard; DNA; 15 BP.
XX
AC ABA02592;
XX
DT 05-FEB-2002 (first entry)
XX
DE HBV targeted ribozyme flanking sequence mlrZ-247.
XX
KW Infection; antisense RNA; ribozyme; DNazyme; antiviral; gene therapy;
KW papilloma virus; hepatitis B virus; cytotoxic; cytostatic; wart;
KW cervical dysplasia; cervical carcinoma; carcinoma; laryngeal papilloma;
KW ss.
XX
OS Unidentified.
XX
FN WO200179524-A2.
XX
PD 25-OCT-2001.
XX
PF 13-APR-2001; 2001WO-US012130.
XX
PR 13-APR-2000; 2000US-00548449.
PR 07-DEC-2000; 2000US-0251810P.
XX
PA (UYSC-) UNIV SOUTH CAROLINA.
PA (PENN-) PENN STATE RES FOUND.
XX
PI Norris JS, Clawson GA, Westwater C, Schofield D, Schmidt MG;
PI Hoel B, Dolan J, Pan W;
DR WPI; 2001-607700/69.
XX
PT Novel nucleic acid for the treatment of papilloma or hepatitis virus
PT induced conditions comprises a catalytic region which produces a
PT cytotoxic or cytostatic effect in the infected cell.
PS
PS Example; Page 97; 143pp; English.

XX The invention relates to the discovery, identification and
CC characterisation of toxic agents lethal to pathogens and methods for
CC targeting such toxic agents to a pathogen or pathogen infected cells in
CC order to treat and/or eradicate the infection. In particular the
CC invention relates to at least one nucleic acid molecule, which
CC specifically hybridises to mRNA encoding at least one viral protein
CC associated with the transformation or plasmid copy number control, which
CC hybridises to a viral polyadenylation signal or a core, pre core or
CC polymeric encoding sequence. Specifically, the invention relates to the
CC delivery of one or more toxic gene products, antisense RNAs, ribozymes,
CC DNazymes or a combination thereof. The nucleic acids have antiviral
CC activity and can be used in gene therapy. They are useful for the
CC treatment of papilloma or hepatitis virus induced conditions and can
CC produce a cytotoxic or cytostatic effect in papillomavirus or hepatitis B
CC infected cells. The papilloma virus induced condition is selected from
CC warts, cervical dysplasia, cervical carcinoma, carcinoma in situ and
CC laryngeal papilloma. ABA02588-ABA02610 comprise ribozyme flanking
CC sequences and ABA02612-ABA02660 comprise DNazyme target sequences, useful
CC to the invention

XX Sequence 15 BP; 3 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 68;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTG 16
Db 13 TCCACCTGCTGCG 1

RESULT 56

ABS64208
ID ABS64208 standard; DNA; 15 BP.
XX
AC ABS64208;
XX
DT 15-NOV-2002 (first entry)
XX
DE Tachykinin receptor gene TACR2, allele-specific primer #18.
XX
KW Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;
KW tachykinin receptor.
XX
OS Homo sapiens.
XX
FN WO200263046-A1.
XX
PD 15-AUG-2002.
XX
PF 09-NOV-2001; 2001WO-US047394.
XX
PR 09-NOV-2000; 2000US-0247649P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Cappola G, Chew A, Gilson CR, Koshy B;
PI WPI; 2002-636600/68.
DR
XX
XX New genetic variants having polymorphisms in the Tachykinin receptor
XX (TACR2) protein, useful for studying the function of TACR2, and for
XX treating disorders associated with abnormal expression or function of
XX TACR2 isogene.

Claim 14; Page 14; 139pp; English.

XX The invention relates to an isolated polypeptide comprising a polymorphic
CC variant of a reference sequence for the Tachykinin receptor (TACR2)
CC protein. Also described is a method for: (1) haplotyping or genotyping
CC the TACR2 gene of an individual; (2) predicting an association between a
CC trait and at least one haplotype or haplotype pair of the TACR2 gene; and
CC (4) isolated oligonucleotide for detecting a single nucleotide
CC polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene
CC are useful in studying the expression and biological function of TACR2,
CC and in identifying drugs targeting TACR2 protein for treating disorders
CC associated with abnormal expression or function of TACR2, e.g. asthma or
CC breast cancer. Polynucleotides comprising a polymorphic gene variant or
CC fragment may be used for therapeutic purposes, where a patient could
CC benefit from expression or increased expression of a particular TACR2
CC protein isoform, or an expression vector encoding the isoform may be
CC administered to the patient. Haplotype information is useful in improving
CC the efficiency and output of several steps in drug discovery and
CC development process, including target validation, identifying lead
CC compounds, and early phase clinical trials. Information on polymorphisms
CC may be applied in studying biological functions of TACR2 as well as in
CC identifying drugs targeting this protein for the treatment of disorders
CC related to its abnormal expression or function. ABS64163-ABS64302
CC represent human TACR2 gene allele-specific oligonucleotide probes and
CC primers used to detect haplotypes of the TACR2 gene of the invention

XX Sequence 15 BP; 3 A; 3 C; 3 G; 5 T; 0 U; 1 Other;

Query Match 39.3%; Score 11.4; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 68;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

Qy 7 ACCTGCTGTGTGACC 21
Db 1 ACTTGCTGTGTAATTC 15

RESULT 57
AAX27264/c
ID AAX27264 standard; DNA; 16 BP.
AC AAX27264;
XX
XX
DT 02-JUN-1999 (first entry)
XX
XX PCR primer for prostate-tumour derived antigen polynucleotide.
XX
XX Prostate-tumour derived polynucleotide; prostate tumour antigen;
XX tumour cell; prostate carcinoma; therapy; PCR primer; ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX WO9909166-A2.
XX
XX
XX 25-FEB-1999.
XX
XX 18-AUG-1998; 98WO-US017058.
XX
XX 20-AUG-1997; 97US-0056110P.
XX
XX 09-JUL-1998; 98US-00112096.
XX
XX (DEND-) DENDREON CORP.
XX
XX Laus R, Shapero MH, Tsavaler L;
XX
XX WPI; 1999-181036/15.
XX
XX Novel human prostate tumour antigens and coding sequences - useful to
XX detect and treat especially prostate carcinoma.
XX
XX Disclosure; Page 40; 85pp; English.
XX
XX This sequence represents a PCR primer for DNA encoding a prostate tumour
XX antigen of the invention. The polynucleotides and polypeptides can be
XX used to detect and treat tumour cells, especially prostate carcinoma
XX
XX Sequence 16 BP; 7 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTGGT 25
Db 16 TGCTGTGTGAAATTTGT 1

RESULT 58
AAD27231/c
ID AAD27231 standard; DNA; 16 BP.
XX
XX AAD27231;
XX
XX
DT 09-APR-2002 (first entry)
XX
XX M13 universal reverse primer used in FDD.
XX
XX Human; congestive heart failure; dilative cardiomyopathy; sudden death;
XX hypertrophic cardiomyopathy; ischaemic cardiomyopathy; rhythm disorder;
XX heart muscle disease; conduction disorder; coronary heart disease;
XX systemic arterial hypertension; pulmonary hypertension; endocarditis;
XX pulmonary heart disease; valvular heart disease; pericardial disease;
XX congenital heart disease; gene therapy; syncope; transgenic animal;
XX primer; ss.

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XX
OS Unidentified.
XX
XX WO200192567-A2.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-EP006165.
XX
XX 30-MAY-2000; 2000US-0207400P.
XX
XX (MEDI-) MEDIGENE AG.
XX
XX Bunk D, Reuner B, Beck J, Henkel T;
XX
XX WPI; 2002-122073/16.
XX
XX Identifying a subject at risk for a heart disease e.g. congestive heart
XX failure, dilative cardiomyopathy, heart muscle disease, by quantifying
XX the polypeptide expressed by genes abnormally expressed in heart tissue.
XX
XX Disclosure; Page 53; 154pp; English.
XX
XX The patent discloses novel target genes abnormally expressed in heart
XX tissues and their corresponding proteins. The invention also relates to
XX methods for assessing the expression level of these genes. The method is
XX used for testing the predisposition of mammals and preferably humans for
XX a heart disease or for an acute state of such a disease. It is also
XX useful to treat diseases of the heart such as congestive heart failure,
XX dilative cardiomyopathy, hypertrophic cardiomyopathy, ischaemic cardio-
XX myopathy, specific heart muscle disease, rhythm and conduction disorders,
XX syncope and sudden death, coronary heart disease, systemic arterial
XX hypertension, pulmonary hypertension, pulmonary heart disease, valvular
XX heart disease, congenital heart disease, pericardial disease and
XX endocarditis. Sequences of the invention are also used in gene therapy. A
XX transgenic non-human mammal comprising the sequences of the invention are
XX useful for the development for medicaments for the treatments of heart
XX diseases. The present DNA sequence is M13 universal reverse priming
XX sequence which is incorporated in M13-ARPX10 arbitrary primer for
XX amplifying cDNAs of the invention. This sequence used in the fluorescence
XX differential display (FDD) method in the exemplification of the invention
XX
XX Sequence 16 BP; 7 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTGGT 25
Db 16 TGCTGTGTGAAATTTGT 1

RESULT 59
ABZ75913/c
ID ABZ75913 standard; DNA; 16 BP.
XX
XX ABZ75913;
XX
XX
XX 15-MAY-2003 (first entry)
XX
XX M13 universal reverse primer.
XX
XX Cardiant; hypotension; antiarrhythmic; gene therapy; heart disease;
XX transgenic; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO2003006687-A2.
XX
XX 23-JAN-2003.
XX
XX 10-JUL-2002; 2002WO-EP007704.
XX

```

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XX PR 10-JUL-2001; 2001US-0304385P.
XX PA (MEDI-) MEDIGENE AG.
XX PI Reuner B, Bunk D, Henkel T;
XX XX WPI; 2003-229493/22.
XX DR Identifying a subject at risk for a disease of the heart, comprises
XX PT quantitating the amount of at least one RNA or a polypeptide in the heart
XX PT tissue or serum of the blood of the subject.
XX PS Example 1; Page 56; 197pp; English.
XX CC The invention relates to identifying a subject at risk for a disease of
XX CC the heart and involves quantitating the amount of at least one RNA or a
XX CC polypeptide in the heart tissue or serum of the blood of the subject. The
XX CC DNA, polypeptides, compounds identified by the methods above, the refined
XX CC or modified compounds, and the monoclonal antibodies are useful for
XX CC manufacturing a pharmaceutical composition for preventing or treating
XX CC heart diseases, e.g. congestive heart failure, dilative cardiomyopathy,
XX CC hypertrophic cardiomyopathy, ischaemic cardiomyopathy, specific heart
XX CC muscle disease, rhythm and conduction disorders, syncope and sudden
XX CC death, coronary heart disease, systemic arterial hypertension, pulmonary
XX CC hypertension and pulmonary heart disease, valvular heart disease,
XX CC congenital heart disease, pericardial disease or endocarditis. Transgenic
XX CC animals are useful for developing medicaments for treating heart
XX CC diseases. The methods are useful for identifying a subject at risk for a
XX CC heart disease, or for identifying compounds for treating heart disease.
XX CC The present sequence represents a M13 universal reverse primer
XX SQ Sequence 16 BP; 7 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTGGT 25
Db 16 TGCTGTGTGAAATGT 1

RESULT 60
ADR70024/c
ID ADR70024 standard; DNA; 16 BP.
XX AC ADR70024;
XX DT 04-NOV-2004 (first entry)
XX DE Human survivin gene modulatory oligonucleotide #92.
XX KW ss: antiangiogenic; cytostatic; antiarteriosclerotic; antipsoriatic;
XX KW antidiabetic; ophthalmological; antiarthritic; antirheumatic;
XX KW antiasthmatic; anticancer; antiallergic; antiinflammatory; dermatological; anti-HIV;
XX KW virucide; survivin antagonist; apoptosis inhibitor;
XX KW cellular proliferation inhibitor; survivin; gene expression;
XX KW abnormal angiogenesis; chemotherapeutic agent; busulfan; myleran;
XX KW carboplatin; paraplatin; Taxol; doxorubicin; adriamycin; atherosclerosis;
XX KW psoriasis; diabetic retinopathy; rheumatoid arthritis; asthma; warts;
XX KW allergic dermatitis; cancer; tumour; sarcoma; glioma; carcinoma;
XX KW melanoma; osteosarcoma; Ewing's sarcoma; chondrosarcoma;
XX KW Paclitaxel; Docetaxel.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..16
XX FT /*tag= b
XX FT /mod_base= OTHER

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```

FT FT /note= "OTHER = phosphorothioate internucleotide
FT FT linkages, all locked nucleic acid (LNA) residues are 5' -
FT FT methyl cytosine residues"
FT FT 1..4
FT FT /mod_base= a
FT FT /note= "OTHER = beta-D-oxy-locked nucleic acid but
FT FT optionally DNA nucleotides, optionally phosphate
FT FT internucleotide linkages"
FT FT 13..16
FT FT /mod_base= c
FT FT /note= "OTHER = beta-D-oxy-locked nucleic acid but
FT FT optionally DNA nucleotides, optionally phosphate
FT FT internucleotide linkages"
XX WO2004069991-A2.
XX PN 19-AUG-2004.
XX PD 10-FEB-2004; 2004WO-DK000096.
XX PF 10-FEB-2003; 2003DK-00000183.
XX PR 18-NOV-2003; 2003DK-00001708.
XX XX (SANT-) SANTARIS PHARMA AS.
XX PA Hansen B, Thru CA, Petersen KD, Westergaard M, Wissenbach M;
XX PI WPI; 2004-625494/60.
XX XX New locked nucleic acid containing oligomeric compound capable of
XX PT modulating survivin expression, useful for treating cancer such as breast
XX PT carcinoma, lung carcinoma, etc.
XX XX Claim 1; SEQ ID NO 93; 122pp; English.
XX PS The invention relates to an oligomeric compound (I) capable of modulating
XX CC survivin expression, having 8-50 nucleotides and/or nucleotide analogues,
XX CC where the compound comprises a subsequence of at least 8 nucleotides or
XX CC nucleotide analogues, where the subsequence is located within a sequence
XX CC chosen from one of 143 sequences given in the specification. (I) is
XX CC useful for treating a mammal suffering from or susceptible from a disease
XX CC caused by abnormal angiogenesis, by administering (I) containing one or
XX CC more LNA units that are targeted to survivin. (I) is useful as a
XX CC medicament and for the manufacture of a medicament for the treatment of
XX CC cancer, in combination with chemotherapeutic agent such as busulfan
XX CC (myleran), carboplatin (paraplatin), Taxol, doxorubicin (adriamycin),
XX CC etc. (I) or a conjugate (II) containing (I) is useful in the preparation
XX CC of a medicament for the treatment of atherosclerosis, psoriasis, diabetic
XX CC retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis.
XX CC (I), (II) or a pharmaceutical (III) containing (I) is useful for treating
XX CC cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen
XX CC from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast
XX CC carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder
XX CC carcinoma, recurrent superficial bladder cancer, stomach carcinoma,
XX CC prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical
XX CC carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma,
XX CC colorectal carcinoma and carcinoma tumours. The malignant melanoma is
XX CC chosen from superficial spreading melanoma, nodular melanoma, lentigo
XX CC maligna melanoma, acral melanoma, amelanotic melanoma, and desmoplastic
XX CC melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma,
XX CC chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's
XX CC sarcoma. The treatment further involves administration of a
XX CC chemotherapeutic agent such as taxanes, preferably taxol, paclitaxel or
XX CC Docetaxel. (I), (II) or (III) is also useful for preventing or limiting
XX CC apoptosis or for preventing cellular proliferation. This sequence
XX CC corresponds to an antisense oligonucleotide targeted to the human
XX CC survivin gene.
XX SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.6%; Score 11.2; DB 1; Length 16;

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Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TCCACCTGCTGTGTGA 19
Db 16 TGCACCTGCTGTGTGA 1

RESULT 61
ADW09956/c
ID ADW09956 standard; DNA; 16 BP.
AC ADW09956;
XX
DT 07-APR-2005 (first entry)
XX
DE Human survivin antisense oligonucleotide 93C, SEQ ID NO:514.
XX
KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW basal cell carcinoma; ovary tumor; breast tumor;
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;
KW endocrine disease; gynecology and obstetrics; genitourinary disease;
KW respiratory disease; musculoskeletal disease; dermatological disease;
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
KW cardiovascular disease; ocular disease; rheumatoid arthritis;
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
KW skin allergy; anti-allergic; anti-inflammatory; dermatological;
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
KW antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_binding 1..16
FT /*tag= b
FT /bound_moiety= "Bases 1248-1233 of human survivin cDNA
FT (SEQ ID NO:1)"
FT modified_base 1..4
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D
FT -oxy-LNA cytosines are 5-methylcytosine"
FT modified_base 5..13
FT /*tag= c
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT modified_base 13..16
FT /*tag= d
FT /mod_base= OTHER
FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are
FT 5-methylcytosine"
XX
FN US2005014712-A1.
XX
XX 20-JAN-2005.
XX
XX 10-FEB-2004; 2004US-00776934.
XX
XX 10-FEB-2003; 2003US-0446372P.
XX 19-NOV-2003; 2003US-0523591P.
XX
XX (HANS/) HANSEN B.
XX (THRU/) THRU C A.
XX (WEST/) WESTERGAARD M.
XX (PETE/) PETERSEN K D.
XX (WISS/) WISSENBACH M.

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PI Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
XX WPI; 2005-100663/11.
XX
XX New oligomeric compound for the modulation of survivin, useful for
PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.
XX
XX Example 10; SEQ ID NO 514; 264pp; English.
XX
XX The invention relates to antisense oligonucleotides consisting of 8-50
CC nucleotides and/or nucleotide analogs which inhibit expression of human
CC survivin, an inhibitor of apoptosis which is also essential for cell
CC division and angiogenesis. The antisense oligonucleotides comprise a
CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
CC subsequence is located within a sequence selected from ADW09444-ADW09586.
CC The oligonucleotides preferably contain one or more (preferably 6-10)
CC nucleotide analogs, especially a locked nucleic acid (LNA), and also
CC preferably contain a linkage group selected from a phosphate group, a
CC phosphorothioate group or a boranophosphate group. The invention also
CC relates to a conjugate comprising a survivin antisense oligonucleotide
CC the invention and one or more non-nucleotide or non-polynucleotide
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical
CC composition comprising a survivin antisense oligonucleotide or conjugate
CC of the invention, optionally further comprising a chemotherapeutic agent.
CC The survivin antisense oligonucleotides, and conjugates and compositions
CC containing them, are useful in the treatment of cancers such as
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
CC gliomas. The survivin antisense oligonucleotides are also useful in the
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
CC dermatitis. They may additionally be used for inhibiting cellular
CC proliferation, for modulating apoptosis and for treating a disease
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides
CC of the invention are shorter than prior art survivin antisense
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC increased specificity and affinity for survivin mRNA, and also have
CC higher biostability and cell permeability. The present sequence
CC represents an antisense oligonucleotide targeted to the human survivin
CC cDNA target sequence shown in ADW09443 used in an example of the
CC invention.
XX
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

```

```

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 TCCACCTGCTGTGTGA 19
Db 16 TGCACCTGCTGTGTGA 1

RESULT 62
ADW09954/c
ID ADW09954 standard; DNA; 16 BP.
XX
XX ADW09954;
AC ADW09954;
XX
DT 07-APR-2005 (first entry)
XX
DE Human survivin antisense oligonucleotide 93A, SEQ ID NO:512.
XX
KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW basal cell carcinoma; ovary tumor; breast tumor;
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;

```

KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;
KW endocrine disease; gynecology and obstetrics; genitourinary disease;
KW respiratory disease; musculoskeletal disease; dermatological disease;
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
KW cardiovascular disease; ocular disease; rheumatoid arthritis;
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
KW skin allergy; anti-allergic; antinflammatory; dermatological;
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
KW antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_binding 1..16
FT /tag= b
FT /bound_moiety= "Bases 1248-1233 of human survivin cDNA
FT (SEQ ID NO:1)"
FT modified_base 1..16
FT /tag= c
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT modified_base 1..4
FT /tag= a
FT /mod_base= OTHER
FT /note= "Beta-D-ox-LNAs (locked nucleic acid). All beta-D
FT -oxy-LNA cytosines are 5-methylcytosine"
FT modified_base 13..16
FT /tag= d
FT /mod_base= OTHER
FT /note= "Beta-D-ox-LNAs. All beta-D-ox-LNA cytosines are
FT 5-methylcytosine"
XX
PN US2005014712-A1.
XX
XX 20-JAN-2005.
XX
XX 10-FEB-2004; 2004US-00776934.
XX
XX 10-FEB-2003; 2003US-0446372P.
PR 19-NOV-2003; 2003US-0523591P.
XX
XX (HANS/) HANSEN B.
PA (THRU/) THRU C A.
PA (WEST/) WESTERGAARD M.
PA (PETE/) PETERSEN K D.
PA (WISS/) WISSENBACH M.
XX
XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
PI WPI; 2005-100663/11.
XX
XX New oligomeric compound for the modulation of survivin, useful for
PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.
XX
XX Example 10; SEQ ID NO 512; 264pp; English.
XX
XX The invention relates to antisense oligonucleotides consisting of 8-50
CC nucleotides and/or nucleotide analogs which inhibit expression of human
CC survivin, an inhibitor of apoptosis which is also essential for cell
CC division and angiogenesis. The antisense oligonucleotides comprise a
CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
CC subsequence is located within a sequence selected from ADW09444-ADW09586.
CC The oligonucleotides preferably contain one or more (preferably 6-10)
CC nucleotide analogs, especially a locked nucleic acid (LNA), and also
CC preferably contain a linkage group selected from a phosphate group, a
CC phosphorothioate group or a boranophosphate group. The invention also
CC relates to a conjugate comprising a survivin antisense oligonucleotide of

CC the invention and one or more non-nucleotide or non-polynucleotide
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical
CC composition comprising a survivin antisense oligonucleotide or conjugate
CC of the invention, optionally further comprising a chemotherapeutic agent.
CC The survivin antisense oligonucleotides, and conjugates and compositions
CC containing them, are useful in the treatment of cancers such as
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
CC gliomas. The survivin antisense oligonucleotides are also useful in the
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
CC dermatitis. They may additionally be used for inhibiting cellular
CC proliferation, for modulating apoptosis and for treating a disease
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides
CC of the invention are shorter than prior art survivin antisense
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC increased specificity and affinity for survivin mRNA, and also have
CC higher biostability and cell permeability. The present sequence
CC represents an antisense oligonucleotide targeted to the human survivin
CC cDNA target sequence shown in ADW09443 used in an example of the
CC invention.
XX
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 4 TCCACCTGCTGTGTGA 19
Db 16 TGCACCTGCTGTGTGA 1
RESULT 63
ADW09555/c
ID ADW09555 standard; DNA; 16 BP.
XX
XX ADW09555;
AC ADW09555;
XX 07-APR-2005 (first entry)
XX Human survivin antisense oligonucleotide 93B, SEQ ID NO:513.
XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW basal cell carcinoma; ovary tumor; breast tumor; bladder tumor;
KW non-small-cell lung cancer; renal cell carcinoma; colon tumor;
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytostatic;
KW endocrine disease; gynecology and obstetrics; genitourinary disease;
KW respiratory disease; musculoskeletal disease; dermatological disease;
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
KW cardiovascular disease; ocular disease; rheumatoid arthritis;
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
KW skin allergy; anti-allergic; antinflammatory; dermatological;
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
KW antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH misc_binding 1..16
FT /tag= b
FT /bound_moiety= "Bases 1248-1233 of human survivin cDNA


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FT modified_base (SEQ ID NO:1)
FT 1..16
FT /*tag= c
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT modified_base 1..4
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D
FT -oxy-LNA cytosines are 5-methylcytosine"
FT modified_base 13..15
FT /*tag= d
FT /mod_base= OTHER
FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are
FT 5-methylcytosine"
FT US2005014712-A1.
FT
FT 20-JAN-2005.
FT
FT 10-FEB-2004; 2004US-00776934.
FT
FT 10-FEB-2003; 2003US-0446372P.
FT
FT 19-NOV-2003; 2003US-0523591P.
FT
FT (HANS// HANSEN B.
FT (THRU// THRU C A.
FT (WEST// WESTERGAARD M.
FT (PETE// PETERSEN K D.
FT (WISS// WISENBACH M.
FT
FT Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
FT WPI; 2005-100663/11.
FT
FT New oligomeric compound for the modulation of survivin, useful for
FT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
FT rheumatoid arthritis, asthma, warts, or allergic dermatitis.
FT
FT Example 10; SEQ ID NO 513; 264pp; English.
FT
FT The invention relates to antisense oligonucleotides consisting of 8-50
FT nucleotides and/or nucleotide analogs which inhibit expression of human
FT survivin, an inhibitor of apoptosis which is also essential for cell
FT division and angiogenesis. The antisense oligonucleotides comprise a
FT subsequence of 8 or more nucleotides or nucleotide analogs wherein the
FT subsequence is located within a sequence selected from ADW09444-ADW09586.
FT The oligonucleotides preferably contain one or more (preferably 6-10)
FT nucleotide analogs, especially a locked nucleic acid (LNA), and also
FT preferably contain a linkage group selected from a phosphate group, a
FT phosphorothioate group or a boranophosphate group. The invention also
FT relates to a conjugate comprising a survivin antisense oligonucleotide of
FT the invention and one or more non-nucleotide or non-polynucleotide
FT moieties covalently attached to the oligonucleotide; and a pharmaceutical
FT composition comprising a survivin antisense oligonucleotide or conjugate
FT of the invention, optionally further comprising a chemotherapeutic agent.
FT The survivin antisense oligonucleotides, and conjugates and compositions
FT containing them, are useful in the treatment of cancers such as
FT carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
FT carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
FT carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
FT stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
FT carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
FT papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid
FT tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
FT malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
FT gliomas. The survivin antisense oligonucleotides are also useful in the
FT treatment of conditions such as atherosclerosis, psoriasis, diabetic
FT retinopathy, rheumatoid arthritis, asthma, warts, and allergic
FT dermatitis. They may additionally be used for inhibiting cellular
FT proliferation, for modulating apoptosis and for treating a disease
FT related to abnormal angiogenesis. The survivin antisense oligonucleotides
FT of the invention are shorter than prior art survivin antisense

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CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC increased specificity and affinity for survivin mRNA, and also have
CC higher biostability and cell permeability. The present sequence
CC represents an antisense oligonucleotide targeted to the human survivin
CC cDNA target sequence shown in ADW09443 used in an example of the
CC invention.
CC
CC SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;
CC
CC Query Match 38.6%; Score 11.2; DB 1; Length 16;
CC Best Local Similarity 81.2%; Pred. No. 80;
CC Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 4 TCCACCTGCTGTGTGA 19
CC | | | | | | | | | |
CC Db 16 TGCCACTGCTGTGTGA 1
CC
CC RESULT 64
CC ADW09535/c
CC ID ADW09535 standard; DNA; 16 BP.
CC XX
CC AC ADW09535;
CC XX
CC DT 07-APR-2005 (first entry)
CC XX
CC DE Human survivin antisense oligonucleotide, SEQ ID NO:93.
CC XX
CC KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
CC basal cell carcinoma; ovary tumor; breast tumor;
CC non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
CC stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
CC uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
CC sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;
CC endocrine disease; gynecology and obstetrics; genitourinary disease;
CC respiratory disease; musculoskeletal disease; dermatological disease;
CC proliferative disorder; atherosclerosis; antiarteriosclerotic;
CC cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
CC immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
CC cardiovascular disease; ocular disease; rheumatoid arthritis;
CC antiarthritic; antiinflammatory; inflammation; asthma; antiasthmatic;
CC skin allergy; antiallergic; antiinflammatory; dermatological;
CC verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
CC angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
CC antisense oligonucleotide; ss.
CC XX
CC OS Homo sapiens.
CC
CC Key Location/Qualifiers
CC misc_binding 1..16
CC /tag= c
CC /bound_moiety= "Bases 1248-1233 of human survivin cDNA
CC (SEQ ID NO:1)"
CC modified_base 1..5
CC /tag= b
CC /mod_base= OTHER
CC /note= "Optionally phosphorothioate linkages when
CC nucleotides 1-4 are beta-D-oxy-LNAs. When nucleotides 1-4
CC are unmodified, the internucleotide linkages are
CC phosphorothioate"
CC modified_base 1..4
CC /tag= a
CC /mod_base= OTHER
CC /note= "Optionally beta-D-oxy-LNAs (locked nucleic acid).
CC All beta-D-oxy-LNA cytosines are 5-methylcytosine"
CC modified_base 5..13
CC /tag= d
CC /mod_base= OTHER
CC /note= "Phosphorothioate linkages"
CC modified_base 13..15
CC /tag= e
CC /mod_base= OTHER
CC /note= "Optionally beta-D-oxy-LNAs. All beta-D-oxy-LNA

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PI Hansen B, Thruue CA, Westergaard M, Petersen KD, Wissenbach M;
XX WPI; 2005-100663/11.
XX
XX New oligomeric compound for the modulation of survivin, useful for
PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.
XX
XX Example 10; SEQ ID NO 515; 264pp; English.
XX
CC The invention relates to antisense oligonucleotides consisting of 8-50
CC nucleotides and/or nucleotide analogs which inhibit expression of human
CC survivin, an inhibitor of apoptosis which is also essential for cell
CC division and angiogenesis. The antisense oligonucleotides comprise a
CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
CC subsequence is located within a sequence selected from ADW09444-ADM09586.
CC The oligonucleotides preferably contain one or more (preferably 6-10)
CC nucleotide analogs, especially a locked nucleic acid (LNA), and also
CC preferably contain a linkage group selected from a phosphate group, a
CC phosphorothioate group or a boranophosphate group. The invention also
CC relates to a conjugate comprising a survivin antisense oligonucleotide of
CC the invention and one or more non-nucleotide or non-polynucleotide
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical
CC composition comprising a survivin antisense oligonucleotide or conjugate
CC of the invention, optionally further comprising a chemotherapeutic agent.
CC The survivin antisense oligonucleotides, and conjugates and compositions
CC containing them, are useful in the treatment of cancers such as
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoïd
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
CC gliomas. The survivin antisense oligonucleotides are also useful in the
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
CC dermatitis. They may additionally be used for inhibiting cellular
CC proliferation, for modulating apoptosis and for treating a disease
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides
CC of the invention are shorter than prior art survivin antisense
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC increased specificity and affinity for survivin mRNA, and also have
CC higher biostability and cell permeability. The present sequence
CC represents an antisense oligonucleotide targeted to the human survivin
CC cDNA target sequence shown in ADW09443 used in an example of the
CC invention.
XX
SQ Sequence 16 BP; 5 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 38.6%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 80;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGA 19
DB 16 TGCACCTGCTGTGTGA 1

RESULT 66
AAZ48742
ID AAZ48742 standard; DNA; 12 BP.
XX
XX AAZ48742;
AC
XX
XX 15-MAR-2000 (first entry)
DT
XX
XX PCR primer for human alpha-antitrypsin gene sequence.
DE
XX
XX PCR primer; oligonucleotide detection; diagnosis; disease screening; COP;
KW competitive oligonucleotide priming; genetic polymorphism detection;
KW genetic disease diagnosis; linkage analysis; tissue typing; gene mapping;
XX

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KW human; alpha-antitrypsin; ss.
XX
XX Homo sapiens.
XX
XX EP333465-A.
XX
XX 20-SEP-1989.
XX
XX 15-MAR-1989; 89EP-00302569.
XX
XX 18-MAR-1988; 88US-00170214.
XX
XX (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Caskey CT, Gibbs RAL;
XX
XX WPI; 1989-272222/38.
XX
XX Detection of mutations in DNA - by adding competitive oligo:nucleotide
XX primers to nucleic acids, hybridising, etc.
XX
XX Example 4; Page 12; 21pp; English.
XX
CC This sequence represents a PCR primer for the human alpha-antitrypsin
CC gene sequence. The invention relates to a method for detecting the
CC presence or absence of a specific known oligonucleotide, or
CC distinguishing between specific and different nucleic acid (NA)
CC sequences, comprising: (1) addition of at least two oligonucleotide
CC primers to a sample or mixture of NA where one primer (a) is
CC substantially complementary to a specific NA sequence and the other
CC primer (b) has a single base mismatch with the specific sequence; (2)
CC preferentially hybridising (a) to the specific NA sequence under
CC competitive conditions; (3) extension of (a) from its 3' terminus to
CC produce an extension product complementary to the strand hybridised to by
CC (a); and (4) identifying the extension product by determining the
CC presence or absence of labels attached to at least one of the primers.
CC The method (referred to as competitive oligonucleotide priming (COP)) can
CC be used in detecting genetic polymorphisms, particularly in detecting
CC genetic diseases, screening for disease association by linkage analysis,
CC tissue typing, gene mapping, screening for neoplasms, and disease screening in
CC pathogens, determining purity of animal strains, and disease screening in
CC animals. With this method, primers may be used that are shorter than
CC those used in PCR, as the binding to template is competitive its sequence
CC can be inferred. The target sequence of the gene need not be precisely
CC known as only the specific sequence for the primers is required
XX
SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 37.9%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ACCTGGTAAAT 29
DB 1 ACCTGGTAAAT 11

RESULT 67
AAQ04007
ID AAQ04007 standard; DNA; 12 BP.
XX
XX AAQ04007;
AC
XX
XX 25-MAR-2003 (revised)
DT 03-SEP-1990 (first entry)
XX
XX Primer used in detecting alpha-1-antitrypsin deficiency.
DE
XX
XX X-chromosome; ornithine transcarbamylase deficiency; muscular dystrophy;
KW dystrophin; ds.
XX
XX Synthetic.
OS
XX

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PN EP364255-A.
 XX 18-APR-1990.
 XX 11-OCT-1989; 89EP-00310424.
 XX 12-OCT-1988; 88US-00256689.
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Caskey CT, Chamberlain JS, Gibbs RAL, Rainer JE, Nguyen PN;
 PI WPI; 1990-117752/16.
 DR
 XX Multiplex genomic DNA amplification for deletion detection - useful for
 PT detecting X-linked diseases such as ornithine transcarbamylase deficiency
 PT and X-linked muscular dystrophy.
 XX Example 8; Page 18; 32pp; English.
 XX Paired oligonucleotide primers are used in detecting deletions
 CC specifically of the X and Y chromosomes. Probe may be used to recognise
 CC mutant (S) allele of alpha-1-antitrypsin. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 12 BP; 4 A; 2 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 37.9%; Score 11; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 ACCTGGTAAAT 29
 DB 1 ACCTGGTAAAT 11
 RESULT 68
 AAF69397
 ID AAF69397 standard; DNA; 15 BP.
 AC AAF69397;
 XX 18-APR-2001 (first entry)
 XX Human IL4Ralpha gene probe #37.
 DE Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
 XX allergic disease; probe; ss.
 KW Homo sapiens.
 XX
 OS WO200104270-A1.
 XX 18-JAN-2001.
 PD 13-JUL-2000; 2000WO-US019094.
 PF 13-JUL-1999; 99US-0143435P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Denton RR, Duda A, Nandabalan K, Stephens JC;
 PI Windemuth AK;
 XX WPI; 2001-103078/11.
 DR New isolated polynucleotide useful for the identification of therapeutics
 XX in allergic diseases is new.
 PT Claim 15; Page 42; 188pp; English.
 XX
 PS The present invention relates to polymorphisms of the human interleukin 4
 CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference

CC sequence). Polynucleotides comprising polymorphic gene variants are
 CC useful for therapeutic purposes. For example, where a patient may benefit
 CC from expression of a particular IL4Ralpha protein isoform, an expression
 CC vector encoding the isoform may be administered to the patient. It may
 CC desirable to decrease or block expression of a particular IL4Ralpha
 CC isogene, which may be done by turning off by transcribing a targeted
 CC organ, tissue or cell population with an expression vector that expresses
 CC high levels of untranslatable mRNA for the isogene. Specific therapeutics
 CC identified by these methods may be useful for the isogene. Specific therapeutics
 CC present sequence is a probe for human IL4R-alpha
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 37.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CACCTGCTGTG 16
 DB 1 CACCTGCTGTG 11
 RESULT 69
 ABA99295/C
 ID ABA99295 standard; DNA; 15 BP.
 XX ABA99295;
 AC ABA99295;
 XX 13-MAY-2002 (first entry)
 DT Human ALDH5 allele-specific oligonucleotide SEQ ID No 15.
 XX ALDH5; human; gene; polymorphism; haplotype; aldehyde dehydrogenase 5;
 KW binding affinity; drug targeting; alcoholism; alcohol-induced disorder;
 KW antialcoholic; ss.
 XX Homo sapiens.
 OS WO200192279-A2.
 PN 06-DEC-2001.
 PD 29-MAY-2001; 2001WO-US017253.
 XX 26-MAY-2000; 2000US-0207508P.
 PR (GENA-) GENAISSANCE PHARM INC.
 XX Duda A, Finkel K, Kazemi A, Messer C, Sanchis A;
 PI WPI; 2002-122054/16.
 XX New genetic variants with polymorphisms in the aldehyde dehydrogenase 5
 PT (ALDH5) gene, useful for studying the function of ALDH5, and for
 PT expressing ALDH5 protein which is useful in screening drugs for treating
 PT ALDH5-related diseases.
 XX Claim 17; Page 77; 96pp; English.
 PS This invention describes a novel isolated genes and haplotypes of the
 CC human aldehyde dehydrogenase 5 (ALDH5) gene containing polymorphic sites.
 CC The polymorphic ALDH5 variant is useful in studying the effect of the
 CC variation on the biological activity of ALDH5 and on the binding affinity
 CC of candidate drugs targeting ALDH5 for the treatment of alcoholism and
 CC alcohol-induced disorders. Polynucleotides comprising a polymorphic gene
 CC variant or fragment may be used for therapeutic purposes. ALDH5 protein
 CC isoforms may be used in assays to measure the binding affinities of one
 CC or more candidate drugs targeting the ALDH5 protein. ALDH5 proteins may
 CC be used to generate antibodies. Haplotyping method can be used by
 CC scientists to validate ALDH5 as a candidate target for treating a
 CC specific condition or disease predicted to be associated with ALDH5
 CC activity, and in the design of clinical trials of candidate drugs for
 CC treating a specific condition or disease predicted to be associated with

CC ALDH5 activity. Information on polymorphisms on the ALDH5 gene can be
 CC applied for studying the biological function of ALDH5 as well as in
 CC identifying drugs targeting this protein for the treatment of disorders
 CC related to its abnormal expression or function. The products of the
 CC invention have antialcoholic activity. This sequence represents a human
 CC ALDH5 allele-specific oligonucleotide described in the disclosure of the
 CC invention
 XX
 SQ Sequence 15 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 1 Other;
 Query Match 37.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 81;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CATCCACTGCTG 14
 |||||: |||||
 DB 14 CATCAVGTGCTG 2
 |||||: |||||
 RESULT 70
 ID ABL45833 standard; DNA; 15 BP.
 XX
 AC ABL45833;
 XX
 DT 26-APR-2002 (first entry)
 XX
 DE Human EDG6 gene allele specific primer SEQ ID NO: 27.
 XX
 KW Human; endothelial differentiation, G-protein coupled receptor 6; EDG6;
 KW haplotype; cancer; angiogenesis; inflammation; chromosome 19p13.3;
 KW cytosolic; antiinflammatory; gene therapy; SNP;
 KW single nucleotide polymorphism; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200206446-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-US022523.
 XX
 PR 17-JUL-2000; 2000US-0218727P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Kliem SE, Koshy B;
 XX
 DR WPI; 2002-171804/22.
 XX
 PT New genetic variants of endothelial differentiation, G-protein coupled
 PT receptor-6 gene for studying expression, function of the gene and
 PT expressing EDG6 protein for use in screening drugs to treat cancer,
 PT inflammation.
 XX
 PS Claim 16; Page 13; 111pp; English.
 XX
 CC The present invention provides the gene, protein and cDNA sequences of
 CC the human endothelial differentiation, G-protein coupled receptor 6
 CC (EDG6). Also identified are single nucleotide polymorphisms (SNPs) found
 CC within the sequences. The sequences can be used in the identification of
 CC the haplotype of an individual, and in the treatment of cancer,
 CC angiogenesis and inflammation. The present sequence is an allele specific
 CC primer for the EDG6 gene, which is found on chromosome 19p13.3
 XX
 SQ Sequence 15 BP; 1 A; 4 C; 4 G; 5 T; 0 U; 1 Other;
 Query Match 37.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CCTGCTGTGTG 18
 |||||: |||||

Db 1 CCTGCTGTGTG 11
 RESULT 71
 ID AAS16726 standard; DNA; 15 BP.
 XX
 AC AAS16726;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human APOA4 allele specific oligonucleotide, ASO, probe #9.
 XX
 KW Human; ss; APOA4; apolipoprotein A-IV; antiatherosclerotic; cardiant;
 KW haplotype; chromosome 11q23-qter; coronary heart disease; obesity;
 KW atherosclerosis; probe.
 XX
 OS Homo sapiens.
 XX
 PN WO200171124-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 03-APR-2001; 2001WO-US010670.
 XX
 PR 05-APR-2000; 2000US-0194362P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Bentivegna SC, Choi JY, Kliem SE, Koshy B;
 XX
 DR WPI; 2002-041281/05.
 XX
 PT New haplotypes of the human apolipoprotein A-IV gene, useful to diagnose
 PT and treat disorders associated with its abnormal expression or function
 PT such as coronary artery disease.
 XX
 PS Claim 16; Page 15; 71pp; English.
 XX
 CC The invention relates to haplotyping the human apolipoprotein A-IV
 CC (APOA4) gene of an individual, comprising determining if the individual
 CC has one of the APOA4 haplotypes or haplotype pairs fully defined in the
 CC specification. Also disclosed are genotyping oligonucleotides (or allele
 CC specific oligonucleotides, ASO) as well as methods for correlating a
 CC particular haplotype pair with a trait e.g. obesity, in a population. The
 CC APOA4 gene is located on chromosome 11q23-qter. The methods of the
 CC invention are useful to diagnose and develop treatment for disorders
 CC associated with abnormal APOA4 expression or function, for example
 CC coronary heart disease and atherosclerosis. The APOA4 isogenes and
 CC screened compounds are useful for the treatment of disorders associated
 CC with abnormal APOA4 expression or function such as coronary artery
 CC disease. The present sequence is an APOA4 allele specific
 CC oligonucleotide, ASO, probe used to detect an APOA4 polymorphism
 XX
 SQ Sequence 15 BP; 4 A; 3 C; 6 G; 1 T; 0 U; 1 Other;
 Query Match 37.9%; Score 11; DB 1; Length 15;
 Best Local Similarity 84.6%; Pred. No. 81;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 CATCCACCTGCTG 14
 |||||: |||||
 DB 15 CCTCCACYTGTG 3
 |||||: |||||
 RESULT 72
 ID AAL39723 standard; DNA; 15 BP.
 XX
 AC AAL39723;
 XX
 DT 05-SEP-2002 (first entry)
 XX

DE	SMOH polymorphism detecting primer SEQ ID No 38.	
XX		
KW	Cytostatic; polymorphic variant; single nucleotide polymorphism; SMOH;	
KW	human smoothened Drosophila homologue; basal cell carcinoma; BCC;	
KW	gene therapy; antisense gene therapy; PCR; primer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200229004-A2.	
XX		
PD	11-APR-2002.	
XX		
PF	04-OCT-2001; 2001WO-US031304.	
XX		
PR	04-OCT-2000; 2000US-0237871P.	
XX		
PA	(GENA-) GENAISSANCE PHARM INC.	
XX		
PI	Bentivegna SC, Choi JY, Koshy B, Lee HH, Sausker EA;	
XX		
DR	WPI; 2002-519113/55.	
XX		
CC	New genetic variants of smoothened Drosophila homolog (SMOH) gene useful	
CC	for therapeutic purposes and for expressing SMOH protein useful in	
PT	identifying drugs to treat basal cell carcinomas.	
XX		
PS	Claim 15; Page 14; 179pp; English.	
XX		
CC	The invention relates to an isolated polynucleotide comprising a sequence	
CC	which is a polymorphic variant of a reference sequence for the human	
CC	smoothened Drosophila homologue (SMOH) gene or its fragment, or a	
CC	polymorphic variant of a reference sequence for a SMOH cDNA or its	
CC	fragment. A new isolated polypeptide is useful for screening for drugs	
CC	targeting the polypeptide. A new method is useful for identifying an	
CC	association between a trait such as a clinical response to a drug	
CC	targeting SMOH and a haplotype or haplotype pair of SMOH gene. The	
CC	methods have applicability in developing diagnostic tests and therapeutic	
CC	treatments for basal cell carcinomas (BCCs). The isolated polynucleotide	
CC	is useful for studying the expression and function of SMOH and expressing	
CC	SMOH protein for use in screening for candidate drugs to treat diseases	
CC	related to SMOH activity. The polymorphism and haplotype data are useful	
CC	for validating whether SMOH is a suitable target for drugs to treat BCCs,	
CC	screening for the drugs and reducing bias in clinical trials of the	
CC	drugs. The isolated polynucleotide is useful for therapeutic purposes.	
CC	The new method, an oligonucleotide and kit of the invention are useful	
CC	for determining whether an individual has one of the haplotypes or the	
CC	haplotype pairs. The polynucleotides of the invention can be used to	
CC	treat disorders by gene therapy and antisense gene therapy. This	
CC	polynucleotide sequence represents a primer used for detecting human	
CC	smoothened Drosophila homologue gene polymorphisms of the invention	
XX		
SQ	Sequence 15 BP; 0 A; 5 C; 5 G; 4 T; 0 U; 1 Other;	
	Query Match 37.9%; Score 11; DB 1; Length 15;	
	Best Local Similarity 100.0%; Pred. No. 81;	
	Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	8 CCTGCTGTGTG 18	
DB	2 CCTGCTGTGTG 12	
RESULT 73		
ACF57574/c		
ID	ACF57574 standard; DNA; 15 BP.	
XX		
XX		
AC	ACF57574;	
XX		
DT	22-APR-2004 (first entry)	
XX		
DE	Human ALDOB gene allele-specific probe SEQ ID NO: 25.	
XX		
XX	Human; ALDOB; fructose-bisphosphate aldolase B; SNP;	
KW		
DE	single nucleotide polymorphism; primer; probe; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003091454-A1.	
XX		
PD	06-NOV-2003.	
XX		
PF	26-APR-2002; 2002WO-US013328.	
XX		
PR	26-APR-2002; 2002WO-US013328.	
XX		
PA	(GENA-) GENAISSANCE PHARM INC.	
XX		
PI	Chew A, Kazemi A, Koshy B;	
XX		
DR	WPI; 2003-877338/81.	
XX		
PS	Claim 39; Page 14; Opp; English.	
XX		
CC	The present invention provides the protein and coding sequences of human	
CC	fructose-bisphosphate aldolase B (ALDOB) and single nucleotide	
CC	polymorphisms (SNPs) which have been identified in each sequence. The	
CC	method of haplotyping the sequences is useful for haplotyping the	
CC	fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for	
CC	validating the ALDOB protein as a candidate target for treating a medical	
CC	condition predicted to be associated with ALDOB activity. The present	
CC	sequence is an allele-specific primer/probe used to identify the	
CC	haplotype of the human ALDOB gene in the exemplification of the invention	
XX		
SQ	Sequence 15 BP; 4 A; 3 C; 2 G; 5 T; 0 U; 1 Other;	
	Query Match 37.9%; Score 11; DB 1; Length 15;	
	Best Local Similarity 84.6%; Pred. No. 81;	
	Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	7 ACCTGCTGTGTGA 19	
DB	15 AACTGCTGTGTGA 3	
RESULT 74		
ADQ30419/c		
ID	ADQ30419 standard; DNA; 15 BP.	
XX		
AC	ADQ30419;	
XX		
DT	09-SEP-2004 (first entry)	
XX		
DE	Human VR1 exon 1d transcription factor binding fragment #138.	
XX		
KW	ds; VR1 receptor; vanilloid receptor type 1; modulator;	
KW	pain transmission; primary sensory neuron; transcription factor;	
KW	detection; MZF1; NPkappaB; NPAT; GATA1; sensitivity disorder; analgesia;	
KW	hypalgesia; hyperalgesia; neuralgia; myalgia; human.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004053120-A2.	
XX		
PD	24-JUN-2004.	
XX		
PF	01-DEC-2003; 2003WO-EP013522.	
XX		
PR	09-DEC-2002; 2002DE-01057421.	
XX		
PA	(CHEF) GRUENENTHAL GMBH.	
XX		
PI	Weihe E, Bieller A, Schaefer WKH;	
XX		
DR	WPI; 2004-468868/44.	
XX		
PT	New nucleic acid that modulates expression of the vanilloid receptor-1,	

useful for control of pain or sensitivity disorders, comprises sequences from control regions of the receptor gene.

Disclosure; Page 54; 68pp; German.

This invention describes a novel nucleic acid containing a specific segment having at least one region that modulates expression of the VRL1 (vanilloid receptor type 1) receptor, or a functional derivative, allele or fragment of this region, or a sequence that hybridizes to it under standard conditions. The VRL1 modulator is derived from one or more of positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or 44731-43231 or 36618-33151 of AF168787 and is involved in transmission of pain, particularly in primary sensory neurons. The invention also describes a vector that contains the VRL1 modulator, host cells containing this vector (other than human germ or embryonal stem cells) and a method for modulating expression of the VRL1 receptor by introducing the modulator or the vector into a cell that contains the VRL1 gene. The products of the invention are used for detecting a transcription factor from its binding to a regulatory sequence for a double-stranded oligonucleotide fragment of it), e.g. by Western blotting or enzyme-linked immunosorbent assay, particularly for diagnosis of diseases associated with overexpression or underexpression of the transcription factor. The region that modulates VRL1 receptor expression includes a binding site for a transcription factor, e.g. MZF1, NFKBpab, NFAT or GATA1. The nucleic acids of the invention, or vectors containing them, are used for prevention or treatment of pain, also for treating sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also neuralgia and myalgia, that are associated with activity of the VRL1 receptor. This sequence represents a fragment of human VRL1 exon 1d DNA which is capable of binding to a transcription factor.

Sequence 15 BP; 4 A; 1 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 37.9%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATCCACCTGC 12
|||||||
Db 14 CATCCACCTGC 4

RESULT 75
AAV92814
ID AAV92814 standard; RNA; 14 BP.

XX AC AAV92814;

XX DT 18-FEB-1999 (first entry)

XX DE Human A-raf target sequence nucleotide position 1828.

XX KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme; target; substrate; catalyst; modulation; expression; Raf gene; delivery; screening; identification; synthesis; deprotection; purification; cancer; inflammation; psoriasis; non-hepatic ascites; infection; genetic drift; restenosis; rheumatoid arthritis; ss.

XX OS Homo sapiens.

XX FN WO9805030-A2.

XX PD 12-NOV-1998.

XX FF 05-MAY-1998; 98WO-US009249.

XX PR 09-MAY-1997; 97US-0046059P.

XX PR 09-JUN-1997; 97US-0049002P.

XX PR 03-JUL-1997; 97US-0051718P.

XX PR 02-AUG-1997; 97US-0056808P.

XX PR 02-OCT-1997; 97US-0061321P.

XX PR 02-OCT-1997; 97US-0061324P.

XX PR 05-NOV-1997; 97US-0064866P.

PR 19-DEC-1997; 97US-0068212P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;

PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;

PI Thompson J, Workman CT, Beaudry A, Sweedler D;

XX WIPI; 1999-009494/01.

XX PT Identifying new catalytic nucleic acid that modulates selected processes - especially ribozymes that cleave Raf RNA for treating cancer, PT restenosis, and also new ribozymes and modified nucleoside triphosphates used as antiviral agents and synthons.

XX PS Claim 179; Page 164; 259pp; English.

XX CC A method has been developed for the identification of a nucleic acid capable of modulating a process in a biological system. The method comprises: (a) introducing into the system a random library of nucleic acid catalysts (NAC) having a substrate binding domain (SBD), comprising a random sequence, and a catalytic domain (CD); and (b) identifying NAC in systems where modulation has occurred and/or determining the sequence of at least part of the SBDs in such systems. Nucleic acid molecules with endonuclease activity and catalytic activity, from the present invention, are used to modulate gene expression in plant and mammalian cells and to cleave target nucleic acid, particularly for treating systemic diseases caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic ascites and infection. They may also be used to detect genetic drift and mutations in diseased cells and to determine c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate expression of the Raf gene, are used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or generally any condition associated with the level of c-raf. Introduction of sugar/phosphate modifications increases stability against nuclease and activity. AAV90522 to AAV93877 represent NACs that can be used in the method, specifically for modulating the expression of a Raf gene

XX SQ Sequence 14 BP; 1 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 14;
Best Local Similarity 57.1%; Pred. No. 83;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CACCTGCTGTGTA 19

Db 1 CGCCGCGUCUGA 14

RESULT 76

AAV48782

ID AAV48782 standard; DNA; 15 BP.

XX AC AAV48782;

XX DT 15-OCT-1998 (first entry)

XX DE Erbb-2 gene antisense oligonucleotide Erbb-2-74.

XX KW Erbb-2; antisense oligonucleotide; modulate; gene expression; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN EP856579-A1.

XX PD 05-AUG-1998.

XX PF 31-JAN-1997; 97EP-00101531.

XX PR 31-JAN-1997; 97EP-00101531.

XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.

XX

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PI Schlingensiepen K, Brysch W;
XX
XX WPI; 1998-400910/35.
XX
XX Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX consecutive guanine or inosine - and have specific ratio of residues
XX able to form two or three hydrogen bonds, have greater activity and
XX reduced toxicity, used therapeutically or to modulate growth of cells in
XX culture.
XX
XX Claim 10; Fig 6b; 286pp; English.
XX
XX AA48709-886 represent antisense oligonucleotides directed against the
XX ErbB-2 gene. Of these, only oligonucleotides AA48709-91 resulted in
XX significant reduction in ErbB-2 protein expression, while
XX oligonucleotides AA48792-886 had little effect. The oligonucleotides
XX exemplify the invention. The specification describes oligonucleotides
XX that contain 8-30 nucleotides, which contain at most 8 nucleotides that
XX can each form three hydrogen bonds to cytosine; do not contain four
XX consecutive nucleotides able to form three H-bonds each to four
XX consecutive cytosines; do not contain two sequences of three consecutive
XX nucleotides each able to form three H-bonds to three consecutive
XX cytosines, and the ratio between residues able to form two H-bonds each
XX (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
XX oligonucleotides are used to modulate expression of genes, particularly
XX the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control
XX proliferation of primary cell cultures (e.g. bone marrow stem, liver or
XX kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
XX oligonucleotides can also be used to analyse function of proteins (by
XX altering their expression or activity) and therapeutically, e.g. in cases
XX of cancer or (targeting TGF) for stimulating the immune system
XX
XX Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACTGCTG 14
Db 1 CCATCCACTGTATG 14

RESULT 77
AAZ62474/c
ID AAZ62474 standard; RNA; 15 BP.
XX
XX AAZ62474;
XX
XX 28-MAR-2000 (first entry)
XX
XX Substrate for HH ribozyme HCV-1282 which cleaves HCV RNA at nt. 1282.
XX
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
XX cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
XX autoimmune disease; ss.
XX
XX Hepatitis C virus.
XX
XX WO9955847-A2.
XX
XX 04-NOV-1999.
XX
XX 26-APR-1999; 99WO-US0009027.
XX
XX 27-APR-1998; 98US-0083217P.
XX
XX 18-SEP-1998; 98US-0100842P.
XX
XX 25-FEB-1999; 99US-00257608.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
PI

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XX
XX WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
XX hepatitis C infection.
XX
XX Claim 1; Page 52; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
XX enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
XX the Hepatitis C virus (HCV) RNA sequence at the base position given in
XX the descriptor line. The HCV sequence was screened for optimal ribozyme
XX target sites using a computer folding algorithm and regions of the mRNA
XX which did not form secondary folding structures and contained potential
XX ribozyme cleavage sites were identified. Ribozymes were synthesised to
XX target these sites and their activities optimised by either varying the
XX length of the binding arms or by modification to prevent degradation by
XX nucleases. The ribozymes of the invention inhibit gene expression and/or
XX viral replication, and are used to treat diseases associated with
XX Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
XX hepatocellular carcinoma. The ribozymes may be used in combination with
XX interferon to treat HCV infection, other infectious diseases, autoimmune
XX diseases, and cancer
XX
XX Sequence 15 BP; 4 A; 4 C; 3 G; 0 T; 4 U; 0 Other;
SQ
Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGTAAAT 29
Db 15 GTGACCTGATACAT 2

RESULT 78
AAH18890
ID AAH18890 standard; DNA; 15 BP.
XX
XX AAH18890;
XX
XX 21-JUN-2001 (first entry)
XX
XX UCP3 polymorphism detection allele specific primer #3.
XX
XX UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
XX
XX Homo sapiens.
XX
XX WO200118232-A2.
XX
XX 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-US024784.
XX
XX 08-SEP-1999; 99US-0152789P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX (STEP/) STEPHENS J C.
XX
XX Chew A, Choi JY, Denton RR, Nandabalan K;
XX
XX WPI; 2001-218562/22.
XX
XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
XX carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
XX useful for the design of drugs for treating obesity.
XX
XX Claim 15; Page 22; 94pp; English.
XX
XX The present invention relates to the human uncoupling protein 3
XX (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
XX polymorphisms are associated with obesity, especially diabetes mellitus
XX

```


CC associated obesity. They polymorphisms may be identified and analysed to
 CC determine whether an individual is susceptible to obesity and may be used
 CC as the basis for targeted design of drugs to treat obesity. The present
 CC sequence was used in the identification and amplification of UCP3
 CC polymorphisms

XX Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
 SQ Score 10.8; DB 1; Length 15;
 Query Match 37.2%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGAC 21
 Db 1 CCTGCCCTGTGACC 14
 ||||| |||||

RESULT 79
 AAF52803
 ID AAF52803 standard; DNA; 15 BP.

XX AC AAF52803;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-1 oligonucleotide #3763.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wraight CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 85; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood

CC vessels or any other hyperplasia
 XX Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;
 SQ Score 10.8; DB 1; Length 15;

Query Match 37.2%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTG 23
 Db 2 TGCTGTGTGACCTG 15
 ||||| |||||

RESULT 80
 AAF45867/C
 ID AAF45867 standard; DNA; 15 BP.

XX AC AAF45867;

XX DT 30-MAR-2001 (first entry)

XX DE IGFBP2 oligonucleotide #706.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wraight CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 6; Page 38; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCT 22
 Db 15 CTGCTCAGTGACCT 2

RESULT 81
 AAF52804
 ID AAF52804 standard; DNA; 15 BP.

XX AC AAF52804;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGF-I oligonucleotide #3764.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wright CV, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 8; Page 85; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 37.2%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCTG 23
 Db 1 TGCTGTGTGACCTG 14

RESULT 82
 AAF45868/c
 ID AAF45868 standard; DNA; 15 BP.

XX AC AAF45868;
 XX DT 30-MAR-2001 (first entry)
 XX DE IGFBP2 oligonucleotide #707.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 6; Page 38; 201pp; English.

XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 4 A; 4 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 37.2%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGACCT 22
 Db 14 CTGCTCAGTGACCT 1

RESULT 83
ADV35524/c
ID ADV35524 standard; RNA; 15 BP.
XX
AC ADV35524;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human anti-HER2 NCH ribozyme substrate sequence #155.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
OS Homo sapiens.
XX
FN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A; Chowrira B;
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Sproat BS;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX
PS obesity and heart disease.
XX
PS Example 7; Page 474; 717pp; English.
XX
CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,
CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular

carcinoma. The enzymatic nucleic acid molecules can also be used as
diagnostic tools to examine genetic drift and mutations within diseased
cells and to detect the presence of specific RNA in a cell. The present
sequence represents a substrate/target sequence for an anti-HER2 NCH
ribozyme used in the examples of the present invention. Note: Some SEQ ID
Nos are repeated more than once in the specification, but these have
different sequences associated with them.
SQ Sequence 15 BP; 4 A; 5 C; 4 G; 0 T; 2 U; 0 Other;
Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 CTGCTGTGTGACCT 22
Db 14 CTGCAGTGGACCT 1
|||||
RESULT 84
ADV35522/c
ID ADV35522 standard; RNA; 15 BP.
XX
AC ADV35522;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human anti-HER2 NCH ribozyme substrate sequence #153.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
OS Homo sapiens.
XX
FN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A; Chowrira B;
PI Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

```

PT obesity and heart disease.
XX
PS Example 7; Page 474; 717pp; English.
XX
CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention of
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2) and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC zynzyme, and/or DNzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for an anti-HER2 NCH
CC ribozyme used in the examples of the present invention. Note: Some SEQ ID
CC Nos are repeated more than once in the specification, but these have
CC different sequences associated with them.
XX
SQ Sequence 15 BP; 3 A; 6 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TCGTGTGTGACCTG 23
Db ||| ||| |||||
15 TGCAGTGGGACCTG 2

RESULT 85
ABX00325/c
ID ABX00325 standard; RNA; 15 BP.
XX
AC ABX00325;
XX
DT 23-DEC-2002 (first entry)
XX
DE Hepatitis C virus substrate #107 for HCV hammerhead ribozyme #107.
XX
KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS Hepatitis C virus.
XX
PN US2002082225-A1.
XX
PD 27-JUN-2002.
XX
PF 23-MAR-1999; 99US-00274553.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS B.
PA (PAVC/) PAVCO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX

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XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS Claim 1; Page 24; 80pp; English.
XX
CC The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDiEntry.html
XX
SQ Sequence 15 BP; 4 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29
Db ||||| ||| |||
15 GTGACCTGATACAT 2

RESULT 86
AEB74235/c
ID AEB74235 standard; RNA; 15 BP.
XX
AC AEB74235;
XX
DT 22-SEP-2005 (first entry)
XX
DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX
KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
KW antiviral; gene therapy; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN US2002013458-A1.
XX
PD 31-JAN-2002.
XX
PF 15-FEB-2000; 2000US-00504231.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS E.
PA (PAVO/) PAVO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX
PT New enzymatic nucleic acid molecule, which specifically cleaves minus
PT strand RNA derived from hepatitis C virus, useful for modulating the
PT expression and/or replication of hepatitis C virus.
XX
XX Example 1; Page 25; 65pp; English.
XX

```

XX The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves minus strand RNA derived from hepatitis C virus
 CC (HCV). The binding arms of the molecule comprise ribozyme sequences. The
 CC molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
 CC Zinzyne motifs. Also described: (1) a pharmaceutical composition
 CC comprising the novel enzymatic nucleic acid; (2) a mammalian cell
 CC including the novel enzymatic nucleic acid; (3) an expression vector
 CC comprising a nucleic acid sequence encoding at least one enzymatic
 CC nucleic acid molecule, in a manner, which allows expression of that
 CC molecule; (4) a mammalian cell including an expression vector of (3); (5)
 CC methods for treating cirrhosis, liver failure or hepatocellular carcinoma
 CC by administering to a patient the novel enzymatic nucleic acid or the
 CC vector of (3); (6) a method of treating a patient having a condition
 CC associated with HCV infection, by contacting cells of the patient with
 CC the nucleic acid molecule, and further employing one or more drug
 CC therapies; (7) a method for inhibiting HCV replication in a mammalian
 CC cell by administering the novel enzymatic nucleic acid; and (8) a method
 CC of cleaving a separate RNA molecule by contacting the novel enzymatic
 CC nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
 CC is useful for modulating the expression and/or replication of hepatitis C
 CC virus (HCV), and for inhibiting the expression of HCV minus strand. The
 CC nucleic acid may also be used to treat or prevent the occurrence of a
 CC disease state in a patient. The present sequence represents an HCV
 CC hammerhead ribozyme target substrate sequence which is used in the
 CC exemplification of the present invention.

XX SQ Sequence 15 BP; 4 A; 4 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 37.2%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 89;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 16 GTGACCTGGTAAAT 29
 DB ||||| ||||| |||||
 15 GTGACCTGTATACAT 2

RESULT 87
 ABL88273/c
 ID ABL88273 standard; DNA; 15 BP.
 XX
 AC ABL88273;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Human CHRNE allele-specific oligonucleotide (ASO) probe, SEQ ID NO:7.
 XX
 KW Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNE;
 KW chromosome 17p13-12; acetylcholine receptor; AChR;
 KW neuromuscular junction; skeletal muscle; postnatal development;
 KW congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;
 KW genetic variant; single nucleotide polymorphism; SNP; gene therapy;
 KW drug screening; allele-specific oligonucleotide; ASO; probe; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200198316-A2.
 XX
 PD 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-US019835.
 XX
 PF 20-JUN-2000; 2000US-0212870P.
 XX
 PR (GENA-) GENAISSANCE PHARM INC.
 XX
 PA Amaro E, Bieglecki KM, Kliem SE, Koshy B, Tanguay DA;
 XX
 PI WPI; 2002-130787/17.
 XX
 DR Novel genetic variants of cholinergic receptor, nicotinic, epsilon
 XX polypeptide gene useful in studying expression and function of the

PT protein, and for screening drugs to treat diseases e.g. congenital
 PT myasthenic syndrome.
 XX
 PS Claim 17; Page 14; 104pp; English.
 XX
 CC The invention relates to a method for haplotyping the cholinergic
 CC receptor, nicotinic, epsilon polypeptide (CHRNE) gene (ABL88268) of an
 CC individual, and also describes 17 novel polymorphic sites within the
 CC human CHRNE gene. The CHRNE gene is located on chromosome 17p13-12 and
 CC contains 12 exons which encode a 493 amino acid protein (ABB49112). The
 CC CHRNE protein is one of the 5 subunits of mammalian acetylcholine
 CC receptors (AChRs) found at neuromuscular junctions in juveniles and
 CC adults, and is essential for the normal postnatal development of skeletal
 CC muscle. Mutations in the CHRNE gene are associated with congenital
 CC myasthenic syndrome (CMS). CHRNE gene sequences can therefore be used in
 CC gene therapy. The CHRNE gene is also useful for studying the expression
 CC and function of CHRNE, and in expressing CHRNE protein for use in
 CC screening for candidate drugs to treat diseases related to CHRNE. The
 CC method of the invention is useful for haplotyping the CHRNE gene in an
 CC individual, and can also be used in pharmaceutical research to validate
 CC CHRNE as a candidate target for, and in design of clinical trials of
 CC candidate drugs for, treating a specific condition drugs or disease
 CC predicted to be associated with CHRNE activity such as CMS. Polymorphisms
 CC in the target region may be determined by the use of allele-specific
 CC oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by
 CC primer extension using oligonucleotide primers comprising sequences
 CC ABL88371-ABL88354. The CHRNE protein is useful for improving the
 CC efficiency and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with CHRNE
 CC activity, and may be used to screen drugs which target CHRNE. Sequences
 CC ABL88270-ABL88286 represent specifically claimed allele-specific
 CC oligonucleotide (ASO) probes used for detecting polymorphisms in the
 CC CHRNE gene

SQ Sequence 15 BP; 5 A; 5 C; 4 G; 0 T; 0 U; 1 Other;

Query Match 36.6%; Score 10.6; DB 1; Length 15;
 Best Local Similarity 90.9%; Pred. No. 97;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 CCTGCTGTGTG 18
 DB ||||| |||||
 15 CCTGCTGTGTG 5

RESULT 88
 ABLK12178
 ID ABLK12178 standard; DNA; 15 BP.
 XX
 AC ABLK12178;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human Tachykinin Receptor 1 allele specific oligonucleotide probe #8.
 XX
 KW Human; ss; probe; TACR1; Tachykinin receptor 1; chromosome 2; SNP;
 KW single nucleotide polymorphism; gene therapy; haplotype; genotype; pain;
 KW depression; vomiting; acute inflammatory diarrhoea; ASO;
 KW opiate addiction; drug screening; allele specific oligonucleotide.
 XX
 OS Homo sapiens.
 XX
 XX WO200216399-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 27-AUG-2001; 2001WO-US026663.
 XX
 PR 25-AUG-2000; 2000US-0227815P.
 XX
 PR (GENA-) GENAISSANCE PHARM INC.
 XX
 PA Anastasio AB, Kazemi A;
 XX
 PI

XX WIPI; 2002-280907/32.
DR
XX
XX Novel isolated polynucleotide which is a polymorphic variant of
PT tachykinin receptor 1 (TACR1) gene useful for expressing TACR1 protein
PT isoform used in screening drug candidates to treat pain, depression,
PT vomiting.
XX
XX Claim 17; Page 14; 89pp; English.
PS
XX
XX The invention relates to an isolated polynucleotide sequence which
CC comprises a tachykinin receptor 1 (TACR1) isogene (SG) that is any one of
CC 16 SG as given in specification, where each SG comprises specific regions
CC of the TACR1 genomic DNA appearing as ABK1169, and is defined by
CC polymorphisms at positions (P) 3164, 3319, 3906, 4339, 4444, 92915,
CC 94601, 94821, 94892, 94960. Also included are fragments of the TACR1
CC isogenes and TACR1 cDNA, a transgenic non-human animal transformed with
CC the TACR1 isogene or coding region, haplotyping (or genotyping) the TACR1
CC of an individual by determining either the haplotype of one or both
CC copies of the TACR1 gene, predicting the haplotype pair for the TACR1
CC gene of an individual, identifying an association between a trait and a
CC haplotype pair, an isolated oligonucleotide for detecting the
CC polymorphisms, a computer system for storing and analysing polymorphism
CC data and a genome anthology for TACR1 gene. The TACR1 isogene is useful
CC for studying expression and function of TACR1 and expressing TACR1
CC protein for use in screening for candidate drugs to treat diseases
CC related to TACR1 activity. The polymorphism and haplotype data is useful
CC for validating whether TACR1 is a suitable target for drugs to treat
CC pain, depression, vomiting, acute inflammatory diarrhoea and opiate
CC addiction, screening for such drugs and reducing bias in clinical trials
CC of such drugs. The genotyping method is useful for determining whether an
CC individual has one of the haplotype pairs. The haplotyping method is
CC useful for improving efficiency and outcome of several steps in discovery
CC and development of drugs for treating the diseases. The haplotyping
CC method is also useful for validating TACR1 as a candidate target for
CC treating a specific condition or disease predicted to be associated with
CC TACR1 activity. The method is also useful for screening compounds to
CC treat a specific condition or disease predicted to be associated with
CC TACR1 activity. The methods are useful for identifying an association
CC between susceptibility to a disease, staging of a disease, or response to
CC a drug. The gene for TACR1 is located on human chromosome 2. The present
CC sequence is an allele specific oligonucleotide (ASO) probe used to detect
CC polymorphisms in the TACR1 gene
XX
SQ Sequence 15 BP; 3 A; 3 C; 3 G; 5 T; 0 U; 1 Other;
Query Match 36.6%; Score 10.6; DB 1; Length 15;
Best Local Similarity 90.9%; Pred. No. 97;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 10 TGCTGTGTGAC 20
Db |||||:||||
2 TGCTGTGTGAC 12
RESULT 89
ACC70394/c
ID ACC70394 standard; DNA; 13 BP.
XX
XX ACC70394;
XX
DT 11-AUG-2003 (first entry)
XX
DE Cytoprotective response element from a shear stress-regulated gene.
XX
XX Cytoprotective response element; CPRE; oxidative stress;
KW cytoprotective enzyme; hemodynamic shear stress; inflammatory disorder;
KW cardiovascular disease; hyperproliferative disorder; neoplasm;
KW lymphoblastic leukemia; skin cancer; radiation therapy;
KW shear stress-regulated gene; ss.
XX
OS Unidentified.
XX

PN WO2003033662-A2.
XX
XX 24-APR-2003.
XX
XX 16-OCT-2002; 2002WO-US033006.
PF
XX
XX 16-OCT-2001; 2001US-0329870P.
PR
XX
XX (ATHE-) ATHEROGENICS INC.
PA
XX
XX Kunsch C, Varner SE, Chen X, Luchoomun J;
PI
XX
XX WIPI; 2003-403211/38.
DR
XX
XX Novel isolated cytoprotective response element nucleic acid for inducing
PT coordinate activation of genes that protect cells from damaging effects
PT of oxidative stress, e.g. during conditions of hemodynamic shear stress.
XX
XX Claim 2; Fig 6; 13pp; English.
PS
XX
XX The present sequence represents a cytoprotective response element (CPRE).
CC The CPRE is an inducer of the coordinate activation of certain genes that
CC protect cells from damaging effects of oxidative stress. It is also a
CC regulator of cytoprotective effects and an inducer of expression of
CC cytoprotective enzymes. The CPRE is useful for inducing the coordinate
CC activation of certain genes that protect cells from damaging effects of
CC oxidative stress, for example during conditions of hemodynamic shear
CC stress. It is useful as a reagent for the identification of a compound
CC (preferably, a drug) with which it directly or indirectly interacts, or
CC for regulating cytoprotective effects by inducing the expression of
CC cytoprotective enzymes or other factors. A compound identified in this
CC way is useful for treating inflammatory disorders, cardiovascular
CC diseases, hyperproliferative disorders (such as neoplasms, lymphoblastic
CC leukemia, skin cancer, or to protect normal tissues and organs from the
CC damaging effects of chemotherapeutic drugs, radiation therapy and disease
CC processes
XX
SQ Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 35.9%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 91;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 CTGCTGTGTGAC 20
Db |||||:||||
12 CTGCTGTGTGAC 1
RESULT 90
ADL72846
ID ADL72846 standard; DNA; 13 BP.
XX
XX ADL72846;
XX
DT 17-JUN-2004 (first entry)
XX
DE CDNA tag for gene expression analysis method primer SEQ ID NO: 46.
XX
KW ss; cDNA tag; gene expression; restriction enzyme; primer; PCR.
XX
OS Synthetic.
XX
XX WO2004024953-A1.
PN
XX
XX 25-MAR-2004.
PD
XX
XX 05-AUG-2003; 2003WO-JP009901.
PF
XX
XX 12-SEP-2002; 2002JP-00267163.
PR
XX
XX (KURE) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
PA

XX Yamamoto M, Yamamoto N, Hirose K, Sakai J;
 XX WPI; 2004-270062/25.
 XX
 XX Preparation of cDNA tags for identifying expressed genes, useful in
 XX analyzing gene expression, by providing complementary deoxyribonucleic
 XX acids and cleaving the cDNAs with a type II restriction enzyme.
 XX
 XX Example 1; Page 63; 70pp; English.
 XX
 XX The present invention relates to a method for the preparation of cDNA
 XX tags for identifying expressed genes, which comprises providing
 XX complementary deoxyribonucleic acids (cDNAs) and cleaving the cDNAs with
 XX a type II restriction enzyme to prepare cDNA fragments. The method is
 XX useful in the preparation of cDNA tags for identifying expressed genes.
 XX The methods and kits are useful in analyzing gene expression. The present
 XX sequence is a PCR primer for use in the method of the invention.
 XX
 XX Sequence 13 BP; 2 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 35.9%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 91;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 13 TGTGTGACCTGG 24
 DB 2 TGTATGACCTGG 13

RESULT 91
 AAQ78352/c
 ID AAQ78352-standard; DNA; 14 BP.
 XX
 XX AAQ78352;
 XX
 XX 25-MAR-2003 (revised)
 XX 27-JUN-1995 (first entry)
 XX
 XX Antisense oligonucleotide hybridising to TGF-beta gene.
 DE
 XX
 XX Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
 XX angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
 XX carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
 XX immunosuppression; oligonucleotide; ss.
 XX
 XX Synthetic.
 XX
 XX WO9425588-A2.
 XX
 XX 10-NOV-1994.
 XX
 XX 29-APR-1994; 94WO-EP001362.
 XX
 XX 30-APR-1993; 93EP-00107089.
 XX
 XX 13-MAY-1993; 93EP-00107849.
 XX
 XX (BT0G-) BIOGOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 XX
 XX Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
 XX Bogdahn U;
 XX
 XX WPI; 1994-358266/44.
 XX
 XX New transforming growth factor beta anti-sense oligo:nucleotide(s) - for
 XX treating immunosuppression, tumours, etc.
 XX
 XX Claim 6; Page 24; 74pp; English.
 XX
 XX The antisense oligonucleotides are useful in the treatment of tumours in
 XX which expression of TGF-beta is of relevance for pathogenicity and/or
 XX inhibition of pathological angiogenesis. They are used especially for the
 XX treatment of the immunosuppressive effect of TGF-beta, augmentation of

CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
 CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
 CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
 CC of skin carcinogenesis, and treatment of oesophageal and gastric
 CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
 CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
 CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
 CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
 CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 14 BP; 3 A; 1 C; 6 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 35.9%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 91.7%; Pred. No. 98;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCATCCACCTGC 12
 DB 13 CTATCCACCTGC 2

RESULT 92
 AAV57016/c
 ID AAV57016 standard; cDNA; 14 BP.
 XX
 XX AAV57016;
 XX
 XX 25-MAR-2003 (revised)
 XX 21-DEC-1998 (first entry)
 XX
 XX Human Notch3 gene exon 8/intron 8 boundary sequence.
 XX
 XX Human; Notch3; transmembrane receptor; lateral inhibition; regulation;
 XX developmental cascade; neurogenic gene; mutant; neurological disorder;
 XX cerebral autosomal dominant arteriopathy; subcortical infarct; CADASIL;
 XX leukoencephalopathy; therapy; intron; exon; ss.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX exon 1..6
 XX FT /*tag= a
 XX FT /number= 8
 XX FT intron 7..14
 XX FT /*tag= b
 XX FT /number= 8
 XX
 XX FR2751986-A1.
 XX
 XX 06-FEB-1998.
 XX
 XX 16-APR-1997; 97FR-00004680.
 XX
 XX 01-AUG-1996; 96FR-00009733.
 XX
 XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 XX Tournier LE, Joutel A, Bousser MG, Bach JF;
 XX
 XX WPI; 1998-133138/13.
 XX
 XX Human Notch3 nucleic acids - and methods for identifying pre-disposition
 XX to cerebral autosomal dominant arteriopathy with sub-cortical infarcts
 XX and leukoencephalopathy.
 XX
 XX Example 3; Page 20; 45pp; French.
 XX
 XX This sequence represents the boundary between exon 8 and intron 8 of the
 XX human Notch3 gene. Notch3 is a transmembrane receptor protein involved in
 XX lateral inhibition and regulating developmental cascades of neurogenic
 XX genes. Mutated Notch3 proteins are thought to be involved in neurological
 XX disorders, especially of the cerebral autosomal dominant arteriopathy
 XX with subcortical infarcts and leukoencephalopathy (CADASIL) type.

CC Blocking expression of a mutated Notch3 gene or by substitution therapy
CC with non-mutated Notch3 gene or protein can be used to treat CADASIL or
CC related disorders. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 14 BP; 1 A; 1 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 98;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 14 CCACCCACCTGC 3
RESULT 93
AAV92815
ID AAV92815 standard; RNA; 14 BP.
XX
AC AAV92815;
XX
XX 18-FEB-1999 (first entry)
DE Human A-raf target sequence nucleotide position 1831.
XX
KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
KW target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
OS Homo sapiens.
XX
XX WO9805030-A2.
XX
XX 12-NOV-1998.
XX
XX 05-MAY-1998; 98WO-US009249.
XX
PR 09-MAY-1997; 97US-0046059P.
PR 09-JUN-1997; 97US-0049002P.
PR 03-JUL-1997; 97US-0051718P.
PR 22-AUG-1997; 97US-0056808P.
PR 02-OCT-1997; 97US-0061321P.
PR 02-OCT-1997; 97US-0061324P.
PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mesziggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
DR WPI; 1999-009494/01.
XX
PT Identifying new catalytic nucleic acid that modulates selected processes
PT - especially ribozymes that cleave Raf RNA for treating cancer,
PT restenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX Claim 179; Page 164; 259pp; English.
XX
CC A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases

CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
SQ Sequence 14 BP; 1 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 58.3%; Pred. No. 98;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 9 CTGCTGTGTGAC 20
Db 1 CUGCUGUCUGAC 12
RESULT 94
ABQ83257
ID ABQ83257 standard; DNA; 14 BP.
XX
AC ABQ83257;
XX
XX 18-JAN-2003 (first entry)
DE Expressed gene identification cDNA tag related oligonucleotide SEQ:30.
XX
XX cDNA tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Homo sapiens.
XX
XX WO200274951-A1.
XX
XX 26-SEP-2002.
XX
XX 13-MAR-2002; 2002WO-JP002338.
XX
XX 15-MAR-2001; 2001JP-00073959.
XX
XX (KURE) KUREHA CHEM IND CO LTD.
XX (YAMA/) YAMAMOTO M.
XX (YAMA/) YAMAMOTO N.
XX
XX Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX
XX WPI; 2002-759896/82.
XX
XX Construction of cDNA tags for identifying expressed genes with specific
PT linkers and recognition sequences, applicable in gene expression
PT analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 22; 59pp; Japanese.
XX
XX The present invention describes a method for constructing a cDNA tag for
XX identifying an expressed gene. The method comprises: (a) preparation of
XX complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX linker Y ligated material; and (e) cleaving the amplification product.
XX The method can be used for the construction of cDNA tags for identifying
XX expressed genes, which is applicable in gene expression analysis, disease
XX diagnosis and identifying target for gene therapy, including the
XX clarification of difference in function or morphology of cells under
XX physiological or pathological conditions. The cDNA or cells for assay can
XX be specifically expressed, with reproducibility and accuracy in the
XX detection of genes. The present sequence represents an expressed gene
XX identification (EGI) cDNA tag related oligonucleotide which is used in an
XX example from the present invention


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XX SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
      Query Match      35.9%; Score 10.4; DB 1; Length 14;
      Best Local Similarity 91.7%; Pred. No. 98;
      Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 13 TGTGTGACCTGG 24
    ||| |||||
Db 2 TGTATGACCTGG 13

RESULT 95
ID AA286497 standard; DNA; 10 BP.
XX AC AA286497;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5731.
XX KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX KW non-metastatic breast tumour tissue; gene therapy; anticancer;
XX KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089883P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
XX PA (ROBE/) ROBERTS B L.
XX PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX DR
XX PT Isolated polynucleotides differentially expressed between metastatic and
XX PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX PT treatment of cancer.
XX PS Claim 1; Page 209; 219pp; English.
XX CC
XX CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX CC that are preferentially transcribed in the metastatic breast tumour
XX CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX CC to AAZ86677 represent tags corresponding to distinct transcripts that are
XX CC preferentially transcribed in the primary or non-metastatic breast tumour
XX CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX CC transcripts can be used for diagnosis, prognosis, monitoring and
XX CC treatment of breast cancer, particularly where metastatic. Diagnosis is
XX CC by standard immunoassays or hybridisation/amplification reactions.
XX CC Compounds that modulate expression of the transcripts are potentially
XX CC useful for treatment of (metastatic) breast cancer, while promoters from
XX CC the transcripts are used to direct expression, in selected cell types, of
XX CC e.g. therapeutic genes (also ribozymes or antisense sequences),
XX CC particularly an antigen-encoding sequence for use in gene or cell-based
XX CC vaccines. Polypeptides encoded by the transcripts are also useful in
XX CC vaccines; for diagnosing breast cancer and for raising specific
XX CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX CC agents. Host cells that produce the polypeptides can be used to expand
XX CC and isolate populations of educated, antigen-specific immune effector

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CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
XX immunotherapy
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
      Query Match      34.5%; Score 10; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 81;
      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 CCTGCTGTGT 17
    |||||
Db 10 CCTGCTGTGT 1

RESULT 96
ID AA95175 standard; DNA; 10 BP.
XX AC AA95175;
XX DT 12-JAN-2001 (first entry)
XX DE Primer #22 for detection of TNFR1 polymorphism by primer extension.
XX KW TNFR1; tumour necrosis factor receptor; polymorphism; human; tumour;
XX KW cancer; apoptosis; bacterial infection; primer; primer extension; ss.
XX OS Homo sapiens.
XX PN WO200050436-A1.
XX PD 31-AUG-2000.
XX PF 23-FEB-2000; 2000WO-US004606.
XX PR 23-FEB-1999; 99US-0121314P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PA (NAND/) NANDABALAN K.
XX PA (SCHU/) SCHULZ V P.
XX PA (STEP/) STEPHENS J C.
XX PA (CHEW/) CHEW A.
XX PI Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX WPI; 2000-543909/49.
XX DR
XX PT Polynucleotides comprising polymorphic variants of a reference sequence
XX PT for tumor necrosis factor receptor 1 (TNFR1), useful for studying the
XX PT biological function of TNFR1 and identifying drugs targeting the protein
XX PT for treating disorders.
XX PS Claim 15; Page 21; 79pp; English.
XX CC
XX CC The present invention relates to polymorphic variants of the tumour
XX CC necrosis factor receptor 1 (TNFR1) gene. The sequence of the gene is
XX CC given in AA95102, AA95103 and AA95104. The polymorphisms were
XX CC identified by amplifying and sequencing regions of the gene. Twelve
XX CC polymorphic loci were discovered. Of these twelve polymorphisms, four can
XX CC cause a change in the TNFR1 protein. The present sequence is the terminal
XX CC sequence of a primer used for detection of a TNFR1 gene polymorphism by
XX CC primer extension. The TNFR1 polymorphisms may be useful for studying the
XX CC biological function of TNFR1 as well as for identifying drugs targeting
XX CC the protein for treatment of disorders related to its abnormal expression
XX CC or function such as tumours, apoptosis related disorders and bacterial
XX CC infection
XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
      Query Match      34.5%; Score 10; DB 1; Length 10;
      Best Local Similarity 100.0%; Pred. No. 81;
      Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 98
ADD71297//
ID ADD7
XX
AC ADD7
XX

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XX 20-DEC-2001; 2001WO-EP015178.
XX PF
XX 03-JAN-2001; 2001DE-01000121.
XX PR
XX (HENK ) HENKEL KGAA.
XX PA
XX Petersohn D, Conradt M, Hofmann K;
XX PI
XX WPI; 2002-528865/56.
XX DR
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX PT screening for cosmetic or therapeutic agents, based on differential gene
XX PT expression.
XX
XX Claim 8; Page 73; 325pp; German.
XX PS
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX CC or animals, are important for skin ageing and/or skin stress by serial
XX CC analysis of gene expression between mixtures of transcribed and
XX CC optionally translated, genetically encoded factors (A) obtained from
XX CC young and aged skin, to identify that genes that show strong differential
XX CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX CC useful for: identifying markers of skin ageing and/or stress; determining
XX CC skin ageing and/or stress; and identifying or determining the effects of
XX CC pharmaceutical or cosmetic agents for control of skin ageing. The present
XX CC sequence is one of a group of human skin ageing/stress related expressed
XX CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
XX
Query Match 34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 ATCCACCTGC 12
Db 1 ATCCACCTGC 10
|||||
|
RESULT 100
ABV66313
ID ABV66313 standard; cDNA; 11 BP.
XX AC
XX ABV66313;
XX
XX 21-OCT-2002 (first entry)
XX DT
XX Human skin EST 4099.
XX DE
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX OS
XX WO200253774-A2.
XX PN
XX 11-JUL-2002.
XX PD
XX 20-DEC-2001; 2001WO-EP015179.
XX PF
XX Human skin EST 4099.
XX PR
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX OS
XX WO200253774-A2.
XX PN
XX 11-JUL-2002.
XX PD
XX 20-DEC-2001; 2001WO-EP015179.
XX PF
XX 03-JAN-2001; 2001DE-01000127.
XX PR
XX (HENK ) HENKEL KGAA.
XX PA
XX Petersohn D, Conradt M, Hofmann K;
XX PI
XX WPI; 2002-590638/63.
XX DR
XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX
XX Disclosure; Page 108; 1345pp; German.
XX PS
XX The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX
XX SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
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XX Disclosure; Page 138; 1345pp; German.
XX PS
XX The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX
XX SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
XX
Query Match 34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 CATCCACCTG 11
Db 1 CATCCACCTG 10
|||||
|
RESULT 101
ABV65203
ID ABV65203 standard; cDNA; 11 BP.
XX AC
XX ABV65203;
XX
XX 21-OCT-2002 (first entry)
XX DT
XX Human skin EST 2989.
XX DE
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX OS
XX WO200253774-A2.
XX PN
XX 11-JUL-2002.
XX PD
XX 20-DEC-2001; 2001WO-EP015179.
XX PF
XX 03-JAN-2001; 2001DE-01000127.
XX PR
XX (HENK ) HENKEL KGAA.
XX PA
XX Petersohn D, Conradt M, Hofmann K;
XX PI
XX WPI; 2002-590638/63.
XX DR
XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX
XX Disclosure; Page 108; 1345pp; German.
XX PS
XX The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
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CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
SQ Sequence 11 BP; 1 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match      34.5%; Score 10; DB 1; Length 11;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19
Db 2 TGCTGTGTGA 11

RESULT 102
ABV63737
ID ABV63737 standard; cDNA; 11 BP.
AC ABV63737;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 1523.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match      34.5%; Score 10; DB 1; Length 11;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
Db 1 ATCCACCTGC 10

RESULT 103
ABV71158
ID ABV71158 standard; cDNA; 11 BP.
XX
AC ABV71158;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 8944.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytosatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
PS WPI; 2002-590638/63.
XX
CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match      34.5%; Score 10; DB 1; Length 11;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
Db 1 ATCCACCTGC 10

RESULT 104
AAD34268/C
ID AAD34268 standard; DNA; 11 BP.
XX
AC AAD34268;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human CYP2D6 gene polymorphic site 1255 detecting sense 5' oligo.
XX
KW Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
KW ligase-based sequenced determination; drug metabolism; chromosome 22; ss.

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XX OS	Homo sapiens.	PA	(CHEF) GRUENENTHAL GMBH.
XX PN	WO200218638-A2.	XX PI	Weihe E, Bieller A, Schaefer MKH;
XX XX		XX DR	WPI; 2004-468868/44.
XX PD	07-MAR-2002.	XX XX	
XX XX	27-AUG-2001; 2001WO-IB001544.	XX PT	New nucleic acid that modulates expression of the vanilloid receptor-1,
XX XX		XX PT	useful for control of pain or sensitivity disorders, comprises sequences
XX PR	30-AUG-2000; 2000GB-00021286.	XX PT	from control regions of the receptor gene.
XX XX	(GEMI-) GEMINI GENOMICS PLC.	XX PS	Disclosure; Page 53; 68pp; German.
XX PA	Risinger C, Andersson MK, Lewander T, Oliasson E;	XX XX	
XX PI	WPI; 2002-329785/36.	XX CC	This invention describes a novel nucleic acid containing a specific
XX XX		XX CC	segment having at least one region that modulates expression of the VR1
XX DR		XX CC	(vanilloid receptor type 1) receptor, or a functional derivative, allele
XX XX		XX CC	or fragment of this region, or a sequence that hybridises to it under
XX PT	New sequence determination oligonucleotides, useful for detecting	XX CC	standard conditions. The VR1 modulator is derived from one or more of
XX PT	polymorphic sites in a 5' flanking region of a CYP2D6 gene, as	XX CC	positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
XX PT	hybridization probes, as components of diagnostic assays, or in ligase-	XX CC	44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
XX XX	based sequence determination.	XX CC	pain, particularly in primary sensory neurons. The invention also
XX PT		XX CC	describes a vector that contains the VR1 modulator, host cells containing
XX XX		XX CC	this vector (other than human germ or embryonal stem cells) and a method
XX PS	Claim 2; Page 23; 63pp; English.	XX CC	for modulating expression of the VR1 receptor by introducing the
XX CC	The invention relates to sequence determination oligonucleotides for	XX CC	modulator or the vector into a cell that contains the VR1 gene. The
XX CC	detecting polymorphic sites in a 5' flanking region of cytochrome P450	XX CC	products of the invention are used for detecting a transcription factor
XX CC	2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many	XX CC	from its binding to a regulatory sequence (or a double-stranded
XX CC	different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The	XX CC	oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
XX CC	oligonucleotides may be used as in situ hybridisation probes, in ligase-	XX CC	linked immunosorbent assay, particularly for diagnosis of diseases
XX CC	based sequence determination, as components of diagnostic assays, as	XX CC	associated with overexpression or underexpression of the transcription
XX CC	probes in sequence determination methods based on mismatches, as	XX CC	factor. The region that modulates VR1 receptor expression includes a
XX CC	hybridisation-based diagnostic assays, and as components of diagnostic	XX CC	binding site for a transcription factor, e.g. MZF1, NFKappaB, NFAT or
XX CC	microarray. CYP2D6 is useful to predict variations in an individual's	XX CC	GATA1. The nucleic acids of the invention, or vectors containing them,
XX CC	ability to metabolise certain drugs. The present sequence is a sense	XX CC	are used for prevention or treatment of pain, also for treating
XX CC	oligonucleotide used for detecting of human CYP2D6 gene 5' flanking	XX CC	sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
XX CC	region single nucleotide polymorphism (SNP)	XX CC	neuralgia and myalgia, that are associated with activity of the VR1
XX XX		XX CC	receptor. This sequence represents a fragment of human VR1 exon 1d DNA
XX SQ	Sequence 11 BP; 2 A; 0 C; 7 G; 2 T; 0 U; 0 Other;	XX XX	which is capable of binding to a transcription factor.
Query Match 34.5%; Score 10; DB 1; Length 11;			
Best Local Similarity 100.0%; Pred. No. 90;			
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 CCATCCACCT 10	QY	3 ATCCACCTGC 12
Db		Db	
	11 CCATCCACCT 2		1 ATCCACCTGC 10
RESULT 105			
ADQ30368		RESULT 106	
ID	ADQ30368 standard; DNA; 11 BP.	ABI43156	
XX		ID	ABI43156 standard; DNA; 12 BP.
AC	ADQ30368;	XX	
XX		AC	ABI43156;
XX		XX	
DT	09-SEP-2004 (first entry)	DT	22-FEB-2002 (first entry)
XX		XX	
DE	Human VR1 exon 1d transcription factor binding fragment #87.	XX	
XX		DE	Oligonucleotide primer SEQ ID NO 343129 for detecting SNP TSC0042904.
XX		XX	
KW	ds; VR1 receptor; vanilloid receptor type 1; modulator;	XX	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	pain transmission; primary sensory neuron; transcription factor;	KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	detection; MZF1; NFKappaB; NFAT; GATA1; sensitivity disorder; analgesia;	KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
KW	hypalgesia; hyperalgesia; neuralgia; myalgia; human.	XX	
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
XX		XX	
PN	WO2004053120-A2.	PN	WO200177384-A2.
XX		XX	
XX		XX	
PD	24-JUN-2004.	PD	18-OCT-2001.
XX		XX	
XX		XX	
PF	01-DEC-2003; 2003WO-EP013522.	PF	06-APR-2001; 2001WO-IB000713.
XX		XX	
XX		XX	
PR	09-DEC-2002; 2002DE-01057421.	PR	07-APR-2000; 2000DE-01019173.
XX		XX	

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 343129; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 34.5%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 3 CCATCCACCT 12
 RESULT 107
 ABI05465
 ID ABI05465 standard; DNA; 12 BP.
 XX
 AC ABI05465;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 305438 for detecting SNP TSC0021446.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 305438; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 34.5%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 3 CCATCCACCT 12
 RESULT 107
 ABI05465
 ID ABI05465 standard; DNA; 12 BP.
 XX
 AC ABI05465;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 305438 for detecting SNP TSC0021446.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 FN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 305438; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 34.5%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 2 CCATCCACCT 11
 RESULT 108
 ADQ30383/c
 ID ADQ30383 standard; DNA; 12 BP.
 XX
 AC ADQ30383;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human VRI exon 1d transcription factor binding fragment #102.
 XX
 KW ds; VRI receptor; vanilloid receptor type 1; modulator;
 KW pain transmission; primary sensory neuron; transcription factor;
 KW detection; MZFI; NPKAPPAB; NFAT; GATAl; sensitivity disorder; analgesia;
 KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.
 XX
 OS Homo sapiens.
 XX
 FN WO2004053120-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 01-DEC-2003; 2003WO-EP013522.
 XX
 PR 09-DEC-2002; 2002DE-01057421.
 XX
 PA (CHEF) GRUENENTHAL GMBH.
 XX
 PI Weihe E, Bieller A, Schaefer MKH;
 XX WPI; 2004-468868/44.
 XX
 DR New nucleic acid that modulates expression of the vanilloid receptor-1,
 XX useful for control of pain or sensitivity disorders, comprises sequences
 PT from control regions of the receptor gene.
 PT
 XX Disclosure; Page 53; 68pp; German.
 XX
 XX This invention describes a novel nucleic acid containing a specific
 CC segment having at least one region that modulates expression of the VRI
 CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
 CC or fragment of this region, or a sequence that hybridises to it under
 CC standard conditions. The VRI modulator is derived from one or more of
 CC positions 221931-22344 of GenBank AL670399, 31673-36359 of AL663116, or
 CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
 CC pain, particularly in primary sensory neurons. The invention also
 CC describes a vector that contains the VRI modulator, host cells containing
 CC this vector (other than human germ or embryonal stem cells) and a method
 CC for modulating expression of the VRI receptor by introducing the
 CC modulator or the vector into a cell that contains the VRI gene. The
 CC products of the invention are used for detecting a transcription factor

CC from its binding to a regulatory sequence (or a double-stranded
 CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
 CC linked immunosorbant assay, particularly for diagnosis of diseases
 CC associated with overexpression or underexpression of the transcription
 CC factor. The region that modulates VRL receptor expression includes a
 CC binding site for a transcription factor, e.g. MZF1, NFKappaB, NFAT or
 CC GATA1. The nucleic acids of the invention, or vectors containing them,
 CC are used for prevention or treatment of pain, also for treating
 CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
 CC neuralgia and myalgia, that are associated with activity of the VRL
 CC receptor. This sequence represents a fragment of human VRL exon 1d DNA
 CC which is capable of binding to a transcription factor.
 XX
 SQ Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ATCCACCTGC 12
 |||||
 Db 12 ATCCACCTGC 3

RESULT 109
 ADQ30420/c
 ID ADQ30420 standard; DNA; 12 BP.
 AC ADQ30420;
 XX
 XX
 DT 09-SEP-2004 (first entry)
 XX
 XX Human VRL exon 1d transcription factor binding fragment #139.
 XX
 KW ds; VRL receptor; vanilloid receptor type 1; modulator;
 KW pain transmission; primary sensory neuron; transcription factor;
 KW detection; MZF1; NFKappaB; NFAT; GATA1; sensitivity disorder; analgesia;
 KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2004053120-A2.
 PN
 XX
 PD 24-JUN-2004.
 XX
 XX
 PF 01-DEC-2003; 2003WO-EP013522.
 XX
 PR 09-DEC-2002; 2002DE-01057421.
 XX
 PA (CHEF) GRUENENTHAL GMBH.
 XX
 PI Weihe E, Bieller A, Schaefer MKH;
 XX
 XX WPI; 2004-468868/44.
 DR
 XX
 PT New nucleic acid that modulates expression of the vanilloid receptor-1,
 PT useful for control of pain or sensitivity disorders, comprises sequences
 PT from control regions of the receptor gene.
 XX
 XX
 PS Disclosure; Page 54; 68pp; German.
 XX

CC This invention describes a novel nucleic acid containing a specific
 CC segment having at least one region that modulates expression of the VRL
 CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
 CC or fragment of this region, or a sequence that hybridises to it under
 CC standard conditions. The VRL modulator is derived from one or more of
 CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
 CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
 CC pain, particularly in primary sensory neurons. The invention also
 CC describes a vector that contains the VRL modulator, host cells containing
 CC this vector (other than human germ or embryonal stem cells) and a method
 CC for modulating expression of the VRL receptor by introducing the
 CC modulator or the vector into a cell that contains the VRL gene. The

CC products of the invention are used for detecting a transcription factor
 CC from its binding to a regulatory sequence (or a double-stranded
 CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
 CC linked immunosorbant assay, particularly for diagnosis of diseases
 CC associated with overexpression or underexpression of the transcription
 CC factor. The region that modulates VRL receptor expression includes a
 CC binding site for a transcription factor, e.g. MZF1, NFKappaB, NFAT or
 CC GATA1. The nucleic acids of the invention, or vectors containing them,
 CC are used for prevention or treatment of pain, also for treating
 CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
 CC neuralgia and myalgia, that are associated with activity of the VRL
 CC receptor. This sequence represents a fragment of human VRL exon 1d DNA
 CC which is capable of binding to a transcription factor.
 XX
 SQ Sequence 12 BP; 3 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ATCCACCTGC 12
 |||||
 Db 12 ATCCACCTGC 3

RESULT 110
 ABC35433
 ID ABC35433 standard; DNA; 13 BP.
 XX
 AC ABC35433;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 XX Oligonucleotide SEQ ID NO 35450 for detecting SNP TSC0011230.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 35450; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

ABCL14106/c	
ID	ABC14106 standard; DNA; 13 BP.
XX	
AC	ABC14106;
XX	
DT	20-FEB-2002 (first entry)
XX	
DE	Oligonucleotide SEQ ID NO 14113 for detecting SNP TSC0003223.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2001-657177/75.
XX	
PT	Set of oligonucleotides, useful for diagnosis and cell typing, is
PT	designed to detect single-nucleotide polymorphisms and cytosine
PT	methylation status.
XX	
PS	Claim 1; SEQ ID NO 14113; 29bp + Sequence Listing; German.
XX	
CC	This invention describes novel oligonucleotide primers or peptide nucleic
CC	acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC	and cytosine methylation status in chemically pretreated genomic DNA. The
CC	oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC	range of diseases including immune system, gastrointestinal, respiratory,
CC	central nervous system, cardiovascular and metabolic disorders. The
CC	oligomers are also used for detecting cell type differentiation. ABC00010
CC	-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC	represent the oligomers described in the invention. NOTE: The sequence
CC	data for this patent did not form part of the printed specification, but
CC	was obtained in electronic format from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 13 BP; 2 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
Query Match	34.5%; Score 10; DB 1; Length 13;
Best Local Similarity	100.0%; Pred.No. 1.1e+02;
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 CCATCCACCT 10
Db	13 CCATCCACCT 4
RESULT 113	
ABCL14104/c	
ID	ABC14104 standard; DNA; 13 BP.
XX	
AC	ABCL14104;
XX	
DT	20-FEB-2002 (first entry)
XX	
DE	Oligonucleotide SEQ ID NO 14111 for detecting SNP TSC0003223.
XX	
KW	SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW	central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX	

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 34.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 1 CCATCCACCT 10
 RESULT 116
 ID ABC35432/C
 XX ABC35432 standard; DNA; 13 BP.
 AC ABC35432;
 XX
 DT 20-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 35449 for detecting SNP TSC0011230.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 35449; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 34.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 1 CCATCCACCT 10
 RESULT 117
 ID ABF12887
 XX ABF12887 standard; DNA; 13 BP.
 AC ABF12887;
 XX
 DT 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 112884 for detecting SNP TSC0028229.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 112884; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
 Query Match 34.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 4 CCATCCACCT 13
 RESULT 118
 ID ABH01640/C
 XX ABH01640 standard; DNA; 13 BP.
 AC ABH01640;
 XX

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 12 CCATCCACCT 3
 RESULT 117
 ID ABF12887
 XX ABF12887 standard; DNA; 13 BP.
 AC ABF12887;
 XX
 DT 21-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 112884 for detecting SNP TSC0028229.
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 112884; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 1 Other;
 Query Match 34.5%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 4 CCATCCACCT 13
 RESULT 118
 ID ABH01640/C
 XX ABH01640 standard; DNA; 13 BP.
 AC ABH01640;
 XX

```

DT XX 22-FEB-2002 (first entry)
DE XX Oligonucleotide SEQ ID NO 201617 for detecting SNP TSC0049588.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 201617; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 3 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
Db 11 CCATCCACCT 2

RESULT 119
ABC14105
ID ABC14105 standard; DNA; 13 BP.
XX
XX ABC14105;
AC
XX
XX 20-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 14112 for detecting SNP TSC0003223.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

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XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 14112; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 13 BP; 4 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
Db 1 CCATCCACCT 10

RESULT 120
ADE14132
ID ADE14132 standard; DNA; 13 BP.
XX
XX ADE14132;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Optineurin promoter motif, repeat element or regulatory region #241.
XX
XX Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX
XX Homo sapiens.
XX
XX US2003190617-A1.
XX
XX 09-OCT-2003.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX 06-MAR-2002; 2002US-00091281.
XX
XX (SIEE/) SI E.
PA (RAYM/) RAYMOND V.
PA (MORI/) MORISSETTE J.
XX
XX Raymond V, Morissette J, Si E;
XX
XX WPI; 2003-864168/80.
XX

```

PT New nucleic acid sequences of the optineurin gene are useful to detect
PT polymorphisms particularly single nucleotide polymorphisms in the
PT optineurin promoter to diagnose, prognose and treat glaucoma and related
PT disorders.
XX
XX Claim 11; SEQ ID NO 243; 159pp; English.
XX
XX The invention relates to an isolated nucleic acid (N1) comprising at
CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
CC promoter appearing as ADE13890. Also included are the optineurin promoter
CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
CC detecting a single nucleotide polymorphism (SNP) in the optineurin
CC promoter, a host cell comprising the promoter operably linked to a
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
CC in a promoter region of the optineurin gene, associated with a glaucoma
CC phenotype), detecting a SNP sequence variation in a sample containing
CC DNA, detecting the presence of an optineurin promoter sequence variation
CC in a sample containing DNA, determining the presence or increased
CC susceptibility to glaucoma or to a progressive ocular hypertensive
CC disorder resulting in loss of visual field in a patient (or the severity
CC or progression of glaucoma in a patient, comprising providing
CC amplification reaction primers that direct amplification of a selected
CC nucleic acid region containing the variation within the optineurin
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
CC obtaining a sample containing human genomic DNA, providing a nucleic acid
CC capable of detecting a SNP located within an optineurin promoter, and
CC detecting the polymorphism). The invention is used to diagnose and
CC prognose glaucoma and also to treat glaucoma related disorders. The
CC present sequence is an optineurin promoter motif, repeat element or
CC putative regulatory region.
XX
XX Sequence 13 BP; 2 A; 6 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 34.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATCCACTGTC 12
DB |||||
2 ATCCACTGTC 11
RESULT 121
AAV92770
ID AAV92770 standard; RNA; 14 BP.
XX
XX AAV92770;
XX
XX 18-FEB-1999 (first entry)
XX
XX Human A-raf target sequence nucleotide position 366.
DE
XX Human; C-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene; delivery;
KW screening; identification; synthesis; deprotection; purification; cancer;
KW inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
KW restenosis; rheumatoid arthritis; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9805030-A2.
PN
XX 12-NOV-1998.
PD
XX
XX 05-MAY-1998; 98WO-US009249.
XX
XX 09-MAY-1997; 97US-0046059P.
PR
XX 03-JUN-1997; 97US-0049002P.
PR
XX 03-JUL-1997; 97US-0051718P.
PR
XX 22-AUG-1997; 97US-0056808P.
PR
XX 02-OCT-1997; 97US-0061321P.
PR
XX 02-OCT-1997; 97US-0061324P.
PR

PR 05-NOV-1997; 97US-0064866P.
PR 19-DEC-1997; 97US-0068212P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Jarvis T, Matulic-Adamic J, Reynolds M, Kisich K, Bellon L;
PI Parry T, Beigelman L, Mcswiggen JA, Karpeisky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
XX
XX WPI; 1999-009494/01.
DR
XX Identifying new catalytic nucleic acid that modulates selected processes
XX -especially ribozymes that cleave Raf RNA for treating cancer,
PT resenosis, and also new ribozymes and modified nucleoside triphosphates
PT used as antiviral agents and synthons.
XX
XX Claim 179; Page 163; 259pp; English.
XX
XX A method has been developed for the identification of a nucleic acid
CC capable of modulating a process in a biological system. The method
CC comprises: (a) introducing into the system a random library of nucleic
CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
CC in systems where modulation has occurred and/or determining the sequence
CC of at least part of the SBDs in such systems. Nucleic acid molecules with
CC endonuclease activity and catalytic activity, from the present invention,
CC are used to modulate gene expression in plant and mammalian cells and to
CC cleave target nucleic acid, particularly for treating systemic diseases
CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
CC ascites and infection. They may also be used to detect genetic drift and
CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
CC with RNA-cleaving activity that modulate expression of the Raf gene, are
CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
CC generally any condition associated with the level of c-raf. Introduction
CC of sugar/phosphate modifications increases stability against nuclease and
CC activity, AAV90922 to AAV93877 represent NACs that can be used in the
CC method, specifically for modulating the expression of a Raf gene
XX
XX Sequence 14 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;
SQ
Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 9 CTGCTGTGTG 18
DB |::|::|
4 CUGCUGUGUG 13
RESULT 122
AAZ64774
ID AAZ64774 standard; RNA; 14 BP.
XX
XX AAZ64774;
XX
XX 28-MAR-2000 (first entry)
DT
XX
XX Substrate for hairpin ribozyme which cleaves HCV at nt. 3887.
DE
XX Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
XX Hepatitis C virus.
OS
XX
XX WO9955847-A2.
PN
XX 04-NOV-1999.
PD
XX 26-APR-1999; 99WO-US009027.
PF
XX 27-APR-1998; 98US-0083217P.
PR
XX 18-SEP-1998; 98US-0100842P.
PR

```

PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
PA (RIBO-) RIBOZYME PHARM INC.
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
XX hepatitis C infection.
XX
XX Claim 2; Page 97; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
XX enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the
XX Hepatitis C virus (HCV) RNA sequence at the base position given in the
XX descriptor line. The HCV sequence was screened for optimal ribozyme
XX target sites using a computer folding algorithm and regions of the mRNA
XX which did not form secondary folding structures and contained potential
XX ribozyme cleavage sites were identified. Ribozymes were synthesised to
XX target these sites and their activities optimised by either varying the
XX length of the binding arms or by modification to prevent degradation by
XX nucleases. The ribozymes of the invention inhibit gene expression and/or
XX viral replication, and are used to treat diseases associated with
XX Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
XX hepatocellular carcinoma. The ribozymes may be used in combination with
XX interferon to treat HCV infection, other infectious diseases, autoimmune
XX diseases, and cancer
XX
XX Sequence 14 BP; 0 A; 3 C; 7 G; 0 T; 4 U; 0 Other;
XX
XX Query Match 34.5%; Score 10; DB 1; Length 14;
XX Best Local Similarity 60.0%; Pred. No. 1.2e+02;
XX Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 9 CTGCTGTGTG 18
Db :|:|:|:|:|
4 CUGCUGUGUG 13

RESULT 123
AAZ37042
ID AAZ37042 standard; DNA; 14 BP.
AC AAZ37042;
XX
XX 27-MAR-2000 (first entry)
XX
XX Probe targeted to the conserved SNP 4.5S RNA of Escherichia coli.
XX
XX Signal recognition particle; SRP; 4.5S RNA; non-viral organism; probe;
XX infection; screening; ss.
XX
XX Synthetic.
XX Escherichia coli.
XX
XX WO9966079-A1.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013799.
XX
XX 19-JUN-1998; 98US-0090063P.
XX
XX (MOSA-) MOSAIC TECHNOLOGIES.
XX
XX Boles TC, Weir L, Stone BB;
XX
XX WPI; 2000-097755/08.
XX
XX Detecting non-viral organisms in samples, useful e.g. in medical
XX diagnosis and for screening medical and food supplies.

```

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XX Claim 19; Page 32; 49pp; English.
XX
XX AAZ37038-45 represent probes targeted to a sequence of the Escherichia
XX coli signal recognition particle (SRP) 4.5S RNA which is conserved across
XX bacteria (see AAZ37037). SRP RNA is found in all non-viral organisms, and
XX has regions that are conserved in phylogenetic groups. Probes targeted to
XX this region will therefore hybridise to all members of that group, but
XX not to organism outside of the specified group. The probes are used in
XX the method of the invention for the detection of a group (e.g. a kingdom
XX or order) of non-viral organisms in a sample (in this case, E. coli). The
XX method comprises using a nucleic acid probe with a SNP RNA from the group
XX to be detected (where the probe is substantially complementary to a
XX subsequence of the SRP RNA). The methods can be used to detect non-viral
XX organisms in samples such as food, clinical, medical, environmental and
XX assay control samples, useful e.g. in medical and veterinary diagnostics
XX (e.g. to diagnose infection with specific organisms), screening medical
XX and food supplies (e.g. to eliminate contaminants in medical supplies
XX such as whole blood) and screening for soil and water contamination. The
XX methods are especially useful to detect non-viral organisms in human
XX samples
XX
XX Sequence 14 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 34.5%; Score 10; DB 1; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 17 TGACCTGGTA 26
Db :|:|:|:|:|
5 TGACCTGGTA 14

RESULT 124
ABX01611
ID ABX01611 standard; RNA; 14 BP.
XX
XX ABX01611;
XX
XX 23-DEC-2002 (first entry)
XX
XX Hepatitis C virus substrate #96 for HCV hairpin ribozyme #96.
XX
XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
XX HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
XX liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
XX type I interferon; interferon alpha; interferon beta; cytostatic;
XX interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
XX substrate; hairpin ribozyme; HP ribozyme; ss.
XX
XX Hepatitis C virus.
XX
XX US2002082225-A1.
XX
XX 27-JUN-2002.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX 23-MAR-1999; 99US-00274553.
XX
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX (ROBE/) ROBERTS B.
XX (PAVC/) PAVCO P A.
XX (MACE/) MACEJACK D.
XX
XX Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX WPI; 2002-617759/66.
XX
XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
XX replication and are useful to treat hepatitis C virus infections and
XX cirrhosis, liver failure or hepatocellular carcinoma.

```

XX PS Claim 2; Page 61; 80pp; English.

XX CC The present invention relates to enzymatic nucleic acids which specifically cleave RNA derived from Hepatitis C virus (HCV). The enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin (HP) motif where the binding arms comprise sequences complementary to one of the substrate sequences defined in the specification. The HCV ribozymes are useful for modulating the expression and/or replication of HCV. They can be used to treat cirrhosis, liver failure and/or hepatocellular carcinoma. The HCV ribozymes are also useful for treating a condition associated with HCV infection in conjunction with one or more other drug therapies, particularly type I interferon, especially interferon alpha, beta or gamma or consensus interferon. The present sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note: Some of the sequence data for this patent did not form part of the printed specification. The complete sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/paipsDIDEntry.html

XX CC seqdata.uspto.gov/paipsDIDEntry.html

XX SQ Sequence 14 BP; 0 A; 3 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
|:|:|:|:|:
Db 4 CUGCUGUGUG 13

RESULT 125
AEB76535
ID AEB76535 standard; RNA; 14 BP.
XX AC AEB76535;
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hairpin ribozyme substrate sequence.
XX KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection; antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002013458-A1.
XX PD 31-JAN-2002.
XX PF 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS E.
PA (PAVO/) PAVO P A.
PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX New enzymatic nucleic acid molecule, which specifically cleaves minus strand RNA derived from hepatitis C virus, useful for modulating the expression and/or replication of hepatitis C virus.
XX Example 1; Page 44; 65pp; English.
XX The invention relates to an enzymatic nucleic acid molecule which specifically cleaves minus strand RNA derived from hepatitis C virus (HCV). The binding arms of the molecule comprise ribozyme sequences. The

CC molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and Zinzyme motifs. Also described: (1) a pharmaceutical composition comprising the novel enzymatic nucleic acid; (2) a mammalian cell including the novel enzymatic nucleic acid; (3) an expression vector comprising a nucleic acid sequence encoding at least one enzymatic nucleic acid molecule, in a manner, which allows expression of that molecule; (4) a mammalian cell including an expression vector of (3); (5) methods for treating cirrhosis, liver failure or hepatocellular carcinoma by administering to a patient the novel enzymatic nucleic acid or the vector of (3); (6) a method of treating a patient having a condition associated with HCV infection, by contacting cells of the patient with the nucleic acid molecule, and further employing one or more drug therapies; (7) a method for inhibiting HCV replication in a mammalian cell by administering the novel enzymatic nucleic acid; and (8) a method of cleaving a separate RNA molecule by contacting the novel enzymatic nucleic acid with the separate RNA molecule. The enzymatic nucleic acid is useful for modulating the expression and/or replication of hepatitis C virus (HCV), and for inhibiting the expression of HCV minus strand. The nucleic acid may also be used to treat or prevent the occurrence of a disease state in a patient. The present sequence represents an HCV hairpin ribozyme target substrate sequence which is used in the exemplification of the present invention.

XX SQ Sequence 14 BP; 0 A; 3 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
|:|:|:|:|:
Db 4 CUGCUGUGUG 13

RESULT 126
AAA06015
ID AAA06015 standard; DNA; 13 BP.
XX AC AAA06015;
XX DT 14-JUN-2000 (first entry)
XX DE CFTR gene analysis oligonucleotide probe SEQ ID NO:25.
XX KW CFTR; cystic fibrosis transmembrane conductance regulator; detection; mutation; probe; human; hybridisation; ss.
XX OS Homo sapiens.
XX PN US6027880-A.
XX PD 22-FEB-2000.
XX PF 10-OCT-1995; 95US-00544381.
XX PR 26-OCT-1993; 93US-00143312.
PR 02-AUG-1994; 94US-00284064.
PR 26-OCT-1994; 94WO-US012305.
PR 02-AUG-1995; 95US-00510521.
XX PA (AFFY-) AFFYMETRIX INC.
XX Huang XC, Chee M, Lobban PE, Hubbell EA, Sheldon EL, Miyada CG;
PI Cronin MT, Lipshutz RU, Morris MS, Fodor SPA;
XX WPI; 2000-194825/17.
XX An array of nucleic acid probes immobilized on a solid support, useful for identifying mutations in the cystic fibrosis transmembrane conductance regulator.
XX Disclosure; Col 73; 114pp; English.

CC The present invention describes an array of nucleic acid probes
 CC immobilised on a solid support, which comprises: (1) a first probe set,
 CC comprising probes with a segment of at least 6 nucleotides complementary
 CC to the CFTR (cystic fibrosis transmembrane conductance regulator) gene,
 CC where the segment includes at least 1 interrogation position
 CC complementary to a nucleotide in the CFTR gene sequence; and (2) second,
 CC third and fourth probe sets, each comprising probes identical to those in
 CC (1) except that the interrogation position is occupied by a different
 CC nucleotide. AAA05991 to AAA06240 represent CFTR gene analysis
 CC oligonucleotide probes for use in the exemplification of the present
 CC invention. The present invention also describes a method of comparing a
 CC target nucleic acid with a reference sequence consisting of a
 CC predetermined sequence of nucleotides, comprising: (a) hybridising a
 CC sample comprising the target nucleic acid to an array of nucleic acid
 CC probes immobilised on a solid support; (b) comparing the relative
 CC specific binding of two corresponding probes from the first and second
 CC probe sets; (c) assigning a nucleotide in the target sequence as the
 CC complement of the interrogation position of the probe having the greater
 CC specific binding; and (d) repeating (b) and (c) by comparing the relative
 CC specific binding of a further two corresponding probes from the first and
 CC second probe sets until each nucleotide of interest in the target
 CC sequence has been assigned. The array is useful for analysis of the CFTR
 CC gene, e.g. detection of mutations
 XX
 SQ Sequence 13 BP; 0 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 33.8%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
 |||||
 Db 1 TGGTGTGTGCCCT 13

RESULT 127
 ABF45366/c
 ID ABF45366 standard; DNA; 13 BP.
 XX
 AC ABF45366;
 XX
 DT 21-FEB-2002 (first entry)
 DE
 DE Oligonucleotide SEQ ID NO 145363 for detecting SNP TSC0036590.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.
 XX
 XX Claim 1; SEQ ID NO 145363; 29pp + Sequence Listing; German.
 XX
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 33.8%; Score 9.8; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGCT 13
 |||||
 Db 13 CCATCCGCTACT 1

RESULT 128

ABF45367
 ID ABF45367 standard; DNA; 13 BP.

XX
 AC ABF45367;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 145364 for detecting SNP TSC0036590.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 XX methylation status.

XX Claim 1; SEQ ID NO 145364; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 XX and cytosine methylation status in chemically pretreated genomic DNA. The
 XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 XX range of diseases including immune system, gastrointestinal, respiratory,
 XX central nervous system, cardiovascular and metabolic disorders. The
 XX oligomers are also used for detecting cell type differentiation. ABC00010
 XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
 XX represent the oligomers described in the invention. NOTE: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 2 A; 7 C; 1 G; 3 T; 0 U; 0 Other;

Query Match	33.8%;	Score 9.8;	DB 1;	Length 13;
Best Local Similarity	84.6%;	Pred. No. 1.2e+02;		
Matches	11;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	1	CCATCCACCTGCT 13		
DB	1	CCATCCGCTACT 13		
RESULT 129				
ABK28875				
ID	ABK28875	standard; DNA; 13 BP.		
XX				
AC	ABK28875;			
XX				
DT	09-APR-2002	(first entry)		
XX				
DE	HPV blocker probe PZ-1.			
XX				
KW	HSV-1; HSV-2; HPV; HBV; ss; probe; microorganism classification;			
KW	infectious disease; genetic abnormality; cancer; capture sequence;			
KW	blocker probe.			
XX				
OS	Human papillomavirus.			
XX				
PN	WO200196608-A1.			
XX				
PD	20-DEC-2001.			
XX				
PF	15-JUN-2001;	2001WO-US019353.		
XX				
PR	15-JUN-2000;	2000US-00594839.		
XX				
PA	(DIGE-) DIGENE CORP.			
XX				
PI	Anthony J, Lorincz A, Williams I, Troy J, Tang Y;			
XX				
DR	WPI; 2002-130748/17.			
XX				
PT	Detecting a target nucleic acid, for identifying microorganisms,			
PT	diagnosing infections or detecting genetic abnormalities, comprises			
PT	producing and detecting double-stranded hybrids between probes and the			
PT	target nucleic acid.			
XX				
PS	Claim 53; Page 24; 128pp; English.			
XX				
CC	The invention relates to detecting a target nucleic acid comprising (a)			
CC	hybridising a single-stranded or partially single-stranded target nucleic			
CC	acid to a capture sequence probe and a signal sequence probe to form			
CC	double-stranded hybrids between the probes and the target nucleic acid,			
CC	where the capture sequence probe and the signal sequence probe are			
CC	capable of hybridising to non-overlapping regions within the target			
CC	nucleic acid and not hybridising to each other, (b) adding a blocker			
CC	probe to the hybridisation reaction, where the blocker probe hybridises			
CC	to excess non-hybridised capture sequence probes, (c) binding the hybrid			
CC	to a solid phase to form a bound hybrid, and (d) detecting the bound			
CC	hybrid. The method is used to detecting a target nucleic acid. The method			
CC	is useful for identifying and classifying microorganisms, diagnosing			
CC	infectious diseases, detecting and characterising genetic abnormalities,			
CC	identifying genetic changes associated with cancer, studying genetic			
CC	susceptibility to disease, and measuring response to various types of			
CC	treatment. The method is also useful for detecting the presence of			
CC	nucleic acid in test samples. The method is not only rapid and sensitive,			
CC	but is also highly specific and capable of discriminating highly			
CC	homologous nucleic acid target sequences. Blocker probes comprising			
CC	oligonucleotides complementary to the capture sequence probes are used in			
CC	the method to eliminate excess capture sequence probe, thus reducing the			
CC	background signal in detection and increasing specificity of the assay.			
CC	The present sequence is a blocker probe derived from HSV-1, HSV-2, HPV or			
CC	HBV sequences			
XX				
SQ	Sequence 13 BP; 1 A; 7 C; 2 G; 3 T; 0 U; 0 Other;			
Query Match	33.8%;	Score 9.8;	DB 1;	Length 13;
Best Local Similarity	84.6%;	Pred. No. 1.2e+02;		
Matches	11;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;

Query Match	33.8%;	Score 9.8;	DB 1;	Length 13;
Best Local Similarity	84.6%;	Pred. No. 1.2e+02;		
Matches	11;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;
QY	5	CCACCTGCTGTGT 17		
DB	1	CCACCTCCTGCT 13		
RESULT 130				
ABZ34180/c				
ID	ABZ34180	standard; DNA; 13 BP.		
XX				
AC	ABZ34180;			
XX				
DT	31-JAN-2003	(first entry)		
XX				
DE	HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:422.			
XX				
KW	Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;			
KW	detection; mutation; anti-HIV drug resistance; polymorphism; resistance;			
KW	probe; ss.			
XX				
OS	Human immunodeficiency virus 1.			
OS	Synthetic.			
XX				
PN	WO200255741-A2.			
XX				
PD	18-JUL-2002.			
XX				
PF	09-JAN-2002;	2002WO-EP000153.		
XX				
PR	11-JAN-2001;	2001EP-00870005.		
PR	20-APR-2001;	2001EP-00870085.		
PR	24-APR-2001;	2001US-0286102P.		
XX				
PA	(INNO-) INNOGENETICS NV.			
XX				
PI	De Smet K, Stuyver L;			
XX				
DR	WPI; 2002-590680/63.			
XX				
PT	Detecting mutations associated with anti-HIV drug resistance comprises			
PT	detecting at least one of the mutations in the HIV reverse transcriptase			
PT	gene by using probes optimized to function together in a reverse-			
PT	hybridization assay.			
XX				
PS	Claim 2; Page 27; 117pp; English.			
XX				
CC	The present invention describes a method for detecting mutations			
CC	associated with anti-HIV drug resistance in a patient by detecting at			
CC	least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,			
CC	G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)			
CC	of HIV strains in a biological sample using a specific set of probes			
CC	optimised to function together in a reverse-hybridisation assay. The			
CC	method and the nucleic acid sequences used in the method are useful for			
CC	determining viral mutations and/or polymorphisms in the HIV RT gene			
CC	associated with resistance. The probes are useful for the genetic			
CC	detection, preferably in vitro detection of the mutations K103N/R,			
CC	V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or			
CC	T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the			
CC	mutation is associated with anti-HIV drug resistance. The method provides			
CC	a rapid, reliable and precise assay or determination and monitoring of			
CC	antiviral drug resistance or mutations associated with drug resistance of			
CC	viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT			
CC	sequences and probes which are used in the exemplification of the present			
CC	invention			
XX				
SQ	Sequence 13 BP; 3 A; 2 C; 5 G; 3 T; 0 U; 0 Other;			
Query Match	33.8%;	Score 9.8;	DB 1;	Length 13;
Best Local Similarity	84.6%;	Pred. No. 1.2e+02;		
Matches	11;	Conservative 0;	Mismatches 2;	Indels 0; Gaps 0;


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Qy      2 CATCCACCTGCTG 14
Db      13 CATCCACGTACTG 1

RESULT 131
ID      AB2341155 standard; DNA; 13 BP.
XX
AC      AB2341155;
XX
DT      31-JAN-2003 (first entry)
XX
DE      HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:397.
XX
KW      Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
KW      detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
KW      probe; ss.
XX
OS      Human immunodeficiency virus 1.
OS      Synthetic.
XX
PN      WO200255741-A2.
XX
18-JUL-2002.
XX
09-JAN-2002; 2002WO-EP000153.
XX
11-JAN-2001; 2001EP-00870005.
XX
20-APR-2001; 2001EP-00870085.
XX
24-APR-2001; 2001US-0286102P.
XX
(INNO-) INNOGENETICS NV.
XX
De Smet K, Stuyver L;
XX
WPI; 2002-590680/63.
XX
Detecting mutations associated with anti-HIV drug resistance comprises
PT detecting at least one of the mutations in the HIV reverse transcriptase
PT gene by using probes optimized to function together in a reverse-
PT hybridization assay.
XX
Claim 2; Page 26; 117pp; English.
XX
The present invention describes a method for detecting mutations
CC associated with anti-HIV drug resistance in a patient by detecting at
CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
CC of HIV strains in a biological sample using a specific set of probes
CC optimised to function together in a reverse-hybridisation assay. The
CC method and the nucleic acid sequences used in the method are useful for
CC determining viral mutations and/or polymorphisms in the HIV RT gene
CC associated with resistance. The probes are useful for the genetic
CC detection, preferably in vitro detection of the mutations K103N/R,
CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
CC mutation is associated with anti-HIV drug resistance. The method provides
CC a rapid, reliable and precise assay or determination and monitoring of
CC antiviral drug resistance or mutations associated with drug resistance of
CC viruses containing RT genes. AB233759 to AB234642 represent HIV RT
CC sequences and probes which are used in the exemplification of the present
CC invention
XX
SQ      Sequence 13 BP; 3 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred.No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 CATCCACCTGCTG 14
Db      13 CATCCACGTACTG 1

RESULT 132
ID      ADF48833 standard; DNA; 13 BP.
XX
AC      ADF48833;
XX
DT      12-FEB-2004 (first entry)
XX
DE      DNA array associated oligonucleotide #25.
XX
SS; DNA array; microfabricated array; DNA chip; CFTR gene mutation;
KW cystic fibrosis gene; uncharacterised mutation identification;
KW simultaneous screening.
XX
OS      Synthetic.
XX
US2003165823-A1.
XX
04-SEP-2003.
XX
22-FEB-2000; 2000US-00510378.
XX
26-OCT-1993; 93US-00143312.
XX
02-AUG-1994; 94US-00284064.
XX
26-OCT-1994; 94WO-US012305.
XX
02-AUG-1995; 95US-00510521.
XX
10-OCT-1995; 95US-00544381.
XX
(CRON/) CRONIN M T.
PA (MIYA/) MIYADA C G.
PA (HUBE/) HUBBELL E A.
PA (CHEE/) CHEE M.
PA (FODO/) FODOR S P A.
PA (HUAN/) HUANG X C.
PA (LIPS/) LIPSHUTZ R J.
PA (LOBE/) LOBBAN P E.
PA (MORR/) MORRIS M S.
PA (SHEL/) SHELTON E L.
XX
Cronin MT, Miyada CG, Hubbell EA, Chee M, Fodor SPA, Huang XC;
PI Lipshutz RJ, Lobban PE, Morris MS, Sheldon EL;
XX WPI; 2004-020546/02.
XX
Arrays of oligonucleotide probes immobilized in microfabricated patterns
PT on chips used for detecting mutations in the cystic fibrosis
PT transmembrane conductance regulator (CFTR) gene.
XX
Disclosure; SEQ ID NO 25; 123pp; English.
XX
The invention relates to an array of oligonucleotide probes immobilised
CC on a solid support, the array comprising at least two sets of
CC oligonucleotide probes (a microfabricated array or DNA chip). The arrays
CC can be used in methods to detect uncommon mutations in the CFTR gene.
CC Prior art methods for analysis of the cystic fibrosis gene do not monitor
CC large regions of the CFTR gene. The invention uses a large number of
CC probes and therefore permits the identification of uncharacterised
CC mutations and the simultaneous screening of large numbers of mutations
CC with a high degree of accuracy. The present sequence is used in the
CC exemplification of the invention.
XX
SQ      Sequence 13 BP; 0 A; 3 C; 5 G; 5 T; 0 U; 0 Other;
XX
Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred.No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      10 TCGTGTGTGACCT 22
Db      1 TGGTGTGTGACCT 13

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred.No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 133
AAQ78366
ID AAQ78366 standard; DNA; 14 BP.
XX AC AAQ78366;
XX DT 25-MAR-2003 (revised)
XX DT 27-JUN-1995 (first entry)
XX DE Antisense oligonucleotide hybridising to TGF-beta gene.
XX KW Transforming growth factor beta; TGF-beta; antisense; treatment; tumour;
KW angiogenesis; breast tumour; neurofibroma; glioma; glioblastoma;
KW carcinogenesis; carcinoma; oesophagus; oesophageal; gastric; gut;
KW immunosuppression; oligonucleotide; ss.
XX OS Synthetic.
XX PN W09425588-A2.
XX PD 10-NOV-1994.
XX PF 29-APR-1994; 94WO-EP001362.
XX PR 30-APR-1993; 93EP-00107089.
XX PR 13-MAY-1993; 93EP-00107849.
XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX PI Schlingensiepen G, Brysch W, Schlingensiepen K, Schlingensiepen R;
PI Bogdahn U;
XX DR WPI; 1994-358266/44.
XX PT New transforming growth factor beta anti:sense oligo:nucleotide(s) - for
XX PT treating immunosuppression, tumours, etc.
XX PS Claim 6; Page 28; 74pp; English.
XX CC The antisense oligonucleotides are useful in the treatment of tumours in
XX CC which expression of TGF-beta is of relevance for pathogenicity and/or
XX CC inhibition of pathological angiogenesis. They are used especially for the
XX CC treatment of the immunosuppressive effect of TGF-beta, augmentation of
XX CC the proliferation of cytotoxic lymphocytes, treatment of endogenous
XX CC hyperexpression of TGF-beta, treatment of breast tumours, neurofibromas
XX CC and malignant gliomas, including glioblastomas, treatment and prophylaxis
XX CC of skin carcinogenesis, and treatment of oesophageal and gastric
XX CC carcinomas. See AAQ78352-Q78488. The sequences given in GENESEQ files
XX CC AAQ78352-Q78407 and AAQ78488 are antisense oligodeoxynucleotides of TGF-
XX CC beta 1. The sequences given in GENESEQ files AAQ78408-78487 are antisense
XX CC oligodeoxynucleotides of TGF-beta 2 in the form of phosphorothioate
XX CC analogues. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 14 BP; 1 A; 3 C; 4 G; 6 T; 0 U; 0 Other;
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 TGCTGTGTGACCT 22
|||||||
DB 1 TGCTGTGTGTACT 13
RESULT 134
AAV48778
ID AAV48778 standard; DNA; 14 BP.
XX AC AAV48778;
XX DT 15-OCT-1998 (first entry)
XX DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:398.
XX KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
XX DE ErbbB-2 gene antisense oligonucleotide ErbbB-2-70.
XX DE ErbbB-2; antisense oligonucleotide; modulate; gene expression; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN EP856579-A1.
XX PD 05-AUG-1998.
XX PF 31-JAN-1997; 97EP-00101531.
XX PR 31-JAN-1997; 97EP-00101531.
XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX PI Schlingensiepen K, Brysch W;
XX DR WPI; 1998-400910/35.
XX PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
XX PT consecutive guanosine or inosine - and have specific ratio of residues
XX PT able to form two or three hydrogen bonds, have greater activity and
XX PT reduced toxicity, used therapeutically or to modulate growth of cells in
XX PT culture.
XX PS Claim 10; Fig 6b; 286pp; English.
XX CC AAV48709-886 represent antisense oligonucleotides directed against the
XX CC ErbbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted in
XX CC significant reduction in ErbbB-2 protein expression, while
XX CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
XX CC exemplify the invention. The specification describes oligonucleotides
XX CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
XX CC can each form three hydrogen bonds to cytosine; do not contain four
XX CC consecutive nucleotides able to form three H-bonds each to four
XX CC consecutive cytosines; do not contain two sequences of three consecutive
XX CC nucleotides each able to form three H-bonds to three consecutive
XX CC cytosines, and the ratio between residues able to form two H-bonds each
XX CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
XX CC oligonucleotides are used to modulate expression of genes, particularly
XX CC the genes for p53, Erbb-2, junB, junD, TGF-beta 1 or beta 2 to control
XX CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
XX CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
XX CC oligonucleotides can also be used to analyse function of proteins (by
XX CC altering their expression or activity) and therapeutically, e.g. in cases
XX CC of cancer or (targeting TGF) for stimulating the immune system
XX SQ Sequence 14 BP; 2 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 11 GCTGTGTGACCTG 23
|||||||
DB 1 GCTGTGTGCACAG 13
RESULT 135
ABZ34156/C
ID ABZ34156 standard; DNA; 14 BP.
XX AC ABZ34156;
XX DT 31-JAN-2003 (first entry)
XX DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:398.
XX KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;

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KW probe; ss.
 XX Human immunodeficiency virus 1.
 OS Synthetic.
 XX WO200255741-A2.
 XX 18-JUL-2002.
 XX 09-JAN-2002; 2002WO-EP000153.
 XX 11-JAN-2001; 2001EP-00870005.
 XX 20-APR-2001; 2001EP-00870085.
 XX 24-APR-2001; 2001US-0286102P.
 XX (INNO-) INNOGENETICS NV.
 XX De Smet K, Stuyver L;
 XX WPI; 2002-590680/63.
 XX
 XX Detecting mutations associated with anti-HIV drug resistance comprises
 XX detecting at least one of the mutations in the HIV reverse transcriptase
 XX gene by using probes optimized to function together in a reverse-
 XX hybridization assay.
 XX
 XX Claim 2; Page 26; 117pp; English.
 XX
 XX The present invention describes a method for detecting mutations
 XX associated with anti-HIV drug resistance in a patient by detecting at
 XX least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
 XX G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
 XX of HIV strains in a biological sample using a specific set of probes
 XX optimised to function together in a reverse-hybridisation assay. The
 XX method and the nucleic acid sequences used in the method are useful for
 XX determining viral mutations and/or polymorphisms in the HIV RT gene
 XX associated with resistance. The probes are useful for the genetic
 XX detection, preferably in vitro detection of the mutations K103N/R,
 XX V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
 XX T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
 XX mutation is associated with anti-HIV drug resistance. The method provides
 XX a rapid, reliable and precise assay or determination and monitoring of
 XX antiviral drug resistance or mutations associated with drug resistance of
 XX viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT
 XX sequences and probes which are used in the exemplification of the present
 XX invention
 XX
 XX Sequence 14 BP; 3 A; 1 C; 5 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 33.8%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CATCCACCTGCTG 14
 Db ||||| |||||
 14 CATCCACATACGT 2
 RESULT 136
 ABZ34175/C
 ID ABZ34175 standard; DNA; 14 BP.
 XX
 XX ABZ34175;
 AC
 XX 31-JAN-2003 (first entry)
 XX
 XX HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:417.
 DE
 XX Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
 XX detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
 KW probe; ss.
 KW
 XX Human immunodeficiency virus 1.
 OS

OS Synthetic.
 XX WO200255741-A2.
 XX 18-JUL-2002.
 XX 09-JAN-2002; 2002WO-EP000153.
 XX 11-JAN-2001; 2001EP-00870005.
 XX 20-APR-2001; 2001EP-00870085.
 XX 24-APR-2001; 2001US-0286102P.
 XX (INNO-) INNOGENETICS NV.
 XX De Smet K, Stuyver L;
 XX WPI; 2002-590680/63.
 XX
 XX Detecting mutations associated with anti-HIV drug resistance comprises
 XX detecting at least one of the mutations in the HIV reverse transcriptase
 XX gene by using probes optimized to function together in a reverse-
 XX hybridization assay.
 XX
 XX Claim 2; Page 27; 117pp; English.
 XX
 XX The present invention describes a method for detecting mutations
 XX associated with anti-HIV drug resistance in a patient by detecting at
 XX least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
 XX G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
 XX of HIV strains in a biological sample using a specific set of probes
 XX optimised to function together in a reverse-hybridisation assay. The
 XX method and the nucleic acid sequences used in the method are useful for
 XX determining viral mutations and/or polymorphisms in the HIV RT gene
 XX associated with resistance. The probes are useful for the genetic
 XX detection, preferably in vitro detection of the mutations K103N/R,
 XX V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
 XX T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
 XX mutation is associated with anti-HIV drug resistance. The method provides
 XX a rapid, reliable and precise assay or determination and monitoring of
 XX antiviral drug resistance or mutations associated with drug resistance of
 XX viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT
 XX sequences and probes which are used in the exemplification of the present
 XX invention
 XX
 XX Sequence 14 BP; 4 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 33.8%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 CATCCACCTGCTG 14
 Db ||||| |||||
 13 CATCCACATACGT 1
 RESULT 137
 ABZ34152/C
 ID ABZ34152 standard; DNA; 14 BP.
 XX
 XX ABZ34152;
 AC
 XX 31-JAN-2003 (first entry)
 XX
 XX HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:394.
 DE
 XX Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
 XX detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
 KW probe; ss.
 KW
 XX Human immunodeficiency virus 1.
 OS Synthetic.
 XX WO200255741-A2.
 PN

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XX PD 18-JUL-2002.
XX PF
XX PR 09-JAN-2002; 2002WO-EP000153.
XX PR 11-JAN-2001; 2001EP-00870005.
XX PR 20-APR-2001; 2001EP-00870085.
XX PR 24-APR-2001; 2001US-0286102P.
XX PA (INNO-) INNOGENETICS NV.
XX PI De Smet K, Stuyver L;
XX PS WPI; 2002-590680/63.
XX PT Detecting mutations associated with anti-HIV drug resistance comprises
XX PT detecting at least one of the mutations in the HIV reverse transcriptase
XX PT gene by using probes optimized to function together in a reverse-
XX PT hybridization assay.
XX PS Claim 2; Page 26; 117pp; English.
XX CC The present invention describes a method for detecting mutations
XX CC associated with anti-HIV drug resistance in a patient by detecting at
XX CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
XX CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
XX CC of HIV strains in a biological sample using a specific set of probes
XX CC optimised to function together in a reverse-hybridisation assay. The
XX CC method and the nucleic acid sequences used in the method are useful for
XX CC determining viral mutations and/or polymorphisms in the HIV RT gene
XX CC associated with resistance. The probes are useful for the genetic
XX CC detection, preferably in vitro detection of the mutations K103N/R,
XX CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
XX CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
XX CC mutation is associated with anti-HIV drug resistance. The method provides
XX CC a rapid, reliable and precise assay or determination and monitoring of
XX CC antiviral drug resistance or mutations associated with drug resistance of
XX CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT
XX CC sequences and probes which are used in the exemplification of the present
XX CC invention
XX SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CATCCACCTGCTG 14
Db ||||| |||
2 CATCCACGTACTG 2

RESULT 138
ABZ34170/C
ID ABZ34170 standard; DNA; 14 BP.
XX AC ABZ34170;
XX DT 31-JAN-2003 (first entry)
XX DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:412.
XX KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
XX KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
XX KW probe; ss.
XX OS Human immunodeficiency virus 1.
XX OS Synthetic.
XX PN WO200255741-A2.
XX PD 18-JUL-2002.
XX PF
XX PR 09-JAN-2002; 2002WO-EP000153.
XX PR 11-JAN-2001; 2001EP-00870005.
XX PR 20-APR-2001; 2001EP-00870085.
XX PR 24-APR-2001; 2001US-0286102P.
XX PA (INNO-) INNOGENETICS NV.
XX PI De Smet K, Stuyver L;
XX PS WPI; 2002-590680/63.
XX PT Detecting mutations associated with anti-HIV drug resistance comprises
XX PT detecting at least one of the mutations in the HIV reverse transcriptase
XX PT gene by using probes optimized to function together in a reverse-
XX PT hybridization assay.
XX PS Claim 2; Page 26; 117pp; English.
XX CC The present invention describes a method for detecting mutations
XX CC associated with anti-HIV drug resistance in a patient by detecting at
XX CC least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
XX CC G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
XX CC of HIV strains in a biological sample using a specific set of probes
XX CC optimised to function together in a reverse-hybridisation assay. The
XX CC method and the nucleic acid sequences used in the method are useful for
XX CC determining viral mutations and/or polymorphisms in the HIV RT gene
XX CC associated with resistance. The probes are useful for the genetic
XX CC detection, preferably in vitro detection of the mutations K103N/R,
XX CC V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
XX CC T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
XX CC mutation is associated with anti-HIV drug resistance. The method provides
XX CC a rapid, reliable and precise assay or determination and monitoring of
XX CC antiviral drug resistance or mutations associated with drug resistance of
XX CC viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT
XX CC sequences and probes which are used in the exemplification of the present
XX CC invention
XX SQ Sequence 14 BP; 3 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
XX
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CATCCACCTGCTG 14
Db ||||| |||
2 CATCCACGTACTG 2

RESULT 139
ABZ34179/C
ID ABZ34179 standard; DNA; 14 BP.
XX AC ABZ34179;
XX DT 31-JAN-2003 (first entry)
XX DE HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:421.
XX KW Human immunodeficiency virus; HIV; reverse transcriptase; RT; enzyme;
XX KW detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
XX KW probe; ss.
XX OS Human immunodeficiency virus 1.
XX OS Synthetic.
XX PN WO200255741-A2.
XX PD 18-JUL-2002.
XX PF
XX PR 09-JAN-2002; 2002WO-EP000153.
XX PR 11-JAN-2001; 2001EP-00870005.
XX PR

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PR 20-APR-2001; 2001EP-00870085.
PR 24-APR-2001; 2001US-0286102P.
XX (INNO-) INNOGENETICS NV.
XX De Smet K, Stuyver L;
XX WPI; 2002-590680/63.
XX
XX Detecting mutations associated with anti-HIV drug resistance comprises
XX detecting at least one of the mutations in the HIV reverse transcriptase
XX gene by using probes optimized to function together in a reverse-
XX hybridization assay.
XX Claim 2; Page 27; 117pp; English.
XX
XX The present invention describes a method for detecting mutations
XX associated with anti-HIV drug resistance in a patient by detecting at
XX least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
XX G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
XX of HIV strains in a biological sample using a specific set of probes
XX optimised to function together in a reverse-hybridisation assay. The
XX method and the nucleic acid sequences used in the method are useful for
XX determining viral mutations and/or polymorphisms in the HIV RT gene
XX associated with resistance. The probes are useful for the genetic
XX detection, preferably in vitro detection of the mutations K103N/R,
XX V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
XX T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
XX mutation is associated with anti-HIV drug resistance. The method provides
XX a rapid, reliable and precise assay or determination and monitoring of
XX antiviral drug resistance or mutations associated with drug resistance of
XX viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT
XX sequences and probes which are used in the exemplification of the present
XX invention
XX
XX Sequence 14 BP; 4 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
Db 13 CATCCACGTACTG 1

RESULT 140
ABZ341172/c
XX ABZ341172 standard; DNA; 14 BP.
XX
XX ABZ341172;
XX
XX 31-JAN-2003 (first entry)
XX
XX HIV-1 reverse transcriptase mutation detection probe SEQ ID NO:414.
XX
XX Human immunodeficiency virus 1.
XX detection; mutation; anti-HIV drug resistance; polymorphism; resistance;
XX probe; ss.
XX
XX Human immunodeficiency virus 1.
XX Synthetic.
XX
XX W0200255741-A2.
XX
XX 18-JUL-2002.
XX
XX 09-JAN-2002; 2002WO-EP000153.
XX
XX 11-JAN-2001; 2001EP-00870005.
XX 20-APR-2001; 2001EP-00870085.
XX 24-APR-2001; 2001US-0286102P.
XX
PR 20-APR-2001; 2001EP-00870085.
PR 24-APR-2001; 2001US-0286102P.
XX (INNO-) INNOGENETICS NV.
XX De Smet K, Stuyver L;
XX WPI; 2002-590680/63.
XX
XX Detecting mutations associated with anti-HIV drug resistance comprises
XX detecting at least one of the mutations in the HIV reverse transcriptase
XX gene by using probes optimized to function together in a reverse-
XX hybridization assay.
XX Claim 2; Page 27; 117pp; English.
XX
XX The present invention describes a method for detecting mutations
XX associated with anti-HIV drug resistance in a patient by detecting at
XX least one of the mutations K103N/R, V106A/I/L, Y181C/I, M184V/I, Y188L,
XX G190A/S/R, T215Y/F/D/S/A and/or Q151M/L in the reverse transcriptase (RT)
XX of HIV strains in a biological sample using a specific set of probes
XX optimised to function together in a reverse-hybridisation assay. The
XX method and the nucleic acid sequences used in the method are useful for
XX determining viral mutations and/or polymorphisms in the HIV RT gene
XX associated with resistance. The probes are useful for the genetic
XX detection, preferably in vitro detection of the mutations K103N/R,
XX V106A/I/L, Y181C/I, Q151M/L, M184V/I, Y188L, G190A/S/R and/or
XX T215Y/F/D/S/A in the RT of HIV strains in a biological sample, where the
XX mutation is associated with anti-HIV drug resistance. The method provides
XX a rapid, reliable and precise assay or determination and monitoring of
XX antiviral drug resistance or mutations associated with drug resistance of
XX viruses containing RT genes. ABZ33759 to ABZ34642 represent HIV RT
XX sequences and probes which are used in the exemplification of the present
XX invention
XX
XX Sequence 14 BP; 4 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
Db 13 CATCCACGTACTG 1

RESULT 141
AEA60845
XX AEA60845 standard; DNA; 14 BP.
XX
XX AEA60845;
XX
XX 11-AUG-2005 (first entry)
XX
XX Blood fluke Sjpp 5'-RACE PCR primer Sjpp-P.
XX
XX Sjpp; RACE; PCR; primer; ss.
XX
XX Fasciola sp.
XX Synthetic.
XX
XX CN1563382-A.
XX
XX 12-JAN-2005.
XX
XX 16-APR-2004; 2004CN-00017743.
XX
XX 16-APR-2004; 2004CN-00017743.
XX (SHAN-) SHANGHAI LIVESTOCK PARASTITIC DISEASE IN.
XX
XX Lin J, Yao L, Fu Z;
XX
XX WPI; 2005-307227/32.
XX
XX Gene of Chinese Mainland Sjpp gene stock of Japanese blood fluke, clone,
XX

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PT expression and application.
XX
PS Example 1; Page 9; 25pp; Chinese.
XX
XX The invention relates to a novel blood fluke gene designated SjPP. Also
CC described are methods for cloning and expressing the SjPP gene. The
CC present sequence represents a 5'-RACE PCR primer for the blood fluke SjPP
CC gene, which is used in an example from the present invention.
XX
SQ Sequence 14 BP; 1 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
    Query Match      33.8%; Score 9.8; DB 1; Length 14;
    Best Local Similarity 84.6%; Pred. No. 1.3e+02;
    Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGTG 16
Db 2 TCCGCATGCTGTG 14

RESULT 142
AAZ18959
ID AAZ18959 standard; DNA; 11 BP.
XX
XX AAZ18959;
AC
XX 22-OCT-1999 (first entry)
DT
XX Murine MRL SAGE tag 1334652.
DE
XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX Mus sp.
OS
XX WO9941364-A2.
PN
XX 19-AUG-1999.
PD
XX 12-FEB-1999; 99WO-US002962.
PF
XX 13-FEB-1998; 98US-0074737P.
PR
XX 26-AUG-1998; 98US-0097937P.
PR
XX 28-SEP-1998; 98US-0102051P.
XX
XX (WIST-) WISTAR INST.
PA
XX Heber-Katz E;
PI
XX WPI; 1999-494533/41.
DR
XX New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
XX Claim 13; Page 73; 136pp; English.
PS
XX This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags

PT from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
SQ Sequence 11 BP; 1 A; 6 C; 1 G; 3 T; 0 U; 0 Other;
    Query Match      32.4%; Score 9.4; DB 1; Length 11;
    Best Local Similarity 90.9%; Pred. No. 1.2e+02;
    Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGT 15
Db 1 CCACCTCCTGT 11

RESULT 143
AAZ18744/c
ID AAZ18744 standard; DNA; 11 BP.
XX
XX AAZ18744;
AC
XX 22-OCT-1999 (first entry)
DT
XX Murine C57BL/6 SAGE tag 1217605.
DE
XX Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
KW healing response; microsatellite marker; treatment; central nerve;
KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
XX
XX Mus sp.
OS
XX WO9941364-A2.
PN
XX 19-AUG-1999.
PD
XX 12-FEB-1999; 99WO-US002962.
PF
XX 13-FEB-1998; 98US-0074737P.
PR
XX 26-AUG-1998; 98US-0097937P.
PR
XX 28-SEP-1998; 98US-0102051P.
XX
XX (WIST-) WISTAR INST.
PA
XX Heber-Katz E;
PI
XX WPI; 1999-494533/41.
DR
XX New mammalian model for enhanced wound healing - useful for identifying
PT enhanced wound healing genes.
XX
XX Claim 13; Page 56; 136pp; English.
PS
XX This invention describes a novel non-MRL healer mouse (M) having at least
CC one quantitative trait locus selected from those given in the
CC specification, exhibiting an enhanced healing response to a wound
CC compared to mice (m) without the locus. The invention describes a novel
CC method of identifying a gene involved in enhanced wound healing by
CC identifying DNA microsatellite markers which can distinguish healer mice
CC from non-healer mice and identifying microsatellite markers which
CC segregate with enhanced wound healing in progeny of the mice, where a
CC chromosomal locus containing at least one enhanced wound healing gene is
CC identified. A method of treating a wound in a mammal is also disclosed.
CC The new methods are useful for treating wounds, especially central and
CC peripheral nerve wound. The methods of the invention are useful for
CC restoring function after nerve injury in a mammal. (M) is useful as a
CC mammalian model of enhanced wound healing, useful for identifying genes
CC and gene products involved in enhanced wound healing, and to provide
CC methods for wound healing. AAZ18691-Z19036 represent murine SAGE tags
from C57BL/6 and MRL mice which are used to illustrate the method of the
CC invention
XX
SQ Sequence 11 BP; 4 A; 5 C; 2 G; 0 T; 0 U; 0 Other;
    Query Match      32.4%; Score 9.4; DB 1; Length 11;

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Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTG 23
Db 11 TGTGTGCCCTG 1

RESULT 144
AAA96508/c
ID AAA96508 standard; DNA; 11 BP.
AC AAA96508;
XX
XX 08-FEB-2001 (first entry)
XX
DE Consensus sequence derived from the human VhIII gene domain.
XX
KW HIV-1; envelope glycoprotein; gp120; ss.
XX
OS Homo sapiens.
XX
PN EP1043407-A2.
XX
PD 11-OCT-2000.
XX
PF 04-APR-2000; 2000EP-00107333.
XX
XX 09-APR-1999; 99IT-M1000729.
XX
PA (DIAP-) DIAPHARM LTD.
XX
XX Veljkovic V, Veljkovic N, Prljic J, Metlas R;
XX
XX WPI; 2000-595765/57.
XX
XX New oligonucleotides for identifying human immunodeficiency virus-1 in
XX biological samples comprise an 8 bp sequence inserted between highly
XX conserved HIV-1 gp120 gene derived sequences.
XX
XX Disclosure; Page 3; 8pp; English.
XX
XX The present sequence represents a consensus sequence derived from the
XX human VhIII gene domain coding the FRI region. The sequence used to
XX design primers which also contain the sequence GCTGGTGG, inserted between
XX highly conserved sequences corresponding to the domain of Human
XX immunodeficiency virus type 1 (HIV-1) envelope glycoprotein gp120. The
XX primer comprises the PCR primer is used to detect the presence of HIV-1
XX isolates in a biological sample
XX
XX Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTG 14
Db 11 TCCACCACTG 1

RESULT 145
ABQ86330
ID ABQ86330 standard; cDNA; 11 BP.
XX
XX ABQ86330;
XX
XX 10-SEP-2002 (first entry)
XX
DE Human skin stress/ageing related EST SEQ ID NO 85.
XX
KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX

OS Homo sapiens.
XX
PN WO200253773-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015178.
XX
PR 03-JAN-2001; 2001DE-01000121.
XX
PA (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX Claim 8; Page 40; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTGA 19
Db 1 CTGCTGAGTGA 11

RESULT 146
ABV64871
ID ABV64871 standard; cDNA; 11 BP.
XX
XX ABV64871;
XX
XX 21-OCT-2002 (first entry)
XX
XX Human skin EST 2657.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX

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DR WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 99; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 32.4%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 CTGTGTGACCT 22
 Db 1 CTGTGTGACCT 11
 ||||| |||||
 RESULT 147
 ABV66455
 ID ABV66455 standard; cDNA; 11 BP.
 XX
 AC ABV66455;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 4241.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 142; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to

CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 2 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 32.4%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 ACTGTGTGTGT 17
 Db 1 ACTGTGTGTGT 11
 ||||| |||||
 RESULT 148
 ABV67092
 ID ABV67092 standard; cDNA; 11 BP.
 XX
 AC ABV67092;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 4878.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 OS WPI; 2002-590638/63.
 XX
 PN In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 159; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 32.4%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
PS Disclosure; Page 108; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ATCCACCTGCT 13
DB 1 ATCCGCTTGCT 11
RESULT 152
ABV67859
ID ABV67859 standard; cDNA; 11 BP.
XX
AC ABV67859;
XX
XX 21-OCT-2002 (first entry)
XX
DE Human skin EST 5645.
XX
XX Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
PT

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XX
PS Disclosure; Page 181; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 CTGCTGTGTGA 19
DB 1 CTGCTGAGTGA 11
RESULT 153
ADQ34760
ID ADQ34760 standard; DNA; 11 BP.
XX
XX ADQ34760;
XX
XX 23-SEP-2004 (first entry)
XX
XX Human facial skin-associated DNA fragment SEQ ID NO 2850.
XX
XX facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX
OS Homo sapiens.
XX
XX DE10260928-A1.
XX
XX 08-JUL-2004.
XX
XX 20-DEC-2002; 2002DE-01060928.
XX
XX 20-DEC-2002; 2002DE-01060928.
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
XX Conradt M, Hofmann K;
XX
XX WPI; 2004-518855/50.
XX
XX In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.
XX
XX Claim 4; SEQ ID NO 2850; 577pp; German.
XX
XX This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test

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CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.

XX SQ Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGT 15
 Db 1 CCACCTGCTTT 11

RESULT 154
 ADQ33707
 ID ADQ33707 standard; DNA; 11 BP.
 XX AC ADQ33707;
 AC ADQ33707;
 DT 23-SEP-2004 (first entry)
 DE Human facial skin-associated DNA fragment SEQ ID NO 1797.
 XX facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; db.
 XX Homo sapiens.
 XX DE10260928-A1.
 XX 08-JUL-2004.
 XX 20-DEC-2002; 2002DE-01060928.
 XX 20-DEC-2002; 2002DE-01060928.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 PI WPI; 2004-518855/50.
 DR In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.
 XX Claim 5; SEQ ID NO 1797; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of

CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.

XX SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCT 13
 Db 1 ATCCGCTGCT 11

RESULT 155
 AAZ48741
 ID AAZ48741 standard; DNA; 12 BP.
 XX AC AAZ48741;
 AC AAZ48741;
 DT 15-MAR-2000 (first entry)
 DE PCR primer for human alphas-antitrypsin gene sequence.
 XX PCR primer; oligonucleotide detection; diagnosis; disease screening; COP;
 KW competitive oligonucleotide priming; genetic polymorphism detection;
 KW genetic disease diagnosis; linkage analysis; tissue typing; gene mapping;
 KW human; alpha-antitrypsin; ss.
 XX Homo sapiens.
 OS EP333465-A.
 PN 20-SEP-1989.
 PD 15-MAR-1989; 89EP-00302569.
 XX 18-MAR-1988; 88US-00170214.
 PR (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Caskey CT, Gibbs RAL;
 PI WPI; 1989-272222/38.
 DR Detection of mutations in DNA - by adding competitive oligo-nucleotide
 PT primers to nucleic acids, hybridising, etc.
 XX Example 4; Page 12; 21pp; English.

XX This sequence represents a PCR primer for the human alpha-antitrypsin
 CC gene sequence. The invention relates to a method for detecting the
 CC presence or absence of a specific known oligonucleotide, or
 CC distinguishing between specific and different nucleic acid (NA)
 CC sequences, comprising: (1) addition of at least two oligonucleotide
 CC primers to a sample or mixture of NA where one primer (a) is
 CC substantially complementary to a specific NA sequence and the other
 CC primer (b) has a single base mismatch with the specific sequence; (2)
 CC preferentially hybridising (a) to the specific NA sequence under
 CC competitive conditions; (3) extension of (a) from its 3' terminus to
 CC produce an extension product complementary to the strand hybridised to by
 CC (a); and (4) identifying the extension product by determining the
 CC presence or absence of labels attached to at least one of the primers.
 CC The method (referred to as competitive oligonucleotide priming (COP)) can
 CC be used in detecting genetic polymorphisms, particularly in detecting
 CC genetic diseases, screening for disease association by linkage analysis,
 CC tissue typing, gene mapping, screening for neoplasms, detection of known
 CC pathogens, determining purity of animal strains, and disease screening in

CC animals. With this method, primers may be used that are shorter than
 CC those used in PCR, as the binding to template is competitive its sequence
 CC can be inferred. The target sequence of the gene need not be precisely
 CC known as only the specific sequence for the primers is required
 XX
 SQ Sequence 12 BP; 5 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 32.4%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 19 ACCTGGTAAAT 29
 Db 1 ACCTGGAAAT 11
 RESULT 156
 AAQ04006
 ID AAQ04006 standard; DNA; 12 BP.
 XX AC AAQ04006;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-SEP-1990 (first entry)
 XX
 DE Primer used in detecting alpha-1-antitrypsin deficiency.
 XX
 KW X-chromosome; ornithine transcarbamylase deficiency; muscular dystrophy;
 KW dystrophin; ds.
 KW
 OS Synthetic.
 OS
 PN EP364255-A.
 XX
 PD 18-APR-1990.
 XX
 PF 11-OCT-1989; 89EP-00310424.
 XX
 PR 12-OCT-1988; 89US-00256689.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Caskey CT, Chamberlain JS, Gibbs RAL, Rainer JE, Nguyen PN;
 XX
 DR WPI; 1990-117752/16.
 XX
 XX Multiplex genomic DNA amplification for deletion detection - useful for
 PT detecting X-linked diseases such as ornithine transcarbamylase deficiency
 PT and X-linked muscular dystrophy.
 XX
 PS Example 8; Page 18; 32pp; English.
 XX
 CC Paired oligonucleotide primers are used in detecting deletions
 CC specifically of the X and Y chromosomes. Probe may be used to recognise
 CC normal (M) allele of alpha-1-antitrypsin. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 12 BP; 5 A; 2 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 32.4%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 19 ACCTGGTAAAT 29
 Db 1 ACCTGGAAAT 11
 RESULT 157
 AAV40900
 ID AAV40900 standard; DNA; 12 BP.
 XX
 AC AAV40900;

XX
 DT 25-SEP-1998 (first entry)
 XX
 DE Primer CBFMYHA:1033L12 for abnormality detection.
 XX
 KW PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
 KW lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
 KW medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9824928-A2.
 XX
 PD 11-JUN-1998.
 XX
 XX 08-DEC-1997; 97WO-DK000556.
 XX
 PR 06-DEC-1996; 96DK-00001401.
 XX
 PA (PALL/) PALLISGAARD N.
 XX
 PI Pallisgaard N, Hokland P;
 XX
 DR WPI; 1998-333344/29.
 XX
 PT Detection of chromosomal abnormalities - by subjecting patient sample
 PT nucleic acids to a multiplex molecular amplification procedure using
 PT primers specific for characteristic nucleic acid sequence.
 XX
 PS Claim 73; Page 58; 126pp; English.
 XX
 CC This sequence represents a primer used in the method of the invention for
 CC the detection of the presence or absence of chromosomal abnormalities, and
 CC each abnormality being associated with a condition in a subject and each
 CC being defined by at least one characteristic nucleic acid sequence. The
 CC method comprises: (a) obtaining a sample of nucleic acids derived from a
 CC subject which may harbour one of the chromosomal abnormalities; (b)
 CC subjecting the sample to a multiplex molecular amplification (MMA)
 CC procedure, where a number of the characteristic sequences, if present in
 CC a sufficient amount, will be amplified; (c) retrieving the product(s)
 CC from step (b), and detecting the presence and/or absence of an amplicon
 CC characteristic of the abnormal sequences to detect the presence or
 CC absence of corresponding chromosomal abnormalities; where the MMA
 CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
 CC in one single reaction mixture, each of the primers defining an end of at
 CC least one characteristic nucleic acid sequence, and where at least one of
 CC the primers defines the first end of at least two characteristic nucleic
 CC acid sequences, the characteristic nucleic acid sequences each being
 CC determined in their opposite ends by MDP selected from the remainder of
 CC the MDP. The methods can be used for detecting chromosomal abnormalities
 CC associated with diseases including numerous leukaemia's, lymphoma's,
 CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
 CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
 XX
 SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 32.4%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 CTGCTGTGTGA 19
 Db 1 CTGCTGGTGA 11
 RESULT 158
 AAA06782
 ID AAA06782 standard; DNA; 12 BP.
 XX
 AC AAA06782;
 XX
 DT 05-JUN-2000 (first entry)

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XX DE VEGF derived short oligonucleotide SEQ ID NO:91.
XX OS
XX OS Synthetic.
XX PN Human; vascular endothelial growth factor; VEGF; phosphorothioate;
XX KW antisense oligonucleotide; inhibition; cytosolic; angiogenic;
XX KW gene therapy; abnormal vascular permeability; cell proliferation;
XX KW cell permeation; angiogenesis; neovascularisation; tumour cell growth;
XX KW metastasis; ss.
XX OS
XX OS Homo sapiens.
XX OS Synthetic.
XX PN EP979869-A1.
XX KW 16-FEB-2000.
XX PD
XX PF 07-AUG-1998; 98EP-00114853.
XX PR
XX PR 07-AUG-1998; 98EP-00114853.
XX OS
XX OS (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX PN Ulmann E, Peyman A, Bitonti AJ, Woessner RD;
XX KW WPI; 2000-258586/23.
XX PD
XX PF 07-AUG-1998; 98EP-00114853.
XX PR
XX PR 07-AUG-1998; 98EP-00114853.
XX OS
XX OS (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX PN Ulmann E, Peyman A, Bitonti AJ, Woessner RD;
XX KW WPI; 2000-258586/23.
XX PD
XX PF Novel oligonucleotides corresponding to a part of a vascular endothelial
XX KW growth factor, useful for treating e.g. tumor cell growth and/or
XX KW metastasis.
XX OS
XX OS Disclosure; Page 13; 73pp; English.
XX OS
XX OS The present invention describes oligonucleotides (I) of 10-15 residues
XX CC corresponding to a part of a vascular endothelial growth factor (VEGF)
XX CC comprising 1 of 6 sequences given in AAA06692 to AAA06697. AAA06698 to
XX CC AAA06783 represent VEGF antisense oligonucleotides used in the
XX CC exemplification of the present invention. The antisense oligonucleotides
XX CC can contain phosphorothioate linkages. Oligonucleotides from the present
XX CC invention have cytostatic and angiogenic activities, and can be used in
XX CC gene therapy. The oligonucleotides are useful for inhibiting the
XX CC expression of VEGF, e.g. for the treatment of diseases associated with
XX CC abnormal vascular permeability, cell proliferation, cell permeation,
XX CC angiogenesis, neovascularisation, tumour cell growth and/or metastasis.
XX CC AAA06784 represents a human VEGF nucleotide sequence from which the
XX CC oligonucleotides are derived
XX OS
XX OS Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
XX SQ
XX Query Match 32.4%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 14 GTGTGACCTGG 24
Db 1 GTGTGACCTGG 11
RESULT 159
AAA06783
ID AAA06783 standard; DNA; 12 BP.
XX
XX AAA06783;
XX AC
XX 05-JUN-2000 (first entry)
XX DT
XX VEGF derived short oligonucleotide SEQ ID NO:92.
XX DE
XX KW Human; vascular endothelial growth factor; VEGF; phosphorothioate;
XX KW antisense oligonucleotide; inhibition; cytosolic; angiogenic;
XX KW gene therapy; abnormal vascular permeability; cell proliferation;
XX KW cell permeation; angiogenesis; neovascularisation; tumour cell growth;
XX KW metastasis; ss.
XX OS
XX OS Homo sapiens.
XX OS Synthetic.
XX PN EP979869-A1.
XX KW 16-FEB-2000.
XX PD
XX PF 07-AUG-1998; 98EP-00114853.
XX PR
XX PR 07-AUG-1998; 98EP-00114853.
XX OS
XX OS (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX PN Ulmann E, Peyman A, Bitonti AJ, Woessner RD;
XX KW WPI; 2000-258586/23.
XX PD
XX PF Novel oligonucleotides corresponding to a part of a vascular endothelial
XX KW growth factor, useful for treating e.g. tumor cell growth and/or
XX KW metastasis.
XX OS
XX OS Disclosure; Page 13; 73pp; English.
XX OS
XX OS The present invention describes oligonucleotides (I) of 10-15 residues
XX CC corresponding to a part of a vascular endothelial growth factor (VEGF)
XX CC comprising 1 of 6 sequences given in AAA06692 to AAA06697. AAA06698 to
XX CC AAA06783 represent VEGF antisense oligonucleotides used in the
XX CC exemplification of the present invention. The antisense oligonucleotides
XX CC can contain phosphorothioate linkages. Oligonucleotides from the present
XX CC invention have cytostatic and angiogenic activities, and can be used in
XX CC gene therapy. The oligonucleotides are useful for inhibiting the
XX CC expression of VEGF, e.g. for the treatment of diseases associated with
XX CC abnormal vascular permeability, cell proliferation, cell permeation,
XX CC angiogenesis, neovascularisation, tumour cell growth and/or metastasis.
XX CC AAA06784 represents a human VEGF nucleotide sequence from which the
XX CC oligonucleotides are derived
XX OS
XX OS Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
XX SQ
XX Query Match 32.4%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 14 GTGTGACCTGG 24
Db 1 GTGTGACCTGG 11
RESULT 160
ABH86901
ID ABH86901 standard; DNA; 12 BP.
XX
XX ABH86901;
XX AC
XX 22-FEB-2002 (first entry)
XX DT
XX Oligonucleotide primer SEQ ID NO 286894 for detecting SNP TSC0012869.
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200177384-A2.
XX KW 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX KW
XX KW 07-APR-2000; 2000DE-01019173.
XX PR
XX PR (EPIG-) EPIGENOMICS AG.
XX OS

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OS Homo sapiens.
OS Synthetic.
PN EP979869-A1.
PD 16-FEB-2000.
XX 07-AUG-1998; 98EP-00114853.
XX 07-AUG-1998; 98EP-00114853.
XX (HMRI ) HOECHST MARION ROUSSEL DEUT GMBH.
XX Ulmann E, Peyman A, Bitonti AJ, Woessner RD;
XX WPI; 2000-258586/23.
XX Novel oligonucleotides corresponding to a part of a vascular endothelial
XX growth factor, useful for treating e.g. tumor cell growth and/or
XX metastasis.
XX Disclosure; Page 13; 73pp; English.
XX The present invention describes oligonucleotides (I) of 10-15 residues
XX corresponding to a part of a vascular endothelial growth factor (VEGF)
XX comprising 1 of 6 sequences given in AAA06692 to AAA06697. AAA06698 to
XX AAA06783 represent VEGF antisense oligonucleotides used in the
XX exemplification of the present invention. The antisense oligonucleotides
XX can contain phosphorothioate linkages. Oligonucleotides from the present
XX invention have cytostatic and angiogenic activities, and can be used in
XX gene therapy. The oligonucleotides are useful for inhibiting the
XX expression of VEGF, e.g. for the treatment of diseases associated with
XX abnormal vascular permeability, cell proliferation, cell permeation,
XX angiogenesis, neovascularisation, tumour cell growth and/or metastasis.
XX AAA06784 represents a human VEGF nucleotide sequence from which the
XX oligonucleotides are derived
XX Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 U; 0 Other;
XX Query Match 32.4%; Score 9.4; DB 1; Length 12;
XX Best Local Similarity 90.9%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 14 GTGTGACCTGG 24
Db 1 GTGTGACCTGG 11
RESULT 160
ABH86901
ID ABH86901 standard; DNA; 12 BP.
XX
XX ABH86901;
XX AC
XX 22-FEB-2002 (first entry)
XX DT
XX Oligonucleotide primer SEQ ID NO 286894 for detecting SNP TSC0012869.
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200177384-A2.
XX KW 18-OCT-2001.
XX PD
XX PF 06-APR-2001; 2001WO-IB000713.
XX KW
XX KW 07-APR-2000; 2000DE-01019173.
XX PR
XX PR (EPIG-) EPIGENOMICS AG.
XX OS

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XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX FT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 286894; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: the sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
XX
Query Match 32.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CATCACCTGC 12
DB 2 CATCACCTAC 12
XX
RESULT 161
AAD54083
ID AAD54083 standard; DNA; 12 BP.
XX AC AAD54083;
XX XX
XX DT 17-JUN-2003 (first entry)
XX DE HNF1-131-1 gene SNP detecting capture probe 1.
XX KW Microfluidic analysis; biomolecule identification; sample analysis;
XX KW single nucleotide polymorphism; SNP; genotyping; probe; HNF1-131-1; ss.
XX OS Unidentified.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 2
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "Methylated LNA nucleotide"
XX FT modified_base 6..8
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "LNA nucleotides"
XX FT modified_base 5
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "Methylated"
XX FT modified_base 11
XX FT /*tag= d
XX FT /mod_base= OTHER
XX FT /note= "LNA nucleotide"
XX XX
XX PN WO200297398-A2.
XX PD 05-DEC-2002.
XX XX
XX PF 25-OCT-2001; 2001WO-IB002902.

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XX PR 25-OCT-2000; 2000US-0243349P.
XX PR 16-JUL-2001; 2001US-0305726P.
XX XX
XX PA (EXIQ-) EXIQON AS.
XX PI Jakobsen MH, Kongsbak L;
XX XX
XX DR WPI; 2003-183891/18.
XX XX
XX PT Closed substrate platform has slide element comprising microfluidic
XX PT analysis platform, enclosed within container having inlet port for
XX PT introducing liquid into sample analysis area and vent for removing air
XX PT from container.
XX PS Example; Page 70; 49pp; English.
XX XX
XX CC The invention relates to a closed substrate platform which has a slide
XX CC element comprising microfluidic analysis platform, enclosed within
XX CC container having inlet port for introducing liquid into sample analysis
XX CC area and vent for removing air from container. The invention is used for
XX CC identifying a nucleic acid sequence capable of binding to a biomolecule
XX CC such as a nucleic acid sequence or polypeptide. It is useful for
XX CC identifying a polypeptide capable of binding to a biomolecule such as a
XX CC nucleic acid sequence, polypeptide, multimeric polypeptide, an antibody,
XX CC a receptor, a hormone, drug or drug candidate. It is also useful for
XX CC sample analysis, especially liquid, and is useful for detecting DNA
XX CC sequence variation, DNA sequencing, deletion analysis, single nucleotide
XX CC polymorphism (SNP) analysis, gene expression, genotyping, etc. The
XX CC present sequence is a capture probe used for detecting HNF1-131-1 gene
XX CC SNP. This sequence is used in the exemplification of the invention
XX XX
XX SQ Sequence 12 BP; 1 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
XX
Query Match 32.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 CCACCTGCTGT 15
DB 2 CCTCCTGCTGT 12
XX
RESULT 162
AAL51397/C
ID AAL51397 standard; DNA; 12 BP.
XX AC AAL51397;
XX XX
XX DT 27-MAR-2003 (first entry)
XX DE Human polyamine oxidase (PAO) exon-intron junction, SEQ ID No 24.
XX KW Human; gene; ds; enzyme; polyamine oxidase; PAO; exon-intron junction;
XX KW polyamine oxidase-related disease.
XX OS Homo sapiens.
XX XX
XX PN WO2002100884-A2.
XX FT 19-DEC-2002.
XX XX
XX PF 13-JUN-2002; 2002WO-US018666.
XX XX
XX PR 13-JUN-2001; 2001US-0297815P.
XX PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PI Casero RA, Wang Y;
XX XX
XX DR WPI; 2003-156944/15.
XX XX
XX PF New purified mammalian polyamine oxidase enzyme, useful as a diagnostic

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PT or prognostic tool, e.g. for determining the etiology and predicting the
 PT optimal treatment regimens for diseases caused by abnormal expression of
 PT this enzyme.

PS Disclosure; Fig 2C; 45pp; English.

XX The invention comprises the amino acid and coding sequence of human
 CC polyamine oxidase (PAO) proteins. The PAO DNA and protein sequences of
 CC the invention are useful as diagnostic and prognostic tools, particularly
 CC to determine the etiology of and predict the optimal treatment regimens
 CC for disease states caused by abnormal expression of this enzyme. The
 CC present DNA sequence represents an exon-intron junction from the human
 CC PAO gene

XX Sequence 12 BP; 2 A; 3 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTG 14

Db 11 TCCACCTGCCG 1

RESULT 163

ID AAA54184/c

ID AAA54184 standard; CDNA; 13 BP.

AC AAA54184;

XX 08-FEB-2001 (first entry)

DE 5' exon-intron junction of exon 8 of BSMAP.

XX Brain specific membrane anchored protein; BSMAP; dopamine; GABA;
 KW receptor; agonist; antagonist; central nervous system; CNS;
 KW brain disease; chromosome 19; CLF-1; depression; dyslexia; dystonia;
 KW eating disorder; epilepsy; migraine; headache; panic disorder;
 KW schizophrenia; obsessive disorder; compulsive disorder;
 KW amyotrophic lateral sclerosis; multiple sclerosis; Alzheimer's disease;
 KW brain tumour; Huntington's disease; Parkinson's disease; stroke; human;
 KW exon; intron; ss.

XX Homo sapiens.

XX WO200055317-A1.

XX 21-SEP-2000.

XX 16-MAR-2000; 2000WO-IB000360.

XX 16-MAR-1999; 99EP-00400636.

XX (FABR) FABRE MEDICAMENT SA PIERRE.

XX Elson G, Bonnefoy J, Gauchat J;

XX WPI; 2000-638200/61.

XX Novel nucleic acid encoding Brain-Specific Membrane Anchored Protein
 PT useful for treating central nervous system associated disorders and
 PT diseases.

XX Disclosure; Page 13; 45pp; English.

XX Several receptors (dopamine receptors, the 5-HT family of receptors and
 CC GABA receptors) have been shown to be useful targets by agonist and
 CC antagonist compounds to treat and/or prevent CNS disorders. Brain
 CC receptors in general are attractive candidates for finding new therapies
 CC for brain diseases. Human chromosome 19 is a short chromosome with a
 CC relatively high GC content which has been found to be involved in CNS
 CC functions. The gene for type I cytokine receptor homologue CLF-1 was

CC recently localised to chromosome 19. Unexpectedly seven other exons
 CC coding in the reverse orientation located adjacent to the CLF-1 exons
 CC have also been found. This new gene was designated brain-specific
 CC membrane anchored protein (BSMAP). Antagonistic compounds directed
 CC against BSMAP are useful for preparing medicaments for treating and/or
 CC preventing central nervous system disorders such as depression, dyslexia,
 CC dystonia, eating disorders, epilepsy, migraine, headache, panic disorder,
 CC schizophrenia, obsessive and compulsive disorders, amyotrophic lateral
 CC sclerosis, multiple sclerosis, Alzheimer's disease, brain tumors,
 CC Huntington's disease, Parkinson's disease and stroke

XX Sequence 13 BP; 1 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 32.4%; Score 9.4; DB 1; Length 13;

Best Local Similarity 90.9%; Pred. No. 1.4e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCTG 11

Db 13 CCACCCACCTG 3

RESULT 164

ABC87602/c

ID ABC87602 standard; DNA; 13 BP.

AC ABC87602;

XX 21-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 87619 for detecting SNP TSC0022039.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 87619; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

```
Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ATCCACCTGCT 13
Db      11 ATCCACCTACT 1

RESULT 165
ABC87603
ID ABC87603 standard; DNA; 13 BP.
AC ABC87603;
XX
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 87620 for detecting SNP TSC0022039.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 87620; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 5 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 ATCCACCTGCT 13
Db      3 ATCCACCTACT 13

RESULT 166
ACC70395/c
ID ACC70395 standard; DNA; 13 BP.
XX
```

```
ACC70395;
XX 11-AUG-2003 (first entry)
XX
XX Cytoprotective response element from a shear stress-regulated gene.
XX
XX Cytoprotective response element; CPRE; oxidative stress;
KW cytoprotective enzyme; hemodynamic shear stress; inflammatory disorder;
KW cardiovascular disease; hyperproliferative disorder; neoplasm;
KW lymphoblastic leukemia; skin cancer; radiation therapy;
KW shear stress-regulated gene; ss.
XX
XX Unidentified.
XX
XX WO2003033662-A2.
XX
XX 24-APR-2003.
XX
XX 16-OCT-2002; 2002WO-US033006.
XX
XX 16-OCT-2001; 2001US-0329870P.
XX
XX (ATHE-) ATHEROGENICS INC.
XX
XX Kunsch C, Varner SE, Chen X, Luchoomun J;
XX
XX WPI; 2003-403211/38.
XX
XX Novel isolated cytoprotective response element nucleic acid for inducing
XX coordinate activation of genes that protect cells from damaging effects
XX of oxidative stress, e.g. during conditions of hemodynamic shear stress.
XX
XX Claim 2; Fig 6; 133pp; English.
XX
XX The present sequence represents a cytoprotective response element (CPRE).
XX The CPRE is an inducer of the coordinate activation of certain genes that
XX protect cells from damaging effects of oxidative stress. It is also a
XX regulator of cytoprotective effects and an inducer of expression of
XX cytoprotective enzymes. The CPRE is useful for inducing the coordinate
XX activation of certain genes that protect cells from damaging effects of
XX oxidative stress, for example during conditions of hemodynamic shear
XX stress. It is useful as a reagent for the identification of a compound
XX (preferably a drug) with which it directly or indirectly interacts, or
XX for regulating cytoprotective effects by inducing the expression of
XX cytoprotective enzymes or other factors. A compound identified in this
XX way is useful for treating inflammatory disorders, cardiovascular
XX diseases, hyperproliferative disorders (such as neoplasms, lymphoblastic
XX leukemia, skin cancer, or to protect normal tissues and organs from the
XX damaging effects of chemotherapeutic drugs, radiation therapy and disease
XX processes
XX
XX Sequence 13 BP; 5 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTGCTGTGTGA 19
Db      12 CTGCTGTGTCA 2

RESULT 167
AAZ79202
ID AAZ79202 standard; DNA; 10 BP.
XX
XX AAZ79202;
XX
XX 10-APR-2000 (first entry)
XX
XX Human dendritic cell SAGE tag, SEQ ID NO:1630.
XX
XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
```


KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX WO9965924-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013800.
 XX 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089901P.
 PR 19-JUN-1998; 98US-0089902P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-011715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 XX
 XX Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 111; 130pp; English.
 XX Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen

CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 CTGTGTGAC 20
 Db 1 CTGTGTGAC 9
 RESULT 168
 AAZ78009
 ID AAZ78009 standard; DNA; 10 BP.
 XX
 AC AAZ78009;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:437.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.
 XX
 XX 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089901P.
 PR 19-JUN-1998; 98US-0089902P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-011715P.

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PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX WPI; 2000-106077/09.
DR
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer.
XX
XX Claim 1; Page 77; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or ESTs
XX (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can lyse
XX the tumour cells, immunostimulatory cofactors also being required for
XX efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell differentially
XX expressed genes, or of their encoded proteins, can be used to identify
XX cells as belonging to the monocyte lineage. Cells containing these genes
XX can be used in active immunotherapy (or to stimulate production of a
XX population of antigen-specific effector cells) and vectors containing
XX them are used in gene therapy. Co-administration of tumour antigens and
XX APC-associated costimulatory factors ensures adequate antigen
XX presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
| | | | |
Db 1 CCACCTGCT 9

RESULT 169
AAZ78129
ID AAZ78129 standard; DNA; 10 BP.
XX
XX AAZ78129;
AC
XX
XX 10-APR-2000 (first entry)
XX
XX Human dendritic cell SAGE tag, SEQ ID NO:557.
XX

```

SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

Homo sapiens.

WO9965924-A2.

23-DEC-1999.

18-JUN-1999; 99WO-US013800.

19-JUN-1998; 98US-0089833P.

19-JUN-1998; 98US-0089844P.

19-JUN-1998; 98US-0089853P.

19-JUN-1998; 98US-0089878P.

19-JUN-1998; 98US-0089911P.

19-JUN-1998; 98US-0089922P.

19-JUN-1998; 98US-0089933P.

19-JUN-1998; 98US-0089944P.

19-JUN-1998; 98US-0089977P.

19-JUN-1998; 98US-0089999P.

19-JUN-1998; 98US-0090000P.

19-JUN-1998; 98US-0090035P.

19-JUN-1998; 98US-0090036P.

19-JUN-1998; 98US-0090039P.

19-JUN-1998; 98US-0090040P.

19-JUN-1998; 98US-0090041P.

19-JUN-1998; 98US-0090042P.

19-JUN-1998; 98US-0090043P.

19-JUN-1998; 98US-0090044P.

19-JUN-1998; 98US-0090045P.

19-JUN-1998; 98US-0090047P.

19-JUN-1998; 98US-0090048P.

19-JUN-1998; 98US-0090072P.

19-JUN-1998; 98US-0090076P.

19-JUN-1998; 98US-0090077P.

19-JUN-1998; 98US-0090078P.

19-JUN-1998; 98US-0090079P.

19-JUN-1998; 98US-0090080P.

08-DEC-1998; 98US-0111715P.

(GENZ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.

Roberts BL, Shankara S;
WPI; 2000-106077/09.

Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.

Claim 1; Page 81; 130pp; English.

Sequences AA277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells

Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
| | | | |
Db 1 CCACCTGCT 9

RESULT 169
AAZ78129
ID AAZ78129 standard; DNA; 10 BP.
XX
XX AAZ78129;
AC
XX
XX 10-APR-2000 (first entry)
XX
XX Human dendritic cell SAGE tag, SEQ ID NO:557.
XX

CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to co-stimulatory APCs and upregulates the APCs for the
 CC presentation of endogenous APCs and upregulates the APCs for the
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 CC
 SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 TGCTGTGTG 18
 Db 1 TGCTGTGTG 9
 RESULT 170
 AAZ85467/C
 ID AAZ85467 standard; DNA; 10 BP.
 XX
 AC AAZ85467;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #4701.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 185; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CATCCACCT 10
 Db 10 CATCCACCT 2
 RESULT 171
 AAZ86332/C
 ID AAZ86332 standard; DNA; 10 BP.
 XX
 AC AAZ86332;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5566.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 206; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 4 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 TGCTGTGTG 18
 |||||
 Db 9 TGCTGTGTG 1
 |||||
 RESULT 172
 AAZ81042
 ID AAZ81042 standard; DNA; 10 BP.
 XX
 AC AAZ81042;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #276.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 65; 219pp; English.
 XX

CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 TGCTGTGTG 18
 |||||
 Db 1 TGCTGTGTG 9
 |||||
 RESULT 173
 AAZ82620
 ID AAZ82620 standard; DNA; 10 BP.
 XX
 AC AAZ82620;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell upregulated transcript tag #1854.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 XX Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106079/09.
 XX
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX

PS Claim 1; Page 108; 219pp; English.

XX AA280767 to AA283941 represent tags corresponding to distinct transcripts

CC that are preferentially transcribed in the metastatic breast tumour

CC tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942

CC to AA286677 represent tags corresponding to distinct transcripts that are

CC preferentially transcribed in the primary or non-metastatic breast tumour

CC tissue (i.e. are downregulated in metastatic breast tumour cells). These

CC transcripts can be used for diagnosis, prognosis, monitoring and

CC treatment of breast cancer, particularly where metastatic. Diagnosis is

CC by standard immunoassays or hybridisation/amplification reactions.

CC Compounds that modulate expression of the transcripts are potentially

CC useful for treatment of (metastatic) breast cancer, while promoters from

CC the transcripts are used to direct expression, in selected cell types, of

CC e.g. therapeutic genes (also ribozymes or antisense sequences),

CC particularly an antigen-encoding sequence for use in gene or cell-based

CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific

CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic

CC agents. Host cells that produce the polypeptides can be used to expand

CC and isolate populations of educated, antigen-specific immune effector

CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive

CC immunotherapy

XX

SQ Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGCTGTGTG 18

Db 2 TGCTGTGTG 10

RESULT 174

AAH63185/c

ID AAH63185 standard; cDNA; 10 BP.

XX

AC AAH63185;

DT 20-SEP-2001 (first entry)

XX

DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 25.

XX

KW Human; transcriptome; gene expression pattern; cancer; drug screening;

KW cancer diagnosis; cell specific gene expression; ss.

XX

OS Homo sapiens.

XX

PN WO200138577-A2.

XX

PD 31-MAY-2001.

XX

PF 21-NOV-2000; 2000WO-US031922.

XX

PR 24-NOV-1999; 99US-00448480.

XX

PA (UYJO) UNIV JOHNS HOPKINS.

XX

PI Velulescu VE, Vogelstein B, Kinzler KW;

XX

DR WPI; 2001-367706/38.

XX

PT New isolated polynucleotides, useful for identifying specific cell type,

PT such as cancer cell, comprises transcriptomes expressed in particular

PT cell types.

XX

PS Claim 11; Page 39; 94pp; English.

XX

CC The present invention describes a method of identifying the type of cell

CC in a sample, involving determining which of the sequences AAH63161-

CC AAH64724 is expressed by the cell. The transcriptomes described in the

CC

CC invention are cell-type specific, cancer specific or ubiquitously

CC expressed in humans. They can also be used to screen for drugs, reduce

CC cancer specific gene expression, standardise expression and restore the

CC function of a diseased cell or tissue. The present sequence is one of the

CC transcripts described in the exemplification of the invention

XX

SQ Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GTGACCTGG 24

Db 10 GTGACCTGG 2

RESULT 175

AAS57316

ID AAS57316 standard; DNA; 10 BP.

XX

AC AAS57316;

XX

DT 16-JAN-2002 (first entry)

XX

DE Human CHRN2 allele specific oligonucleotide PCR primer terminus #41.

XX

KW Human; cholinergic receptor, nicotinic, beta polypeptide 2; neuronal;

KW CHRN2; memory disorder; Alzheimer's disease; epilepsy; learning;

KW chromosome 1q21; schizophrenia; attention deficit/hyperactivity disorder;

KW ADHD; autosomal dominant nocturnal frontal lobe epilepsy; ADFLE; ss;

KW allele specific oligonucleotide; ASO; PCR primer.

XX

OS Homo sapiens.

XX

PN WO200174833-A2.

XX

PD 11-OCT-2001.

XX

PF 03-APR-2001; 2001WO-US010666.

XX

PR 03-APR-2000; 2000US-0194155P.

PR 13-JUL-2000; 2000US-0217952P.

XX

PA (GENA-) GENAISANCE PHARM INC.

XX

XX

PI Choi JY, Kliem SE, Koshy B, Lee HH, Sanchis A;

XX

DR WPI; 2001-626374/72.

XX

PT Genotyping cholinergic receptor, nicotinic, beta-polypeptide 2 gene of an

PT individual involves determining for two copies of the gene, the identity

PT of nucleotide pair at polymorphic sites selected from PSI-24.

XX

PS Claim 17; Page 15; 82pp; English.

XX

CC The invention relates to genotyping/haplotyping the cholinergic receptor,

CC nicotinic, beta-polypeptide 2 (neuronal) (CHRN2) gene of an individual,

CC comprising determining for the two copies of the CHRN2 gene present in

CC the individual, the identity of the nucleotide pair at one or more

CC polymorphic sites selected from PSI-24. Also include are oligonucleotides

CC for performing the method and the nucleotide sequence of the polymorphic

CC variants of CHRN2. The method is useful for detecting novel CHRN2

CC polymorphisms and for determining if an individual has a haplotype or

CC haplotype pairs defined in the specification and to validate CHRN2 as a

CC candidate agent for treating a specific condition or disease predicted to

CC be associated with CHRN2 activity (e.g. a memory disorder, Alzheimer's

CC disease, epilepsy, a learning disorder, schizophrenia, attention

CC deficit/hyperactivity disorder, ADHD) and autosomal dominant nocturnal

CC frontal lobe epilepsy (ADNFLE)), and in the design of clinical trials of

CC candidate drugs for treating a specific condition or disease predicted to

CC be associated with CHRN2 activity. The method is useful to screen for

CC compounds targeting CHRN2 to treat a specific conditions or disease

CC associated with CHRN2 activity. The polymorphic nucleic acids are useful
 CC in studying the expression and function of CHRN2, and in expressing
 CC CHRN2 protein for use in screening for candidate drugs to treat diseases
 CC related to CHRN2 activity and are useful for therapeutic purposes. The
 CC CHRN2 gene is located on chromosome 1q21. The present sequence is an
 CC allele specific oligonucleotide (ASO) PCR primer (3' terminus) for
 CC performing the method of the invention

XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GTGACCTGG 24
 |||||
 Db 1 GTGACCTGG 9

RESULT 176
 AAH32728
 ID AAH32728 standard; cDNA; 10 BP.
 AC AAH32728;
 DT 13-AUG-2001 (first entry)
 XX LPS activated human monocyte expression gene cDNA tag SEQ:101.
 DE Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.
 XX Homo sapiens.
 OS JP2001069993-A.
 PN 21-MAR-2001.
 XX 28-APR-2000; 2000JP-00131079.
 XX 08-JUL-1999; 99JP-00195103.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX WPI; 2001-304369/32.
 DR LPS activated human monocyte expression gene group.

XX Claim 10; Page 24; 52pp; Japanese.
 XX The present invention describes an lipopolysaccharide (LPS) activated
 CC human monocyte expression gene group consisting of the high-ranking 50
 CC genes of the highest expression among the genes expressed by human
 CC monocyte stimulated by LPS in which the cDNA of each gene has the base
 CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
 CC CATG-3' nearest to the polyA region. The gene group is useful for the
 CC development of new means for the diagnosis and the treatment of various
 CC human diseases in which human monocyte plays an important role. AAH32628
 CC to AAH32943 represent specifically claimed LPS activated human monocyte
 CC expression gene cDNA tags from the present invention. AAH32944 represents
 CC an LPS activated human monocyte expression gene cDNA sequence encoding
 CC AA98009, which are given in the exemplification of the present invention

XX SQ Sequence 10 BP; 1 A; 3 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GTGTGACCT 22
 |||||
 Db 2 GTGTGACCT 10

RESULT 177
 ABA81652
 ID ABA81652 standard; DNA; 10 BP.
 XX ABA81652;
 AC ABA81652;
 DT 24-JAN-2002 (first entry)
 XX Human phospholipid transfer protein gene PCR primer SEQ ID NO: 101.
 DE Human; phospholipid transfer protein; PLTP; SNP; atherosclerosis;
 KW single nucleotide polymorphism; high-density lipoprotein metabolism;
 KW PCR primer; ss.
 XX Homo sapiens.
 OS WO200172761-A2.
 PN 04-OCT-2001.
 XX 15-MAR-2001; 2001WO-US008283.
 XX 24-MAR-2000; 2000US-0192127P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX Chew A, Choi JY, Koshy B;
 XX WPI; 2001-662922/76.
 XX Genotyping phospholipid transfer protein gene of individual for
 PT haplotyping individual's gene, comprises determining identity of
 PT nucleotide pair at polymorphic sites for two copies of PLTP gene present
 PT in the individual.
 XX Claim 17; Page 14; 98pp; English.
 XX The present invention relates to a method for haplotyping the human
 CC phospholipid transfer protein (PLTP) gene, involving determining the
 CC identity of the nucleotide present at one or more of the 25 polymorphic
 CC sites within the gene. This can be used to aid drug development for the
 CC treatment of diseases associated with different haplotypes of the PLTP
 CC gene, possibly including atherosclerosis. The present sequence is a PCR
 CC primer used for detecting polymorphisms in the PLTP gene

XX SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCTGTGTGGA 19
 |||||
 Db 1 GCTGTGTGGA 9

RESULT 178
 AAF35559
 ID AAF35559 standard; DNA; 10 BP.
 XX AAF35559;
 AC AAF35559;
 DT 23-MAR-2001 (first entry)
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2298.
 DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX Saccharomyces cerevisiae.
 OS

```
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 82; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression of
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 U; 0 Other;
Query Match 31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 CTGCTAAAT 29
Db 1 CTGCTAAAT 9
RESULT 179
AAF34581
ID AAF34581 standard; DNA; 10 BP.
XX AC AAF34581;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1320.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
```

```
KW linker; PCR primer; ds.
OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velulescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 47; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression of
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CACCTGCTG 14
Db 2 CACCTGCTG 10
RESULT 180
AAF37646/C
ID AAF37646 standard; DNA; 10 BP.
XX AC AAF37646;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4385.
```

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 XX Saccharomyces cerevisiae.
 XX
 XX WO200077214-A2.
 XX
 XX 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 XX
 XX 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX
 XX WPI; 2001-061874/07.
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 156; 419pp; English.
 XX
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCACCTGCT 13
 Db 10 CCACCTGCT 2
 |||||
 RESULT 181
 ABL52170/c
 ID ABL52170 standard; DNA; 10 BP.
 XX
 XX ABL52170;
 XX
 XX 12-JUL-2002 (first entry)
 DT

XX Human PER1 preferred oligonucleotide primer SEQ ID NO:95.
 DE
 XX Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
 KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
 KW single nucleotide polymorphism; SNP; gene; primer; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200222650-A2.
 XX
 XX 21-MAR-2002.
 XX
 XX 13-SEP-2001; 2001WO-US028780.
 XX
 XX 13-SEP-2000; 2000US-0232468P.
 XX
 XX (GENA-) GENAISANCE PHARM INC.
 XX
 XX Duda A, Kiem SE, Koshy B;
 XX
 XX WPI; 2002-393941/42.
 XX
 XX Novel isolated human period Drosophila homolog 1 polynucleotide, useful
 PT for therapeutic purposes, for studying the expression and function of the
 PT polynucleotide, and for expressing the homolog.
 XX
 XX Claim 19; Page 15; 162pp; English.
 PS
 XX The present invention describes an isolated human period (Drosophila)
 CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
 CC polymorphic variant for a reference sequence (ABL52077) for the PER1 gene
 CC or its fragment, or a polymorphic variant of a reference sequence
 CC (ABL52078) for a PER1 cDNA or its fragment. The present invention also
 CC describes methods for genotyping and haplotyping the PER1 gene of an
 CC individual. (I) is useful in studying the expression and function of
 CC PER1, and in expressing PER1 protein for use in screening for candidate
 CC drugs to treat diseases related to PER1 activity. (I) is useful for
 CC therapeutic purposes. A recombinant non-human organism transformed or
 CC transfected with (I) can be used for studying expression of the PER1
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted
 CC against PER1 protein, and for testing the efficacy of therapeutic agents
 CC and compounds for disorders associated with circadian rhythm regulation.
 CC The present sequence represents a preferred oligonucleotide primer for
 CC human PER1, which is used in the exemplification of the present invention
 XX
 XX Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
 SQ
 Query Match 31.0%; Score 9; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CACCTGCTG 14
 Db 10 CACCTGCTG 2
 |||||
 RESULT 182
 AAS94664
 ID AAS94664 standard; DNA; 10 BP.
 XX
 XX AAS94664;
 AC
 XX 14-FEB-2002 (first entry)
 DT
 XX
 XX Human PLTP gene allele-specific oligonucleotide PCR primer #23.
 DE
 XX Human; phospholipid transfer protein; PLTP; haplotyping; haplotype pair;
 KW single nucleotide polymorphism; genotyping; gene therapy; drug screening;
 KW binding affinity; atherosclerosis; ss; sequencing primer; PCR primer;
 KW probe.
 XX
 XX Homo sapiens.
 OS


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XX PR 06-MAR-2002; 2002US-00091281.
XX PA (SIEE/) SI E.
XX PA (RAYM/) RAYMOND V.
XX PA (MORI/) MORISSETTE J.
XX PA Raymond V, Morissette J, Si E;
XX PI WPI; 2003-864168/80.
XX DR
XX PT New nucleic acid sequences of the optineurin gene are useful to detect
XX PT polymorphisms particularly single nucleotide polymorphisms in the
XX PT optineurin promoter to diagnose, prognose and treat glaucoma and related
XX PT disorders.
XX PS Claim 11; SEQ ID NO 244; 159pp; English.
XX PS
XX CC The invention relates to an isolated nucleic acid (N1) comprising at
XX CC least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX CC promoter appearing as ADE13890. Also included are the optineurin promoter
XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin
XX CC promoter; a host cell comprising the promoter operably linked to a
XX CC heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX CC obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX CC in a promoter region of the optineurin gene, associated with a glaucoma
XX CC phenotype), detecting a SNP sequence variation in a sample containing
XX CC DNA, detecting the presence of an optineurin promoter sequence variation
XX CC in a sample containing DNA, determining the presence or increased
XX CC susceptibility to glaucoma or to a progressive ocular hypertensive
XX CC disorder resulting in loss of visual field in a patient (or the severity
XX CC or progression of glaucoma in a patient, comprising providing
XX CC amplification reaction primers that direct amplification of a selected
XX CC nucleic acid region containing the variation within the optineurin
XX CC promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX CC obtaining a sample containing human genomic DNA, providing a nucleic acid
XX CC capable of detecting a SNP located within an optineurin promoter, and
XX CC detecting the polymorphism). The invention is used to diagnose and
XX CC prognose glaucoma and also to treat glaucoma related disorders. The
XX CC present sequence is an optineurin promoter motif, repeat element or
XX CC putative regulatory region.
XX SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCACCTGC 12
Db 1 TCCACCTGC 9

RESULT 185
ADQ30369
ID ADQ30369 standard; DNA; 10 BP.
XX AC
XX AC ADQ30369;
XX DT
XX DT 09-SEP-2004 (first entry)
XX DE Human VR1 exon 1d transcription factor binding fragment #88.
XX DE
XX KW ds; VR1 receptor; vanilloid receptor type 1; modulator;
XX KW pain transmission; primary sensory neuron; transcription factor;
XX KW detection; MZF1; NFKappaB; NFAT; GATA1; sensitivity disorder; analgesia;
XX KW hypalgesia; hyperalgesia; neuralgia; myalgia; human.
XX OS Homo sapiens.
XX PN WO2004053120-A2.
XX PD 21-JAN-1999.

PD 24-JUN-2004.
XX PF 01-DEC-2003; 2003WO-EP013522.
XX PR 09-DEC-2002; 2002DE-01057421.
XX PA (CHEF ) GRUENENTHAL GMBH.
XX PI Weihe E, Bieller A, Schaefer MKH;
XX PI WPI; 2004-468868/44.
XX DR
XX PT New nucleic acid that modulates expression of the vanilloid receptor-1,
XX PT useful for control of pain or sensitivity disorders, comprises sequences
XX PT from control regions of the receptor gene.
XX PS Disclosure; Page 53; 68pp; German.
XX PS
XX CC This invention describes a novel nucleic acid containing a specific
XX CC segment having at least one region that modulates expression of the VR1
XX CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
XX CC or fragment of this region, or a sequence that hybridises to it under
XX CC standard conditions. The VR1 modulator is derived from one or more of
XX CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
XX CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
XX CC pain, particularly in primary sensory neurons. The invention also
XX CC describes a vector that contains the VR1 modulator, host cells containing
XX CC this vector (other than human germ or embryonal stem cells) and a method
XX CC for modulating expression of the VR1 receptor by introducing the
XX CC modulator or the vector into a cell that contains the VR1 gene. The
XX CC products of the invention are used for detecting a transcription factor
XX CC from its binding to a regulatory sequence (or a double-stranded
XX CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
XX CC linked immunosorbant assay, particularly for diagnosis of diseases
XX CC associated with overexpression or underexpression of the transcription
XX CC factor. The region that modulates VR1 receptor expression includes a
XX CC binding site for a transcription factor, e.g. MZF1, NFKappaB, NFAT or
XX CC GATA1. The nucleic acids of the invention, or vectors containing them,
XX CC are used for prevention or treatment of pain, also for treating
XX CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
XX CC neuralgia and myalgia, that are associated with activity of the VR1
XX CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA
XX CC which is capable of binding to a transcription factor.
XX SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCCACCTGC 12
Db 1 TCCACCTGC 9

RESULT 186
AAIX19836
ID AAX19836 standard; DNA; 11 BP.
XX AC
XX AC AAX19836;
XX DT
XX DT 11-JUN-1999 (first entry)
XX DE Transcription factor binding site E-box.
XX DE
XX KW Transcriptional regulatory region; tissue specific; identification;
XX KW gene expression; transcription factor binding site; ss.
XX OS Synthetic.
XX PN WO9902737-A1.
XX PD 21-JAN-1999.

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XX 14-JUL-1998; 98WO-US014901.
PF
XX
XX 14-JUL-1997; 97US-0052403P.
PR
XX
XX (GENE-) GENEMEDICINE INC.
PA
XX
XX Schwartz RJ, Eastman EM, Li X, Nordstrom J;
PI
XX
XX WPI; 1999-120937/10.
DR
XX
XX Identifying transcriptional regulatory regions - by identifying binding
PT sites for transcription factors and evaluating whether a selective gene
PT is expressed in cells.
XX
XX Example 1; Page 36; 106pp; English.
PS
XX
XX A method has been developed for identifying transcription factor binding
CC sites comprising identifying the oligonucleotides (ONs) in ON-protein
CC complexes formed between one or more proteins of a cellular or nuclear
CC extract and any double stranded (ds) ON fragments in a mixture of the
CC fragments and the extract, where the complexes are separated from free
CC ONs in the mixture using size exclusion chromatography; and where the
CC presence of the ON in the complex is indicative that the ON comprises a
CC binding site. The synthetic regulatory regions obtained using the method
CC can be used in gene delivery or gene therapy to achieve desired gene
CC expression in targeted cells. They can also be used to achieve the
CC production of recombinant proteins at high levels. The present sequence
CC represents a transcription factor binding site given in an example from
CC the present invention
XX
XX Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CACCTGCTG 14
DB 3 CACCTGCTG 11
RESULT 187
AAAI6595/c
ID AAAI6595 standard; DNA; 11 BP.
XX
XX AAAI6595;
AC
XX
XX 16-JUN-2000 (first entry)
DT
XX
XX Human MN gene 5' donor consensus splice sequence SEQ ID NO:73.
DE
XX
XX Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW MN/CA IX isoenzyme; ds.
XX
XX Homo sapiens.
OS
XX
XX US6027887-A.
FN
XX
XX 22-FEB-2000.
PD
XX
XX 24-JAN-1997; 97US-00787739.
PF
XX
XX 21-OCT-1992; 92US-00964589.
PR
XX 30-DEC-1993; 93US-00177093.
PR
XX 15-JUN-1994; 94US-00260190.
PR
XX 07-JUN-1995; 95US-00477504.
PR
XX 07-JUN-1995; 95US-00481658.
PR
XX 07-JUN-1995; 95US-00485049.
PR
XX 07-JUN-1995; 95US-00485862.
PR
XX 07-JUN-1995; 95US-00485863.
PR
XX 07-JUN-1995; 95US-00486756.

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PR 07-JUN-1995; 95US-00487077.
XX (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
PA
XX Pastorek J, Zavada J, Pastorekova S;
PI
XX WPI; 2000-194827/17.
XX
XX Nucleic acid based assay for diagnosing a wide variety of
PT preneoplastic/neoplastic disease comprises screening for the presence of
PT abnormal MN gene expression in a vertebrate.
XX
XX Disclosure; Col 16; 87pp; English.
PS
XX
XX The present invention describes a method of screening for
CC preneoplastic/neoplastic disease. The method comprises: (1) determining
CC whether abnormal MN gene expression is present in a vertebrate; and (2)
CC if abnormal MN gene expression is determined to be present in the
CC vertebrate, determining that the vertebrate has a significant risk of
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC in a vertebrate, preferably a human. The disease detected is mammary.
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC mucosa, pancreatic duct epithelium or liver duct epithelium
CC preneoplastic/neoplastic disease. AAAI6540 to AAAI6617 and AAY53228 to
CC AAY53245 represent sequences used in the exemplification of the present
CC invention
XX
XX Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CCACCTGCT 13
DB 9 CCACCTGCT 1
RESULT 188
AAAI652514/c
ID AAAI652514 standard; DNA; 11 BP.
XX
XX AAAI652514;
AC
XX
XX 25-SEP-2000 (first entry)
DT
XX
XX Human MN gene intron 7 splice donor sequence.
DE
XX
XX MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW abnormal expression; neoplastic disease; cancer; gene therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200024913-A2.
PN
XX
XX 04-MAY-2000.
PD
XX
XX 22-OCT-1999; 99WO-US024879.
PF
XX
XX 23-OCT-1998; 98US-00177776.
PR
XX 23-OCT-1998; 98US-00178115.
PR
XX (FARB ) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
PA
XX

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PI Zavada J, Pastorekova S, Pastorek J;
XX WPI; 2000-350752/30.
XX
XX A molecule which specifically binds to a site on MN protein (oncoprotein)
XX and prevents adhesion of vertebrate cells to the protein, useful for
XX treating preneoplastic or neoplastic diseases such as cancer.
XX
XX Disclosure; Page 26; 154pp; English.
XX
XX The invention relates to the inhibition of cell adhesion mediated by the
XX MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
XX protein). The MN protein is a tumour-associated adhesion molecule which
XX comprises a proteoglycan-like (PG) domain (AA903017) which contains the
XX protein's binding site, and a carbonic anhydrase (CA) domain (AA903018).
XX Abnormal expression of the MN protein is associated with tumorigenicity.
XX The invention encompasses molecules (e.g., proteins and peptides) which
XX which specifically bind to a site on the MN protein, thereby preventing
XX adhesion of vertebrate cells to the protein in a cell adhesion assay. It
XX also encompasses MN proteins or MN protein fragments which can be added
XX to the extracellular environment to prevent the adhesion of vertebrate
XX cells to each other. The invention also relates to the identification of
XX the binding site of the MN protein and to a method of identifying a site
XX on an MN protein to which cells adhere, comprising testing a series of
XX overlapping peptides from the protein in a cell adhesion assay. The
XX invention encompasses a vector comprising an expression control sequence
XX operatively linked to a nucleic acid encoding the variable domains of a
XX MN-specific antibody, where the domains are separated by a flexible
XX linker peptide (AA903035) and the vector inhibits the growth of a
XX vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
XX protein. The invention also encompasses a vector comprising a nucleic
XX acid encoding a cytotoxic protein or peptide operatively linked to the MN
XX gene promoter, which inhibits the growth of a vertebrate preneoplastic or
XX neoplastic cell. Also claimed is a repressor complex that binds to the MN
XX gene promoter (AA52473). MN proteins and peptides, MN-binding proteins
XX and peptides, and expression vectors encoding such proteins and peptides
XX are useful for treating patients with preneoplastic or neoplastic disease
XX (e.g., cancers) associated with or characterised by abnormal MN
XX expression. The present sequence represents a fragment of the human MN
XX gene (AA52462) specified in the invention
XX
XX Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CCACCTGCT 13
Db 9 CCACCTGCT 1
RESULT 189
ABQ86329/C
ID ABQ86329 standard; cDNA; 11 BP.
XX
XX ABQ86329;
AC
XX
XX 10-SEP-2002 (first entry)
DT
XX
XX Human skin stress/ageing related EST SEQ ID NO 84.
DE
XX
XX Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253773-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP015178.
PF
XX
XX 03-JAN-2001; 2001DE-01000121.
PR
XX
XX The invention relates to in vitro identification (M1) of genes expressed
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```
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-528865/56.
XX
XX Identifying genes involved in skin stress and aging, useful e.g. in
XX screening for cosmetic or therapeutic agents, based on differential gene
XX expression.
XX
XX Claim 8; Page 40; 325pp; German.
XX
XX The invention relates to identifying (M1) genes in vitro that, in humans
XX or animals, are important for skin ageing and/or skin stress by serial
XX analysis of gene expression between mixtures of transcribed and
XX optionally translated, genetically encoded factors (A) obtained from
XX young and aged skin, to identify that genes that show strong differential
XX expression. (A) comprises protein or mRNAs or their fragments. (M1) is
XX useful for: identifying markers of skin ageing and/or stress; determining
XX skin ageing and/or stress; and identifying or determining the effects of
XX pharmaceutical or cosmetic agents for control of skin ageing. The present
XX sequence is one of a group of human skin ageing/stress related expressed
XX sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2
RESULT 190
ABV62312/C
ID ABV62312 standard; cDNA; 11 BP.
XX
XX ABV62312;
AC
XX
XX 21-OCT-2002 (first entry)
DT
XX
XX Human skin EST 98.
DE
XX
XX Human; skin; dermatological; vulnerrary; antipsoriatic; antiseborrhoeic;
XX immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200253774-A2.
PN
XX
XX 11-JUL-2002.
PD
XX
XX 20-DEC-2001; 2001WO-EP015179.
PF
XX
XX 03-JAN-2001; 2001DE-01000127.
PR
XX
XX (HENK ) HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Disclosure; Page 28; 1345pp; German.
XX
XX The invention relates to in vitro identification (M1) of genes expressed
```

CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2
|||||

RESULT 191
ABV69491
ID ABV69491 standard; cDNA; 11 BP.
XX
AC ABV69491;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7277.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Disclosure; Page 228; 1345pp; German.
XX

CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGCTGTGTG 18
Db 1 TGCTGTGTG 9
|||||

RESULT 192
ABV69733/C
ID ABV69733 standard; cDNA; 11 BP.
XX
AC ABV69733;
XX
DT 21-OCT-2002 (first entry)
XX
DE Human skin EST 7519.
XX
KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO200253774-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-EP015179.
XX
PR 03-JAN-2001; 2001DE-01000127.
XX
PA (HENK) HENKEL KGAA.
XX
PI Petersohn D, Conradt M, Hofmann K;
XX
DR WPI; 2002-590638/63.
XX
PT In vitro identification of skin-expressed genes, useful for determining
PT homeostasis and identifying cosmetic or pharmaceutical agents against
PT e.g. skin cancer.
XX
PS Claim 24; Page 237; 1345pp; German.
XX

CC The invention relates to in vitro identification (M1) of genes expressed
CC in the skin of humans or animals by subjecting a mixture of genetically
CC encoded factors from skin, to serial analysis of gene expression (SAGE)
CC so as to identify skin-expressed genes and quantify their expression.
CC (M1) is useful for identifying genes involved in skin homeostasis; to
CC determine skin homeostasis and to test agent (A) that maintains or
CC promotes skin homeostasis or that can be used for treating skin
CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC skin. The present sequence is that of a human expressed sequence tag
CC (EST) of the invention
XX
SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2
|||||

RESULT 193
ABL91944/C
ID ABL91944 standard; cDNA; 11 BP.

```
XX ABL91944;
AC
XX 30-MAY-2002 (first entry)
DT
XX
XX Human Pan-Endothelial Marker SEQ ID NO 42.
DE
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW normal endothelial marker; pan-endothelial marker; immunostimulant;
KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW psoriasis; ss.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200210217-A2.
FN
XX
XX 07-FEB-2002.
PD
XX
XX 01-AUG-2001; 2001WO-US024031.
PF
XX
XX 02-AUG-2000; 2000US-0222599P.
PR
XX
XX 11-AUG-2000; 2000US-0224360P.
PR
XX
XX 11-APR-2001; 2001US-0282850P.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX St Croix B, Kinzler KW, Vogelstein B;
PI
XX
XX WPI; 2002-291856/33.
DR
XX
XX An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Example 4; Page 325; 331pp; English.
PS
XX
XX The invention relates to an isolated molecule comprising an antibody
CC variable region which specifically binds to an extracellular domain of a
CC tumor endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC bearing a vascularised tumour, polycystic kidney disease, diabetic
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC are disclosed, as are marker oligonucleotide sequences: tumour
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC (PEM) ABL91903-ABL91995. The present sequence is that of an
CC oligonucleotide marker useful to the invention
XX
XX Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2
RESULT 194
ABX71869/c
ID ABX71869 standard; DNA; 11 BP.
XX
XX ABX71869;
AC
XX
XX 12-MAR-2003 (first entry)
DT
XX
XX DNA tag used to identify human gene encoding PEM 42.
DE
XX
XX
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```
KW Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
KW Tumour endothelial marker; normal endothelial marker; PEM;
KW pan-endothelial marker; polycystic kidney disease; psoriasis;
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW neoangiogenesis; immune response; cytostatic; anti-diabetic;
KW ophthalmological; anti-rheumatic; anti-arthritis; antipsoriatic; ds.
KW
XX
XX Homo sapiens.
OS
XX
XX WO200283874-A2.
FN
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US008253.
PF
XX
XX 11-APR-2001; 2001US-0282850P.
PR
XX
XX 06-FEB-2002; 2002US-0354262P.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
PA
XX
XX Carson-Walter B, St Croix B, Kinzler KW, Vogelstein B;
PI
XX
XX WPI; 2003-093016/08.
DR
XX
XX New purified human transmembrane protein, designated as tumor endothelial
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors;
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT psoriasis.
XX
XX Disclosure; Page 94; 374pp; English.
PS
XX
XX The present invention relates to a novel method for the isolation of
CC endothelial cells (ECs), and the identification of genes expressed in
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
CC identified in human ECs. The human EC marker proteins and the
CC polynucleotide sequences encoding them are useful for detecting,
CC diagnosing or treating tumours as well as polycystic kidney disease,
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
CC inducing an immune response to tumour endothelial cells in a patient, or
CC for identifying candidate drugs for treating tumours. ABX71828-ABX71999
CC represent DNA tags for human PEM, TEM or NEM genes
XX
XX Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2
RESULT 195
ADK41823/c
ID ADK41823 standard; DNA; 11 BP.
XX
XX ADK41823;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human MN gene intron-exon boundary sequence SeqID52.
DE
XX
XX carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
KW human; vertebrate; cytostatic; vaccine; gene therapy;
KW renal cell carcinoma; breast cancer; colorectal cancer; splice acceptor;
KW ds.
KW
XX
XX Homo sapiens.
OS
XX
XX WO2004005348-A1.
PN
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XX PD 15-JAN-2004.
XX XX
XX PF 22-FEB-2003; 2003WO-US005137.
XX PR 23-MAY-2002; 2002US-0383068P.
XX PR 05-DEC-2002; 2002US-0431499P.
XX XX
XX PA (FARB ) BAYER CORP.
XX PA (VIRO-) INST VIROLOGY.
XX PI Zavada J, Pastorekova S, Pastorek J, Zavadova Z;
XX PT WPI; 2004-0833500/08.
XX DR
XX PT New soluble form of the carbonic anhydrase IX (CA IX) protein for
XX PT screening, diagnosing or prognosing diseases associated with abnormal
XX PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
XX PT colorectal cancer.
XX XX
XX PS Disclosure; SEQ ID NO 52; 159pp; English.
XX CC
XX CC This invention relates to a novel soluble form of the carbonic anhydrase
XX CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
XX CC precancerous and/or cancerous cells of a vertebrate into a body fluid.
XX CC The invention may be useful for the development of compounds with a
XX CC cytostatic activity or a vaccine whilst the disclosed sequences may be
XX CC used for gene therapy. The protein and method are useful for screening,
XX CC diagnosing or prognosing diseases associated with abnormal expression of
XX CC carbonic anhydrase IX protein, such as precancerous and cancerous
XX CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.
XX CC The monoclonal antibody may also be used for treating or preventing
XX CC precancerous and cancerous diseases. The present sequence is that of a
XX CC splice acceptor site from a human MN gene intron-exon boundary which is
XX CC related to the invention.
XX XX
XX SQ Sequence 11 BP; 2 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
Db 9 CCACCTGCT 1
|||||

RESULT 196
ABH83073/c
ID ABH83073 standard; DNA; 12 BP.
XX AC ABH83073;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 283066 for detecting SNP TSC0011130.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (BPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 283066; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABG99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CATCCACCT 10
Db 9 CATCCACCT 1
|||||

RESULT 197
ABI66469/c
ID ABI66469 standard; DNA; 12 BP.
XX AC ABI66469;
XX XX
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 366442 for detecting SNP TSC0055762.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 366442; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

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CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
  Query Match 31.0%; Score 9; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2 CATCCACCT 10
  Db 9 CATCCACCT 1
  |||||
  |||||
RESULT 198
ABI17481
ID ABI17481 standard; DNA; 12 BP.
XX
AC ABI17481;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 317454 for detecting SNP TSC0028024.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 317454; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
  Query Match 31.0%; Score 9; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2 CATCCACCT 10
  Db 9 CATCCACCT 1
  |||||
  |||||
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 CCATCCACC 9
  Db 2 CCATCCACC 10
  |||||
  |||||
RESULT 199
ABI77789/c
ID ABI77789 standard; DNA; 12 BP.
XX
AC ABI77789;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 377762 for detecting SNP TSC0007285.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 377762; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
  Query Match 31.0%; Score 9; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.5e+02;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2 CATCCACCT 10
  Db 11 CATCCACCT 3
  |||||
  |||||
RESULT 200
ABI74143/c
ID ABI74143 standard; DNA; 12 BP.
XX
AC ABI74143;
```



```

XX 22-FEB-2002 (first entry)
DT Oligonucleotide primer SEQ ID NO 374116 for detecting SNP TSC0060503.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 374116; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Claim 1; SEQ ID NO 374116; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATCCACC 9
Db 9 CCATCCACC 1
RESULT 201
AB117480
ID AB117480 standard; DNA; 12 BP.
XX
XX ABI117480;
XX
XX 22-FEB-2002 (first entry)
DT Oligonucleotide primer SEQ ID NO 317453 for detecting SNP TSC0028024.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 374116; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATCCACC 9
Db 9 CCATCCACC 1
RESULT 202
ABH73202/c
ID ABH73202 standard; DNA; 12 BP.
XX
XX ABH73202;
XX
XX 22-FEB-2002 (first entry)
DT Oligonucleotide primer SEQ ID NO 273187 for detecting SNP TSC0003081.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 317453; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATCCACC 9
Db 2 CCATCCACC 10
RESULT 203
ABH73202/c
ID ABH73202 standard; DNA; 12 BP.
XX
XX ABH73202;
XX
XX 22-FEB-2002 (first entry)
DT Oligonucleotide primer SEQ ID NO 273187 for detecting SNP TSC0003081.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 317453; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCATCCACC 9
Db 2 CCATCCACC 10

```

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 273187; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATCACCT 10
Db 10 CATCCACCT 2
|||||

RESULT 203
ABI56716
ID ABI56716 standard; DNA; 12 BP.
XX
AC ABI56716;
XX
XX 22-FEB-2002 (first entry)
DT
XX
DE Oligonucleotide primer SEQ ID NO 356689 for detecting SNP TSC0050259.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 356689; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATCACCT 10
Db 10 CATCCACCT 2
|||||

RESULT 204
AAL44624
ID AAL44624 standard; DNA; 12 BP.
XX
AC AAL44624;
XX
XX 26-APR-2002 (first entry)
DT
XX
DE Muscle creatine kinase MCK-R control element #1.
XX
XX Muscle-specific enhancer; gene therapy; regulatory element; haemostatic;
XX antibacterial; antiviral; antitumor; antiinflammatory; anti-HIV;
XX cytostatic; antilipemic; antidiabetic; antianaemic; MCK; MCK-R;
XX muscle creatine kinase control element; ds.
XX
XX Unidentified.
OS
XX
XX WO200206495-A2.
XX
XX 24-JAN-2002.
PD
XX
XX 13-JUL-2001; 2001WO-US022092.
PF
XX
XX 14-JUL-2000; 2000US-0218436P.
PR
XX
XX (UNMI) UNIV MICHIGAN.
PA
XX
XX Chamberlain JS, Hauschka SD;
PI
XX
XX WPI; 2002-171809/22.
DR
XX
XX Composition comprising nucleic acid which comprises mutant muscle-
PT specific enhancer region having two muscle creatine kinase-R control
PT elements, useful in gene therapy, drug screening, and diagnostic assays.
XX
XX Disclosure; Fig 16; 61pp; English.
PS
XX
XX The present invention relates to a composition comprising a nucleic acid,
CC where the nucleic acid contains a mutant muscle-specific enhancer region
CC which comprises at least 2 muscle creatine kinase (MCK)-R control
CC elements. The nucleic acid can be used in gene therapy, particularly
CC where the therapy is directed at muscle cells and in the treatment of
CC endocrine, metabolic, haematologic, cardiovascular, neurologic,
CC musculoskeletal, urologic, pulmonary and immune disorders such as
CC inflammatory diseases, autoimmune disease, chronic and infectious
CC diseases such as AIDS, cancer, hypercholesterolaemia, insulin disorders
CC such as diabetes, growth disorders, various blood disorders including
CC anaemia, thalassaemia, haemophilia, genetic defects such as cystic
CC fibrosis, Gaucher's disease, Hurler's disease, adenosine deaminase (ADA)
CC deficiency, and emphysema. The present sequence is an MCK-R control
CC element
XX
XX Sequence 12 BP; 3 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
SQ

Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACC 9
Db 4 CCATCCACC 12
|||||

CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACC 9
Db 4 CCATCCACC 12
|||||

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QY      6 CACCTGCTG 14
Db      3 CACCTGCTG 11
      |||||
      |||||

RESULT 205
ADF78489/c
ID      ADF78489 standard; DNA; 12 BP.
XX
AC      ADF78489;
XX
DT      26-FEB-2004 (first entry)
XX
DE      Chromosomal abnormality detection-related PCR primer 70.
XX
KW      chromosomal abnormality; maternal locus; genetic disorder; foetus;
KW      mutation; translocation; transversion; monosomy; trisomy; trisomy 21;
KW      chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;
KW      chromosome addition; chromosome amplification; chromosome translocation;
KW      chromosome rearrangement; single nucleotide polymorphism detection;
KW      SNP detection; pregnant female; PCR; primer; ss.
XX
OS      Homo sapiens.
XX
PN      WO2003074723-A2.
XX
PD      12-SEP-2003.
XX
PF      28-FEB-2003; 2003WO-US006198.
XX
PR      01-MAR-2002; 2002US-0360232P.
PR      11-MAR-2002; 2002US-00093618.
PR      08-MAY-2002; 2002US-0378354P.
XX
PA      (DHALL/) DHALLAN R.
XX
PI      Dhallan R;
XX
WPI; 2003-845073/78.
XX
Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
PT      invasively in a fetus, comprises forming a ratio of amounts of alleles at
PT      a locus of interest and a different heterozygous locus.
XX
Example 11; Page 214; 164pp; English.
XX
This invention relates to a novel method of detecting chromosomal
CC      abnormalities by determining the sequence of alleles of a locus of
CC      interest from template DNA, determining which alleles are present and
CC      comparing to amounts of alleles at a different, selected heterozygous
CC      locus (for example on another chromosome or a maternal locus); relative
CC      amounts are expressed as a ratio indicating presence or absence of the
CC      abnormality. The method is useful for the detection of genetic disorders,
CC      especially in a fetus, including chromosomal abnormalities and
CC      mutations, for example translocations, transversions, monosomies,
CC      trisomies (for example trisomy 21 in which an additional copy of
CC      chromosome 21 results in Down's Syndrome) and other aneuploidies,
CC      deletions, additions, amplifications, translocations and rearrangements.
CC      It can be used to detect any alterations in a gene sequence, especially
CC      single nucleotide polymorphisms (SNPs), and may be used to detect
CC      numerous abnormalities simultaneously, for example if several SNPs are
CC      associated with a particular disease. The method provides a rapid, non-
CC      invasive method for determining the sequence of DNA from a foetus using a
CC      sample from a pregnant female, for example to detect genetic disorders as
CC      above or to determine if a foetus is a carrier of a disease or
CC      predisposed to a disease.
XX
Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GCTGTGTGA 19
Db      1 GCTGTGTGA 9
      |||||
      |||||

RESULT 207
ADR98065/c
ID      ADR98065 standard; DNA; 12 BP.
XX
AC      ADR98065;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Human SNP TSC1261039 multiplex PCR primer #1.

```

```

QY      15 TGTGACCTG 23
Db      11 TGTGACCTG 3
      |||||
      |||||

RESULT 206
ADO08498
ID      ADO08498 standard; DNA; 12 BP.
XX
AC      ADO08498;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Human papillomavirus (HPV) detection-related PNA probe XII SeqID30.
XX
KW      detection; typing; Human Papilloma Virus; HPV; infection; PNA probe;
KW      high-risk; infectious organism; probe; ss.
XX
OS      Human papillomavirus.
XX
PN      WO2004042071-A2.
XX
PD      21-MAY-2004.
XX
PF      07-OCT-2003; 2003WO-US031841.
XX
PR      01-NOV-2002; 2002US-00286387.
XX
PA      (CYTY-) CYTYC CORP.
XX
PI      Cohenford MA, Lentricchia BB;
XX
WPI; 2004-400683/37.
XX
New peptide-nucleic acids, useful as a probe for detecting and typing
PT      Human Papilloma Virus infection, or in screening assay toward the
PT      diagnostically most-relevant strains or species of a disease organism.
XX
Example 4; SEQ ID NO 30; 26pp; English.
XX
This invention relates to a novel method for detection and typing of a
CC      Human Papilloma Virus (HPV) infection using PNA primers or probes,
CC      including methods for detecting high-risk types of HPV infection with
CC      minimal numbers of PNA probes or using PNA primers to selectively amplify
CC      only high-risk types of HPV. Specifically claimed are novel primer/probe
CC      sequences which are useful as primers/probes for detecting and typing HPV
CC      infection. The methods are used in a screening assay toward the
CC      diagnostically most-relevant strains or species of a disease organism or
CC      to selectively amplify high-risk strains of an infectious organism. The
CC      present sequence is that of a HPV PNA probe which was used in the
CC      exemplification of the invention.
XX
Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GCTGTGTGA 19
Db      1 GCTGTGTGA 9
      |||||
      |||||

RESULT 207
ADR98065/c
ID      ADR98065 standard; DNA; 12 BP.
XX
AC      ADR98065;
XX
DT      02-DEC-2004 (first entry)
XX
DE      Human SNP TSC1261039 multiplex PCR primer #1.

```

XX ss; chromosomal abnormality; detection; foetus; translocation;
KW transversion; monosomy; trisomy; aneuploidy; deletion; addition;
KW amplification; prenatal diagnosis; PCR; primer; SNP;
KW single nucleotide polymorphism; human; multiplex; TSC1261039.
XX
OS Homo sapiens.
XX
XX WO2004079011-A1.
XX
XX PD 16-SEP-2004.
XX
XX PF 29-AUG-2003; 2003WO-US027308.
XX
XX PR 28-FEB-2003; 2003WO-US006198.
XX
XX PA (RAVG-) RAVGEN INC.
XX
XX PI Dhallan R;
XX
XX DR WPI; 2004-677127/66.
XX
XX DR Detecting a chromosomal abnormality, e.g. translocations, transversions,
XX monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises
XX determining the sequence of alleles of a locus of interest in the sample
XX from template DNA.
XX
XX Example 12; Page 200; 429pp; English.
XX
XX This invention describes a novel method for detecting a chromosomal
XX abnormality in a sample which comprises determining the sequence of
XX alleles of a locus of interest in a sample from template DNA where
XX determining the sequence of the alleles comprises amplifying the locus of
XX interest, hybridising the amplified loci to GeneChip array, washing
XX GeneChip array, staining the GeneChip array with detectable reagents, and
XX scanning GeneChip array. The amplification method is self-sustained
XX sequence reaction, ligase chain reaction, rapid amplification of cDNA
XX ends, PCR and ligase chain reaction, Q-beta phage amplification, strand
XX displacement amplification, or splice overlap extension PCR, preferably
XX PCR. The determination of the sequence of the alleles comprises
XX amplifying the locus of interest, fragmenting the amplicon, hybridising
XX fragmented amplicons to CodeLink Arrays, extension reaction to
XX incorporate a nucleotide and detecting incorporated nucleotides. The
XX amplicon fragmentation is by exonuclease digestion. Detecting a
XX chromosomal abnormality in a sample comprises determining the sequence of
XX alleles of a locus of interest from template DNA, where determining the
XX sequence of the alleles comprises using BeadArray Technology. The
XX determination of the locus of interest, dephosphorylation of the unused
XX reagents, in vitro transcription reaction of the products, RNase A
XX cleavage of the products, mixing the products with Cleanesin,
XX transferring products to SpectroCHIP, and analysing the SpectroCHIP. The
XX dephosphorylation reaction is with shrimp alkaline phosphatase.
XX Alternatively, the determination of the sequence of the alleles comprises
XX amplifying the locus of interest, dephosphorylation of the unused
XX reagents, hybridising a primer to the locus of interest, incorporating a
XX nucleotide, mixing the products with Cleanesin, transferring products to
XX SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer
XX is adjacent to the locus of interest. The determination of the sequence
XX of the alleles may also comprise amplifying the locus of interest,
XX treating the products with exonuclease, single stranded DNA is annealed
XX to an oligonucleotide, incorporating a nucleotide using the annealed
XX template and primer, and detecting the incorporated nucleotide. The
XX method is useful for detecting a chromosomal abnormality in a sample.
XX Specifically, the method is useful for detecting chromosomal
XX abnormalities in a fetus including translocations, transversions,
XX monosomies, trisomies, and other aneuploidies, deletions, additions,
XX amplifications, and arrangements. The method of the invention can also be
XX used for prenatal diagnosis. This sequence represents a multiplex PCR
XX primer used to amplify the human SNP TSC1261039.
XX
XX Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;
QY 15 TGTGACCTG 23
| | | | | | | | | |
Db 11 TGTGACCTG 3
RESULT 208
ADS08752/c
ID ADS08752 standard; DNA; 12 BP.
XX
XX AC ADS08752;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Human DNA PCR primer #89.
XX
XX Human; PCR; primer; ss; nucleic acid detection; cell lysis;
KW chromosomal abnormality; cancer; carcinoma; bladder; breast; bronchus;
KW colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas;
KW stomach; cervix; thyroid; prostate; skin; small cell lung cancer;
KW squamous cell carcinoma; leukaemia; lymphoma; myelodysplastic syndrome;
KW fibrosarcoma; rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma;
KW schwannoma; melanoma; seminoma; teratocarcinoma; osteosarcoma.
XX
XX OS Homo sapiens.
XX
XX PN WO2004078994-A2.
XX
XX PD 16-SEP-2004.
XX
XX PF 01-MAR-2004; 2004WO-US006337.
XX
XX PR 28-FEB-2003; 2003WO-US006198.
XX
XX PA (RAVG-) RAVGEN INC.
XX
XX PI Dhallan R;
XX
XX DR WPI; 2004-662434/64.
XX
XX PT Detecting presence or absence of nucleic acid, containing mutation,
XX involves isolating nucleic acid from sample containing cell lysis
XX inhibitor, and detecting presence or absence of nucleic acid.
XX
XX Example 12; Page 209; 440pp; English.
XX
XX The invention relates to a method for detecting a nucleic acid, involving
XX isolating a nucleic acid from a sample, where an agent that impedes cell
XX lysis was added to the sample, and detecting the presence or absence of
XX the nucleic acid. The invention also relates to a method for detecting
XX chromosomal abnormalities in a DNA sample and determining the sequence of
XX foetal DNA from a sample of a pregnant female. The nucleic acid contains
XX at least one mutation chosen from a single point mutation, multiple point
XX mutations, an insertion, a frameshift, a truncation, a deletion, a
XX duplication and a transversion. The method is useful for detecting
XX nucleic acid in a sample obtained from a source chosen from bacteria,
XX viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,
XX non-humans, multi-cellular parasites, animals and archaeobacteria. The
XX method is useful for detecting, diagnosing or monitoring a disease such
XX as cancer chosen from carcinoma of the bladder, breast, pancreas, stomach,
XX kidney, liver, lung, oesophagus, gall bladder, ovary, prostate, colon,
XX cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell
XX carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute
XX lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-
XX cell-lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell
XX lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage,
XX acute and chronic myelogenous leukaemias, myelodysplastic syndrome and
XX promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and
XX rhabdomyosarcoma, tumours of the central and peripheral nervous system,
XX astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma,

CC teratocarcinoma and osteosarcoma. The method is also useful for
CC monitoring response to treatment chosen from surgery, radiation,
CC lifestyle change, dietary protocol and supplementation and administration
CC of a drug. The drug is chosen from chemotherapeutic agents, anti-
CC bacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer
CC drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents.
CC This sequence represents a PCR primer used in the scope of the invention.

XX
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 31.0%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TGTGACCTG 23
|||||||
Db 11 TGTGACCTG 3

RESULT 209
AAQ86030/c
ID AAQ86030 standard; DNA; 12 BP.

XX AC AAQ86030;

XX XX
DT 25-MAR-2003 (revised)
DT 05-MAY-1995 (first entry)

XX ITr10C3 coding region, exon 7-intron border.

XX transporter protein; ITr10C3; superfamily; tetracycline resistance;
KW exon amplification; PCR: D4S95; Huntington's disease; dementia;
KW choreiform movements; cognitive decline; neurodegenerative; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH exon 1..6
FT /*tag= a
FT /number= exon 7
FT intron 7..12
FT /*tag= b

XX EP617125-A2.

XX 28-SEP-1994.

XX 23-MAR-1994; 94EP-00302092.

XX 23-MAR-1993; 93US-00035928.

XX (GEO) GEN HOSPITAL CORP.

XX Duyao MP, Macdonald MF, Gusella JF;

XX WPI; 1994-295776/37.

XX New transporter protein ITr10C3 and related nucleic acid - vectors and
PT antibodies, for diagnosis and treatment, of e.g. neuro-degenerative
PT disorders, derived from the Huntington's disease region of chromosome 4.

XX Example 2; Fig 5; 36pp; English.

XX A series of nucleotide sequences (AAQ86018-35) showing the exon-intron
CC borders of the gene for the novel transporter protein ITr10C3. The
CC composite DNA sequence presented (AAQ73384) covers 1788 bp including a
CC 1365 bp open reading frame with a 29-mer poly A-tail. The gene encodes a
CC protein of 455 amino acids with strong similarity to a superfamily of
CC transporter protein typified by tetracycline resistance proteins. The
CC gene was isolated from a human frontal cortex cDNA library with cosmid
CC Y24 and trapped, uncloned exon PCR products. The products were used to
CC rescreen the library and pull out a series of clone whose sequence form
CC the composite of AAQ73384. The gene maps distal to D4S95 in the

CC Huntington's region. Probes to this gene can be used for presymptomatic
CC (e.g. prenatal) diagnosis of ITr10C3-related diseases e.g. choreiform
CC movements, dementia, cognitive decline and/or neurodegenerative disorders
CC such as Huntington's disease. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTG 14
|||||||
Db 12 ACCCACCTACTG 1

RESULT 210
AAQ88466
ID AAQ88466 standard; DNA; 12 BP.

XX AC AAQ88466;

XX XX
DT 19-DEC-1995 (first entry)

XX Human mitochondrial D-loop region DNA probe 11-2.

XX Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
KW D-loop region; biological chip; hybridisation fingerprint;
KW interrogation position; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 12
FT /*tag= a
FT /note= "3'-end of probe is covalently attached to chip
FT surface"

XX WO9511995-A1.

XX 04-MAY-1995.

XX 26-OCT-1994; 94WO-US012305.

XX 26-OCT-1993; 93US-00143312.

XX 02-AUG-1994; 94US-00284064.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
PI Lipshutz RJ, Lobbann PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX WPI; 1995-178887/23.

XX New arrays of oligo-nucleotide probes - used for comparing known
PT sequences with variants for detection of mutation(s) and sequencing.

XX Disclosure; Page 107; 223pp; English.

XX A DNA chip was prepared for analysing sequences contained in a 1.3kb
CC fragment of human mitochondrial DNA from the D-loop region, the most
CC polymorphic region of human mitochondrial DNA. The chip comprised a set
CC of 288 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
CC x 1cm array. Each position in the sequence was represented by at least
CC one probe (usually 2 or more). DNA was amplified from six human donors
CC and then transcribed to give the 1.3kb RNA transcripts which were
CC fragmented and hybridised to the chip. For each individual, a unique
CC hybridisation fingerprint was produced on the chip; all differences could
CC be correlated with differences in the cloned genomic DNA sequence
XX
XX Sequence 12 BP; 0 A; 1 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGG 24
 Db 1 TGTGTGTGCTGG 12

RESULT 211
 AAA59759
 ID AAA59759 standard; DNA; 12 BP.
 XX AC AAA59759;
 XX DT 06-OCT-2000 (first entry)
 XX DE Bacteriophage M13mpl18 nucleotide sequence SEQ ID 3.
 XX KW Replaceable matrix formulation; biomacromolecule separation;
 KW capillary electrophoresis; nucleic acid sequencing; differential display;
 KW dideoxyfingerprinting; short tandem repeat analysis; ds.
 XX OS Bacteriophage M13mpl18.
 XX WO200028314-A1.
 XX 18-MAY-2000.
 XX 10-NOV-1999; 99WO-US026465.
 XX 10-NOV-1998; 98US-0107798P.
 XX 13-AUG-1999; 99US-00374174.
 XX (CURA-) CURAGEN CORP.
 XX Ruiz-Martinez MC;
 XX WPI; 2000-376654/32.
 XX Replaceable matrix formulation, used for the separation of biological
 macromolecules using capillary electrophoresis, comprises linear
 polyacrylamide solution and at least one denaturant.
 XX Disclosure; Page 30; 33pp; English.
 XX The invention relates to a replaceable matrix formulation, comprising a
 linear polyacrylamide solution, at least one denaturant, a buffer, and 6M
 urea. Also included in the invention is a method of biomacromolecule
 separation using a capillary electrophoresis device, comprising the
 replaceable matrix formulation and a buffer. The method is used for
 capillary array electrophoresis and biomacromolecule separation. The
 biomacromolecule separation method is used in nucleic acid sequencing, to
 determine the molecular size of a biomacromolecule, for differential
 display of mRNA, in dideoxyfingerprinting, or in short tandem repeat
 (STR) analysis. The present sequence represents a fragment of
 bacteriophage M13mpl18 DNA, and is disclosed in the course of the
 invention

XX SQ Sequence 12 BP; 1 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 30.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCCACCTGCTGT 15
 Db 1 TCCACCTGGTTT 12

RESULT 212
 ABI24861/c

ID ABI24861 standard; DNA; 12 BP.
 XX AC ABI24861;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 324834 for detecting SNP TSC0032247.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 designed to detect single-nucleotide polymorphisms and cytosine
 methylation status.
 XX Claim 1; SEQ ID NO 324834; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 and cytosine methylation status in chemically pretreated genomic DNA. The
 oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 range of diseases including immune system, gastrointestinal, respiratory,
 central nervous system, cardiovascular and metabolic disorders. The
 oligomers are also used for detecting cell type differentiation. ABC00010
 -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 represent the oligomers described in the invention. NOTE: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 30.3%; Score 8.8; DB 1; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 13 TGTGTGACCTGG 24
 Db 12 TGTGTGAAGTGG 1

RESULT 213
 ABI11597
 ID ABI11597 standard; DNA; 12 BP.
 XX AC ABI11597;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide primer SEQ ID NO 311570 for detecting SNP TSC0024559.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.

central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCT 13
Db 12 CATCCAACTACT 1

RESULT 216
ABI52832/c
ID ABI52832 standard; DNA; 12 BP.
XX AC ABI52832;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 352805 for detecting SNP TSC0048107.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 352805; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 3 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCT 13
Db 12 CATCCAACTACT 1

RESULT 217
ABI39693
ID ABI39693 standard; DNA; 12 BP.
XX AC ABI39693;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 339666 for detecting SNP TSC0041130.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 339666; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 1 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
Db 1 CCATCTCTCCGC 12

RESULT 218
ABH80092/c
ID ABH80092 standard; DNA; 12 BP.
XX AC ABH80092;
XX DT 22-FEB-2002 (first entry)

Qy 2 CATCCACCTGCT 13
Db 12 CCTCCACCTCCT 1

RESULT 217
ABI39693
ID ABI39693 standard; DNA; 12 BP.
XX AC ABI39693;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 339666 for detecting SNP TSC0041130.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
XX PS Claim 1; SEQ ID NO 339666; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 12 BP; 1 A; 8 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
Db 1 CCATCTCTCCGC 12

RESULT 218
ABH80092/c
ID ABH80092 standard; DNA; 12 BP.
XX AC ABH80092;
XX DT 22-FEB-2002 (first entry)


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XX DE Oligonucleotide primer SEQ ID NO 280085 for detecting SNP TSC0008178.
XX DE
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX 18-OCT-2001.
XX PD
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX
XX DR WPI; 2001-657177/75.
XX XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 280085; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 1 A; 1 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCATCCACCTGC 12
Db 12 CAATCCACCCGC 1
|||||
|

RESULT 219
ABH77417
ID ABH77417 standard; DNA; 12 BP.
XX
XX AC ABH77417;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 277410 for detecting SNP TSC0004463.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX

```

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PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX
XX PS Claim 1; SEQ ID NO 277410; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 2 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
XX
Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCT 13
Db 1 CATCTACCTTCT 12
|||||
|

RESULT 220
ABH83668/c
ID ABH83668 standard; DNA; 12 BP.
XX
XX AC ABH83668;
XX XX
XX DT 22-FEB-2002 (first entry)
XX XX
XX DE Oligonucleotide primer SEQ ID NO 283661 for detecting SNP TSC0011446.
XX XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX XX
XX PD 18-OCT-2001.
XX XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX XX
XX PR 07-APR-2000; 2000DE-01019173.
XX XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.

```



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RESULT 223
ABI60766/c
ID ABI60766 standard; DNA; 12 BP.
XX
XX
AC ABI60766;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 360739 for detecting SNP TSC0052264.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 360739; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 CCATCCACCTGC 12
DB 12 CCATCCATCTCC 1
XX
XX
RESULT 224
ABI62806
ID ABI62806 standard; DNA; 12 BP.
XX
XX ABI62806;
XX
DT 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 362779 for detecting SNP TSC0053443.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW

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```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 362779; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 CCATCCACCTGC 12
DB 1 CCATCCACATCC 12
XX
XX
RESULT 225
ABI17729
ID ABI17729 standard; DNA; 12 BP.
XX
XX ABI17729;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 317702 for detecting SNP TSC0028181.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX (EPIG-) EPIGENOMICS AG.
XX

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XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 317702; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCT 13
Db 1 CATCTACCTACT 12

RESULT 226
ABH94984/c
ID ABH94984 standard; DNA; 12 BP.
XX AC ABH94984;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 294977 for detecting SNP TSC0016386.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 294977; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCT 13
Db 1 CATCTACCTACT 12

RESULT 227
ABI26645/c
ID ABI26645 standard; DNA; 12 BP.
XX AC ABI26645;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 326618 for detecting SNP TSC0033177.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 326618; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

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Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  4  TCCACCTGCTGT 15
Db  12 TCCACCTGCTGT 1

RESULT 228
ABI39600
ID  ABI39600 standard; DNA; 12 BP.
XX
AC  ABI39600;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 339573 for detecting SNP TSC0041077.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
PP  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 339573; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;

Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  13 TGTGTGACCTGG 24
Db  1  TGTGTGACGAGG 12

RESULT 229
ABI59140/C
ID  ABI59140 standard; DNA; 12 BP.
XX

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```

AC  ABI59140;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 359113 for detecting SNP TSC0009017.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.
XX
PD  18-OCT-2001.
XX
PF  06-APR-2001; 2001WO-IB000713.
XX
PR  07-APR-2000; 2000DE-01019173.
XX
PA  (EPIG-) EPIGENOMICS AG.
XX
PI  Olek A, Piepenbrock C, Berlin K;
XX
PP  WPI; 2001-657177/75.
XX
PT  Set of oligonucleotides, useful for diagnosis and cell typing, is
PT  designed to detect single-nucleotide polymorphisms and cytosine
PT  methylation status.
XX
PS  Claim 1; SEQ ID NO 359113; 29pp + Sequence Listing; German.
XX
CC  This invention describes novel oligonucleotide primers or peptide nucleic
CC  acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC  and cytosine methylation status in chemically pretreated genomic DNA. The
CC  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC  range of diseases including immune system, gastrointestinal, respiratory,
CC  central nervous system, cardiovascular and metabolic disorders. The
CC  oligomers are also used for detecting cell type differentiation. ABC00010
CC  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC  represent the oligomers described in the invention. NOTE: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 12 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  CATCCACCTGCT 13
Db  12 CATCCACCTACT 1

RESULT 230
ABI60733
ID  ABI60733 standard; DNA; 12 BP.
XX
AC  ABI60733;
XX
DT  22-FEB-2002 (first entry)
XX
DE  Oligonucleotide primer SEQ ID NO 360706 for detecting SNP TSC0052238.
XX
KW  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW  peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW  central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS  Homo sapiens.
XX
PN  WO200177384-A2.

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XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 360706; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 15 TGTGACCTGGTA 26
Db 1 TGTGATTGGTA 12
RESULT 231
ABI26571
ID ABI26571 standard; DNA; 12 BP.
XX AC ABI26571;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 326544 for detecting SNP TSC0033133.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 277037; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 15 TGTGACCTGGTA 26
Db 1 TGTGATTGGTA 12
RESULT 232
ABH77044
ID ABH77044 standard; DNA; 12 BP.
XX AC ABH77044;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 277037 for detecting SNP TSC0004364.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 277037; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 1 CCATCCACATAC 12
RESULT 233
ABH77044
ID ABH77044 standard; DNA; 12 BP.
XX AC ABH77044;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 277037 for detecting SNP TSC0004364.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 277037; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 4 A; 6 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 1 CCATCCACATAC 12

```


KW Human; optineurin; ds; ophthalmological; single nucleotide polymorphism;
KW SNP; glaucoma; progressive ocular hypertensive disorder;
KW glaucoma related disorder; motif; repeat element; regulatory region.
XX Homo sapiens.
XX US2003190617-A1.
XX 09-OCT-2003.
XX 06-MAR-2002; 2002US-00091281.
XX 06-MAR-2002; 2002US-00091281.
XX (SIEE/) SI E.
XX (RAYM/) RAYMOND V.
XX (MORI/) MORISSETTE J.
XX Raymond V, Morissette J, Si E;
XX WPI; 2003-864168/80.
XX New nucleic acid sequences of the optineurin gene are useful to detect
XX polymorphisms particularly single nucleotide polymorphisms in the
XX optineurin promoter to diagnose, prognose and treat glaucoma and related
XX disorders.
XX Claim 11; SEQ ID NO 54; 159pp; English.
XX The invention relates to an isolated nucleic acid (NI) comprising at
XX least 20 but not more than 1500 consecutive nucleotides of the optineurin
XX promoter appearing as ADE13890. Also included are the optineurin promoter
XX operably linked to a heterologous nucleic acid, a nucleic acid capable of
XX detecting a single nucleotide polymorphism (SNP) in the optineurin
XX promoter, a host cell comprising the promoter operably linked to a
XX heterologous sequence, diagnosing or prognosing glaucoma in a sample
XX obtained from a cell or bodily fluid (comprising detecting a polymorphism
XX in a promoter region of the optineurin gene, associated with a glaucoma
XX phenotype), detecting a SNP sequence variation in a sample containing
XX DNA, detecting the presence of an optineurin promoter sequence variation
XX in a sample containing DNA, determining the presence or increased
XX susceptibility to glaucoma or to a progressive ocular hypertensive
XX disorder resulting in loss of visual field in a patient (or the severity
XX or progression of glaucoma in a patient, comprising providing
XX amplification reaction primers that direct amplification of a selected
XX nucleic acid region containing the variation within the optineurin
XX promoter and amplifying the DNA) and detecting a polymorphism (comprising
XX obtaining a sample containing human genomic DNA, providing a nucleic acid
XX capable of detecting a SNP located within an optineurin promoter, and
XX detecting the polymorphism). The invention is used to diagnose and
XX prognose glaucoma and also to treat glaucoma related disorders. The
XX present sequence is an optineurin promoter motif, repeat element or
XX putative regulatory region.
XX Sequence 12 BP; 2 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 ATCCACCTGCTG 14
XX |||||
XX Db 1 ATGCAGCTGCTG 12
XX
XX RESULT 236
XX ABZ77024/c
XX ID ABZ77024 standard; DNA; 12 BP.
XX AC ABZ77024;
XX AC ABZ77024;
XX DT 07-MAY-2003 (first entry)
XX XX

DE Bovine DGAT exon-intron junction oligonucleotide #14.
XX Acyl CoA:diacylglycerol transferase; DGAT; enzyme; chromosome 14; bovine;
KW milk; meat marbling; low fat; polymorphic; SNP; gene; ds;
KW single nucleotide polymorphism.
XX Bos taurus.
XX Synthetic.
XX WO2003004630-A2.
XX 16-JAN-2003.
XX 05-JUL-2002; 2002WO-EP007520.
XX 06-JUL-2001; 2001EP-00116412.
XX 13-MAY-2002; 2002US-0379412P.
XX (ARBE-) ARBEITSGEMEINSCHAFT DEUT RINDERZUECHTER.
XX Fries H, Winter A;
XX WPI; 2003-239205/23.
XX New nucleic acid molecule comprising a sequence of an allele of a
XX polymorphic bovine acyl CoA:diacylglycerol transferase gene useful for
XX testing a mammal for its predisposition for fat content of milk and for
XX meat marbling.
XX Disclosure; Page 40; 91pp; English.
XX The present invention describes a nucleic acid molecule (NA) (I) encoding
XX a bovine acyl CoA:diacylglycerol transferase (DGAT) contributing to or
XX indicative for low fat content of milk and to low meat marbling
XX (intramuscular fat content). Human DGAT is located to chromosome 8, and
XX bovine DGAT is located to chromosome 14. (I) is useful for testing a
XX mammal for its predisposition for fat content of milk and/or its
XX predisposition for meat marbling. The method comprises analysing the gene
XX encoding DGAT for nucleotide polymorphisms (e.g. single nucleotide
XX polymorphisms (SNPs)) which are connected with the predisposition. The
XX nucleotide polymorphisms are located in the coding region of the DGAT
XX gene and result in substitution, deletion and/or addition of an amino
XX acid sequence of the polypeptide which is encoded by the gene. The
XX nucleic acid molecule has at the position 10433 and 10434 of the DGAT
XX gene a guanine and a cytosine residue, at position 3343 a cytosine or
XX guanine, 11030 a guanine, 11048 a cytosine or thymine and 11033 a
XX thymine, which correlate with a predisposition for low fat content of
XX milk and low meat marbling. The nucleic acid molecule has at the position
XX corresponding to position 10433 and 10434 of the DGAT gene two adenine
XX residues which correlate with a predisposition for high content of milk
XX and high meat marbling. The nucleotide polymorphisms are located in a
XX region which is responsible for the regulation of the expression of the
XX product of the gene encoding DGAT. ABZ76924 to ABZ77045 and ABZ96035 to
XX ABZ96046 represent sequences used in the exemplification of the present
XX invention
XX Sequence 12 BP; 2 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 3 ATCCACCTGCTG 14
XX | || || || ||
XX Db 12 ACCCACCTGATG 1
XX
XX RESULT 237
XX ADZ24155/c
XX ID ADZ24155 standard; DNA; 12 BP.
XX AC ADZ24155;
XX AC ADZ24155;
XX XX


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DT 16-JUN-2005 (first entry)
DE Human SNP detection related oligonucleotide #1122.
XX ss; haplotype mapping; SNP detection; tumor; cytostatic; neoplasm;
KW immune disorder; cardiovascular disease; metabolic disorder;
KW respiratory disease; musculoskeletal disease; renal disease;
KW nephrotropic; endocrine disease; genitourinary disease.
XX
XX Homo sapiens.
XX
XX WO2005030952-A1.
XX
XX 07-APR-2005.
XX
XX 30-SEP-2004; 2004WO-JP014784.
XX
XX 30-SEP-2003; 2003JP-00342519.
XX
XX 28-MAY-2004; 2004JP-00158717.
XX
XX (RIKE ) RIKEN KK.
XX (STAG-) STAGEN CO LTD.
XX (SEKI/) SEKINE A.
XX (IIDA/) IIDA A.
XX (SAIT/) SAITO S.
XX
XX Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
XX WPI; 2005-305936/31.
XX
XX Analyzing haplotype, by detecting polymorphism in drug-related genes,
XX electing common polymorphism (CP), building haplotype block using CP,
XX specifying CP within block, specifying tag polymorphism from CP within
XX block.
XX
XX Disclosure; SEQ ID NO 1122; 1290pp; Japanese.
XX
XX The invention relates to a method of analyzing haplotype, by detecting
XX gene polymorphism in drug-related genes such as aryl acetylarnide
XX deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
XX sub-family A (ABCL), member 1. The method is useful for analyzing
XX of a medicine or a foreign material, for selecting appropriate dosage of
XX preventing or treating diseases, for determining appropriate dosage of
XX medicine for preventing or treating a disease, for analyzing a drug
XX interaction, and for determining the related polymorphism relative to the
XX sensitivity of the medicine, foreign material or disease. The diseases
XX include malignant tumor, immune disorder circulatory disease, metabolic
XX disease, kidney disease, respiratory disease and muscle associated
XX disease. The method enables analysis of the individual differences
XX related to the sensitivity of a medicine, using a haplotype, without
XX using each single nucleotide polymorphism. The present sequence
XX represents a human SNP detection related oligonucleotide.
XX
XX Sequence 12 BP; 4 A; 5 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 30.3%; Score 8.8; DB 1; Length 12;
XX Best Local Similarity 83.3%; Pred. No. 1.7e+02;
XX Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 13 TGTGTGACCTGG 24
XX ||| ||| |||
XX 12 TGTATGACCTGG 1
XX
XX RESULT 238
XX ADS77727/c
XX ID ADS77727 standard; DNA; 11 BP.
XX
XX AC ADS77727;
XX
XX 30-DEC-2004 (first entry)
XX
XX

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DE Breast cancer detection oligonucleotide #1509.
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 6; SEQ ID NO 1509; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX specification, and (c) if the gene is expressed in the test sample at a
XX lower level than in a control normal breast tissue sample, diagnosing the
XX test sample as containing cancer cells. The method is used for diagnosing
XX breast cancer. This sequence corresponds to an oligonucleotide primer
XX used in the method of the invention.
XX
XX Sequence 11 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 1 Other;
XX
XX Query Match 29.7%; Score 8.6; DB 1; Length 11;
XX Best Local Similarity 81.8%; Pred. No. 1.7e+02;
XX Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 7 ACCTGCTGTGT 17
XX : || || || || ||
XX 11 HCTTGCTGTGT 1
XX
XX RESULT 239
XX ADS77874/c
XX ID ADS77874 standard; DNA; 11 BP.
XX
XX AC ADS77874;
XX
XX 30-DEC-2004 (first entry)
XX
XX Breast cancer detection oligonucleotide #1656.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX

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```

SQ Sequence 12 BP; 0 A; 3 C; 4 G; 4 T; 0 U; 1 Other;
Query Match          29.7%; Score 8.6; DB 1; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTGT 17
Db 4 CTGCTGTGY 12

RESULT 242
AAQ97150
ID AAQ97150 standard; DNA; 10 BP.
XX
XX AC AAQ97150;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 132.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
XX 14-FEB-1995; 95WO-AU000063.
XX
XX 14-FEB-1994; 94AU-00003864.
XX 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 193; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX
SQ Sequence 10 BP; 4 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
Db 10 CCTGCTGTGT 1

RESULT 244
AAQ97151
ID AAQ97151 standard; DNA; 10 BP.
XX
XX AC AAQ97151;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 133.
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
XX

```


Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
 Db 1 CTGTGTGTG 10

RESULT 247
 AAV34960/C
 ID AAV34960 standard; DNA; 10 BP.
 XX AC AAV34960;
 XX DT 13-OCT-1998 (first entry)
 XX DE Synthetic Agaricus bisporus RAPD primer.
 XX KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
 XX OS Synthetic.
 XX PN WO9821975-Al.
 XX PD 28-MAY-1998.
 XX PF 19-NOV-1996; 96WO-US018686.
 XX PR 19-NOV-1996; 96WO-US018686.
 XX PA (AMYC-) AMYCEL INC.
 XX PI Loftus MG, Lodder SC, Legg EJ;
 XX DR WPI; 1998-312054/27.
 XX PT New strains of Agaricus bisporus with improved cap whiteness - compared
 PT with the U1 strain but retaining other desirable features of this strain.
 XX PS Disclosure; Page 10; 26pp; English.
 XX CC The sequence is that of an RAPD (random amplified DNA) primer which was
 CC used in the isolation of an Agaricus bisporus mushroom strain which has
 CC whiter caps, less scaling than known strains, particularly for mushrooms
 CC produced in the first break, so it is more valuable (suitable for
 CC marketing fresh rather than canning). It also retains the desirable
 CC characteristics (good cap shape and shelf life, thick stem and veil) of
 CC the U1 strain
 XX SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 GTGACCTGGT 25
 Db 10 GTGACCGGT 1

RESULT 248
 AAV03254
 ID AAV03254 standard; DNA; 10 BP.
 XX AC AAV03254;
 XX DT 25-MAR-2003 (revised)
 XX DT 08-JUN-1998 (first entry)
 XX DE Homo sapiens mutant melanocortin 4 receptor Ile137Thr PCR primer.
 XX KW Melanocortin 4 receptor; MC4-R gene; body weight disorder; treatment;

KW obesity; anorexia; cachexia; Ile137Thr; mutant; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX PN WO9747316-Al.
 XX PD 18-DEC-1997.
 XX PF 09-JUN-1997; 97WO-US009969.
 XX PR 10-JUN-1996; 96US-0062560.
 PR 08-JAN-1997; 97US-00780749.
 PR 06-JUN-1997; 97US-00870511.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX PI Lee F, Huszar D, Gu W;
 XX DR WPI; 1998-052026/05.
 XX PT Drug screening assays to identify compounds for body weight disorder
 PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin 4
 PT receptor as target.
 XX PS Disclosure; Page 57; 11pp; English.
 XX CC The sequence is that of a PCR primer which may be used in the
 CC identification of the mutant melanocortin 4 receptor (MC4-R) Ile137Thr.
 CC This may be of use in the treatment of body weight disorders e.g.
 CC obesity, anorexia and cachexia. (Updated on 25-MAR-2003 to correct PR
 CC field.)
 XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACTGC 12
 Db 1 ATCCACTGC 10

RESULT 249
 AAX18637/C
 ID AAX18637 standard; DNA; 10 BP.
 XX AC AAX18637;
 XX DT 06-MAY-1999 (first entry)
 XX DE p53 serial analysis of gene expression tag #38.
 XX KW p53; serial analysis of gene expression; SAGE tag; cancer; neoplastic;
 KW rat embryo fibroblast; REF; tumour suppressor; cell cycle control;
 KW tumorigenesis; diagnosis; ss.
 XX OS Synthetic.
 OS OS Rattus sp.
 XX PN WO9901581-Al.
 XX PD 14-JAN-1999.
 XX PF 02-JUL-1998; 98WO-US013903.
 XX PR 02-JUL-1997; 97US-0051573P.
 XX PA (GENZ) GENZYME CORP.
 XX PI Madden SL, Galella EA, Bertelsen AH, Beaudry GA;
 XX PI

DR WPI; 1999-106079/09.

XX Diagnosis of cancer in potentially neoplastic samples - by comparing the

PT level of transcription between RNA transcripts in two tissue samples,

PT useful for providing an extensive profile of gene expression in rat

PT embryo fibroblast (REF) cells.

XX

XX Example 2; Page 16; 32pp; English.

XX

CC A method has been developed for the diagnosis of cancer in potentially

CC neoplastic samples. The method comprises comparing the level of

CC transcription between RNA transcripts in two tissue samples (which are of

CC the same type), where the first sample is potentially neoplastic, and the

CC second sample is normal human tissue. The first sample is categorized as

CC neoplastic if its level of transcription is lower than that of the second

CC sample. The transcript is selected from ALU, RAS, U6 snRNA, 16S RNA, EGR-

CC 1, ribosomal protein S27, ETS-1, 28S RNA, CGR11, and LIMK-2, and it is

CC identified by a tag selected from ribosomal protein L13a, alpha-tubulin

CC (T1) and (T2), thymosin beta-4 and gamma- actin. The present sequence

CC represents a serial analysis of gene expression (SAGE) tag from the

CC present invention. The use of SAGE tags provides an extensive profile of

CC gene expression in rat embryo fibroblast (REF) cells containing the (non)

CC -functional p53 tumour suppression gene. The discovery of new SAGE tags,

CC which are regulated by p53, enables the diagnosis of genes that are

CC related to cell cycle control and tumourigenesis

XX

XX Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

XX

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCACCTG 11

Db 10 CACCACCTG 1

RESULT 250

AAZ11274/c

ID AAZ11274 standard; DNA; 10 BP.

AC AAZ11274;

XX

XX 15-NOV-1999 (first entry)

DT

XX

XX Splice donor site #1 for VP16 gene trap vector.

XX

XX Splice donor; VP16 gene trap vector; protein-cell interaction; detection;

KW protein-protein interaction; transcriptional activator domain; ds.

XX

XX Synthetic.

OS

XX

XX Key Location/Qualifiers

FT misc_feature 1..5

FT /*tag= a

FT /label= sticky_end

FT /note= "the 5' end of the complementary strand overhangs

FT the 3' end of this strand by the sequence 5'-GATC-3'"

XX

XX WO9943848-A1.

XX

XX 02-SEP-1999.

XX

XX 25-FEB-1999; 99WO-CA000173.

XX

XX 25-FEB-1998; 98CA-02224475.

XX

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX

XX Ong CJ, Jirik FR;

XX

XX WPI; 1999-540605/45.

XX

PT New protein interaction and transcription factor trap used for

PT identification of unknown genes encoding transcriptional activator

PT domains.

XX

XX Example 1; Page 26; 40pp; English.

XX

CC This sequence represents a splice donor site that can be used in a VP16

CC gene trap vector used in the method of the invention. The method is for

CC detecting interaction between an endogenous protein of a cell and a test

CC protein. The cell contains a first DNA sequence encoding a reporter under

CC transcriptional control of a transcriptional regulatory element, and a

CC second DNA sequence that is expressed by the cell and which encodes a

CC first hybrid protein comprising a first transcriptional regulatory

CC protein moiety (TRP) selected from a DNA-binding domain that recognises a

CC binding site on the transcriptional regulatory element controlling

CC transcription of the first DNA sequence and, a transcriptional

CC activator functional in the cell; and a test protein. The method

CC comprises: (a) placing into the cell a DNA construct comprising one or

CC more mRNA splice sites, and a third DNA sequence encoding a second TRP

CC which, when combined with the first TRP, will reconstitute a TRP capable

CC of binding to and activating the transcriptional regulatory element

CC controlling transcription of the first DNA sequence; and (b) determining

CC whether the reporter is expressed by the cell, as an indicator of

CC expression of a second hybrid protein comprising the second TRP and an

CC endogenous protein of the cell capable of interaction with the test

CC protein. The method is used for the identification and characterisation

CC of unknown genes according to protein-protein interactions or for

CC identification of genes encoding transcriptional activator domains

XX

XX Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

XX

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACCTGG 24

Db 10 TGCACCTGG 1

RESULT 251

AAZ78697

ID AAZ78697 standard; DNA; 10 BP.

XX

XX AAZ78697;

AC

XX

XX 10-APR-2000 (first entry)

DT

XX

XX Human dendritic cell SAGE tag, SEQ ID NO:1125.

DE

XX

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;

KW APC; monocyte-derived dendritic cell; differential gene expression;

KW immunostimulatory cofactor; costimulatory factor; CTL;

KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX

XX Homo sapiens.

OS

XX

XX WO9965924-A2.

PN

XX

XX 23-DEC-1999.

PD

XX

XX 18-JUN-1999; 99WO-US013800.

PF

XX

XX 19-JUN-1998; 98US-0089833P.

PR

XX

XX 19-JUN-1998; 98US-0089844P.

PR

XX

XX 19-JUN-1998; 98US-0089853P.

PR

XX

XX 19-JUN-1998; 98US-0089878P.

PR

XX

XX 19-JUN-1998; 98US-0089911P.

PR

XX

XX 19-JUN-1998; 98US-0089922P.

PR

XX

XX 19-JUN-1998; 98US-0089933P.

PR

XX

XX 19-JUN-1998; 98US-0089944P.

PR

XX

XX 19-JUN-1998; 98US-0089979P.

PR

XX

XX 19-JUN-1998; 98US-0089999P.

19-JUN-1998; 98US-0090000P.
 19-JUN-1998; 98US-00900035P.
 19-JUN-1998; 98US-00900036P.
 19-JUN-1998; 98US-00900039P.
 19-JUN-1998; 98US-00900040P.
 19-JUN-1998; 98US-00900041P.
 19-JUN-1998; 98US-00900042P.
 19-JUN-1998; 98US-00900043P.
 19-JUN-1998; 98US-00900044P.
 19-JUN-1998; 98US-00900045P.
 19-JUN-1998; 98US-00900047P.
 19-JUN-1998; 98US-00900048P.
 19-JUN-1998; 98US-00900072P.
 19-JUN-1998; 98US-00900076P.
 19-JUN-1998; 98US-00900077P.
 19-JUN-1998; 98US-00900078P.
 19-JUN-1998; 98US-00900079P.
 19-JUN-1998; 98US-00900080P.
 08-DEC-1998; 98US-0111715P.
 (GENZ) GENZYME CORP.
 (ROBE/) ROBERTS B L.
 (SHAN/) SHANKARA S.
 Roberts BL, Shankara S;
 WPI; 2000-106077/09.
 Isolated polynucleotides differentially expressed in antigen-presenting
 cells, useful in gene vaccines against cancer.
 Claim 1; Page 97; 130pp; English.
 Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 expression) tags used to identify mRNA transcripts encoding
 immunostimulatory cofactor proteins which are preferentially or
 differentially expressed in monocyte-derived dendritic cells compared
 with monocytes. Some of the transcripts correspond to known genes or ESTs
 (expressed sequence tags) which were previously unknown to be
 preferentially or differentially expressed in dendritic cells, while
 other transcripts correspond to novel genes. Antigen-presenting cell
 (APC)-associated costimulatory factors play an important role in the
 activation of the cytotoxic immune response, particularly against tumour
 cells. Tumour antigen presentation via the MHC (major histocompatibility
 complex) and subsequent recognition by T-cell receptors is alone
 insufficient to activate a robust cytotoxic immune response that can lyse
 the tumour cells. Immunostimulatory cofactors also being required for
 efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 sequences identified using the SAGE tags have several potential uses.
 They may be used in vaccines to induce an immune response, particularly
 against a tumour antigen; to modulate the genotype of an APC; to screen
 for agents that modulate expression of differentially expressed genes in
 an APC; and as hybridisation probes/amplification primers for the
 diagnosis, prognosis and monitoring of diseases related to abnormal
 expression of these genes. Detection of the dendritic cell differentially
 expressed genes, or of their encoded proteins, can be used to identify
 cells as belonging to the monocyte lineage. Cells containing these genes
 can be used in active immunotherapy (or to stimulate production of a
 population of antigen-specific effector cells) and vectors containing
 them are used in gene therapy. Co-administration of tumour antigens and
 APC-associated costimulatory factors ensures adequate antigen
 presentation to endogenous APCs and upregulates the APCs for the
 presentation of co-stimulatory signals, migration to T cell-rich sites,
 secretion of T cell growth factors and secretion of chemokines for
 recruitment of immune effector cells
 Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Caps 0;
 3 ATCCACCTGC 12

Db 1 ATCCGCTGC 10
 RESULT 252
 AAZ77846/C
 ID AAZ77846 standard; DNA; 10 BP.
 XX
 AC AAZ77846;
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:274.
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965924-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-00898833P.
 PR 19-JUN-1998; 98US-00898844P.
 PR 19-JUN-1998; 98US-00898853P.
 PR 19-JUN-1998; 98US-00898878P.
 PR 19-JUN-1998; 98US-00898911P.
 PR 19-JUN-1998; 98US-00898922P.
 PR 19-JUN-1998; 98US-00898933P.
 PR 19-JUN-1998; 98US-00898994P.
 PR 19-JUN-1998; 98US-00898997P.
 PR 19-JUN-1998; 98US-00898999P.
 PR 19-JUN-1998; 98US-00900000P.
 PR 19-JUN-1998; 98US-00900035P.
 PR 19-JUN-1998; 98US-00900036P.
 PR 19-JUN-1998; 98US-00900039P.
 PR 19-JUN-1998; 98US-00900040P.
 PR 19-JUN-1998; 98US-00900041P.
 PR 19-JUN-1998; 98US-00900042P.
 PR 19-JUN-1998; 98US-00900043P.
 PR 19-JUN-1998; 98US-00900044P.
 PR 19-JUN-1998; 98US-00900045P.
 PR 19-JUN-1998; 98US-00900047P.
 PR 19-JUN-1998; 98US-00900048P.
 PR 19-JUN-1998; 98US-00900072P.
 PR 19-JUN-1998; 98US-00900076P.
 PR 19-JUN-1998; 98US-00900077P.
 PR 19-JUN-1998; 98US-00900078P.
 PR 19-JUN-1998; 98US-00900079P.
 PR 19-JUN-1998; 98US-00900080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 (GENZ) GENZYME CORP.
 (ROBE/) ROBERTS B L.
 (SHAN/) SHANKARA S.
 Roberts BL, Shankara S;
 WPI; 2000-106077/09.
 Isolated polynucleotides differentially expressed in antigen-presenting
 cells, useful in gene vaccines against cancer.
 Claim 1; Page 72; 130pp; English.
 Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 expression) tags used to identify mRNA transcripts encoding
 immunostimulatory cofactor proteins which are preferentially or
 differentially expressed in monocyte-derived dendritic cells compared
 with monocytes. Some of the transcripts correspond to known genes or ESTs
 (expressed sequence tags) which were previously unknown to be
 preferentially or differentially expressed in dendritic cells, while
 other transcripts correspond to novel genes. Antigen-presenting cell
 (APC)-associated costimulatory factors play an important role in the
 activation of the cytotoxic immune response, particularly against tumour
 cells. Tumour antigen presentation via the MHC (major histocompatibility
 complex) and subsequent recognition by T-cell receptors is alone
 insufficient to activate a robust cytotoxic immune response that can lyse
 the tumour cells. Immunostimulatory cofactors also being required for
 efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 sequences identified using the SAGE tags have several potential uses.
 They may be used in vaccines to induce an immune response, particularly
 against a tumour antigen; to modulate the genotype of an APC; to screen
 for agents that modulate expression of differentially expressed genes in
 an APC; and as hybridisation probes/amplification primers for the
 diagnosis, prognosis and monitoring of diseases related to abnormal
 expression of these genes. Detection of the dendritic cell differentially
 expressed genes, or of their encoded proteins, can be used to identify
 cells as belonging to the monocyte lineage. Cells containing these genes
 can be used in active immunotherapy (or to stimulate production of a
 population of antigen-specific effector cells) and vectors containing
 them are used in gene therapy. Co-administration of tumour antigens and
 APC-associated costimulatory factors ensures adequate antigen
 presentation to endogenous APCs and upregulates the APCs for the
 presentation of co-stimulatory signals, migration to T cell-rich sites,
 secretion of T cell growth factors and secretion of chemokines for
 recruitment of immune effector cells


```

Qy 9 CTGCTGTGTG 18
    |||||
Db 1 CTGCTATGTG 10

RESULT 254
AAZ84055
ID AAZ84055 standard; DNA; 10 BP.
XX
AC AAZ84055;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3289.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 147; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACTGC 12
    |||||
Db 1 ACCCACTGC 10

RESULT 255
AAZ81988
ID AAZ81988 standard; DNA; 10 BP.
XX
AC AAZ81988;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1222.
XX
DE Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 91; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

```

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 13 TGTGTGACCT 22
 | | | | | | | |
 DB 1 TCTGTGACCT 10

RESULT 256
 AAZ83343/C
 ID AAZ83343 standard; DNA; 10 BP.
 AC AAZ83343;
 XX
 XX
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell upregulated transcript tag #2577.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS
 FN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic and
 non-metastatic breast cancer cells, useful for diagnosis, prevention and
 treatment of cancer.
 PT
 XX
 PS Claim 1; Page 128; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 that are preferentially transcribed in the metastatic breast tumour
 tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 to AAZ86677 represent tags corresponding to distinct transcripts that are
 preferentially transcribed in the primary or non-metastatic breast tumour
 tissue (i.e. are downregulated in metastatic breast tumour cells). These
 transcripts can be used for diagnosis, prognosis, monitoring and
 treatment of breast cancer, particularly where metastatic. Diagnosis is
 by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 useful for treatment of (metastatic) breast cancer, while promoters from
 the transcripts are used to direct expression, in selected cell types, of
 e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 immunotherapy
 CC
 XX

SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 14 GTGTGACCTG 23
 | | | | | | | |
 DB 10 GTATGACCTG 1

RESULT 257
 AAZ83792/C
 ID AAZ83792 standard; DNA; 10 BP.
 XX AC
 XX AAZ83792;
 XX
 DT 07-APR-2000 (first entry)
 DE Metastatic breast tumour cell upregulated transcript tag #3026.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 OS
 FN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 DR WPI; 2000-106079/09.
 XX
 PT Isolated polynucleotides differentially expressed between metastatic and
 non-metastatic breast cancer cells, useful for diagnosis, prevention and
 treatment of cancer.
 PT
 XX
 PS Claim 1; Page 140; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 that are preferentially transcribed in the metastatic breast tumour
 tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 to AAZ86677 represent tags corresponding to distinct transcripts that are
 preferentially transcribed in the primary or non-metastatic breast tumour
 tissue (i.e. are downregulated in metastatic breast tumour cells). These
 transcripts can be used for diagnosis, prognosis, monitoring and
 treatment of breast cancer, particularly where metastatic. Diagnosis is
 by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 useful for treatment of (metastatic) breast cancer, while promoters from
 the transcripts are used to direct expression, in selected cell types, of
 e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 immunotherapy
 CC
 XX

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CC immunotherapy
XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13
Db ||||||| 1
TCCACCTGGT 1

RESULT 258
AAZ86544
ID AAZ86544 standard; DNA; 10 BP.
XX AC AAZ86544;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5778.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WI WI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 211; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand

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CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;
SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCT 22
Db ||||||| 1
TGTGTGAGCT 10

RESULT 259
AAZ81303
ID AAZ81303 standard; DNA; 10 BP.
XX AC AAZ81303;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell upregulated transcript tag #537.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX PN WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WI WI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX Claim 1; Page 72; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand

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CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy

SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
 |||||
 Db 1 ATCCACCGC 10

RESULT 260

AAC74087
 ID AAC74087 standard; cDNA; 10 BP.
 XX
 AC AAC74087;
 XX
 DT 02-FEB-2001 (first entry)
 XX Human dendritic cell and monocyte expressed gene oligonucleotide #174.
 DE Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmune disease; tumour; ss.
 XX Homo sapiens.
 OS
 XX WO200060074-A1.
 PN
 XX 12-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-JP002019.
 PF
 XX 01-APR-1999; 99JP-00095481.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Hashimoto S, Matsushima K, Suzuki T;
 PI WPI; 2000-619172/59.
 XX

Groups of genes expressed in human dendritic cells at a greater or lesser
 extent than in monocytes for investigation and diagnosis of autoimmune
 disease and tumors.
 PS Claim 10; Page 13; 95pp; Japanese.
 XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterised in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases

PS Claim 10; Page 13; 95pp; Japanese.

XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterised in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases

SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCT 22
 |||||
 Db 1 TGTGTGACCT 10

RESULT 261

AAC73981/c
 ID AAC73981 standard; cDNA; 10 BP.
 XX
 AC AAC73981;
 XX
 DT 02-FEB-2001 (first entry)
 XX Human dendritic cell cDNA base sequence oligonucleotide #68.
 DE Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW Human; dendritic cell; monocyte; immune system; diagnosis; cancer;
 KW autoimmune disease; tumour; ss.
 XX Homo sapiens.
 OS
 XX WO200060074-A1.
 PN
 XX 12-OCT-2000.
 PD
 XX 30-MAR-2000; 2000WO-JP002019.
 PF
 XX 01-APR-1999; 99JP-00095481.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA Hashimoto S, Matsushima K, Suzuki T;
 PI WPI; 2000-619172/59.
 XX

Groups of genes expressed in human dendritic cells at a greater or lesser
 extent than in monocytes for investigation and diagnosis of autoimmune
 disease and tumors.

PS Claim 1; Page 10; 95pp; Japanese.

XX The present invention describes a group of genes consisting of 100 genes
 CC which are highly expressed in human dendritic cells; a group of genes
 CC which are expressed at a higher frequency in human dendritic cells than
 CC in human monocytes; and a group of genes which are expressed at lower
 CC frequency in human dendritic cells than in human monocytes. Each group of
 CC genes are characterised in that cDNAs of these genes respectively have
 CC the base sequences of SEQ ID NO:1 to 100 (AAC73914 to AAC74013), SEQ ID
 CC NO:101 to 200 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114
 CC to AAC74213), each is continuous with the base sequence 5'-CATG-3',
 CC located most closely to the poly-A region. The sequences can be used for
 CC the investigation of the role and mechanism of the involvement of
 CC dendritic cells in the immune system and for the study and diagnosis of
 CC diseases in which dendritic cells play a significant role, e.g. cancers
 CC and autoimmune diseases

SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
 |||||
 Db 10 CTTGCTGTGT 1

RESULT 262

AAA56364/c
 ID AAA56364 standard; DNA; 10 BP.
 XX
 AC AAA56364;
 XX
 DT 07-SEP-2000 (first entry)

```

XX DE Human macrophage gene Tag oligonucleotide sequence SEQ ID NO:258.
XX KW Human; monocyte; macrophage; GM-macrophage; M-macrophage; tag;
XX KW granulocyte-macrophage colony-stimulating factor; characterisation;
XX KW GM-CSF; identification; diagnosis; gene specificity; oncogenesis;
XX KW disease onset mechanism; genetic disease; drug development; ss.
XX OS Homo sapiens.
XX XX
XX PN W0200024892-A1.
XX PD 04-MAY-2000.
XX XX
XX PF 28-OCT-1999; 99WO-JP005982.
XX PR 28-OCT-1998; 98JP-00307532.
XX PR (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PA Hashimoto S, Matsushima K, Suzuki T;
XX PI WPI; 2000-350734/30.
XX DR
XX PS Claim 13; Page 90; 138pp; Japanese.
XX CC The present invention describes 100 human genes, which are expressed most
XX CC frequently in human monocytes. The cDNA of each gene has a sequence fully
XX CC defined in the specification, and lacking the CATG sequence located
XX CC adjacent to polyA region. Also described are: (1) an antibody
XX CC specifically for the protein encoded by any of the genes; (2)
XX CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
XX CC which are expressed most frequently in human macrophages, differentiated
XX CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
XX CC the cDNA of each gene has a fully defined sequence, given in the
XX CC specification, lacking the base sequence CATG located most closely to the
XX CC poly A region; (4) an antibody specifically for the protein encoded by
XX CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
XX CC sequences of (3). The genes and cDNAs, are used for the study of gene
XX CC specificity and disease onset mechanism e.g. oncogenesis, genetic
XX CC diseases, drug development and diagnosis. AA56107 to AA56586 represent
XX CC specifically claimed oligonucleotide tag sequences for human genes
XX CC expressed in monocytes and macrophages
XX SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGCTGTGT 17
Db 10 CTGCTGTGT 1

RESULT 263
AAZ91928/C
ID AAZ91928 standard; DNA; 10 BP.
XX AC AAZ91928;
XX XX
XX DT 08-JUN-2000 (first entry)
XX OS
XX DE PCR primer for murine mahogany protein genomic sequence.
XX KW Mahogany gene; mouse; mg gene; regulatory defect; gene therapy; obesity;
XX KW weight regulation; cell therapy; body weight disorder; cachexia;
XX KW anorexia; hyperpigmentation; increased metabolic rate disorder;
XX KW hyperphagia; Antiobesity; antianorexic; anticachexic; PCR primer; ss.

```

```

XX OS Mus sp.
XX PN W0200005373-A2.
XX PD 03-FEB-2000.
XX XX
XX PF 21-JUL-1999; 99WO-US016484.
XX PR 21-JUL-1998; 98US-0093630P.
XX PR 20-OCT-1998; 98US-0104978P.
XX PR 05-FEB-1999; 99US-00245041.
XX XX
XX PA (MILL-) MILLENIUM PHARM INC.
XX XX
XX PI Moore K, Nagle DL;
XX XX
XX DR WPI; 2000-195103/17.
XX PT New human and murine mahogany genes, useful, e.g. for diagnosis and
XX PT treatment of body weight disorders.
XX PS Example; Page 83; 188pp; English.
XX CC This sequence represents a PCR primer for a murine mahogany gene of the
XX CC invention. The mahogany genes are used: (i) to produce recombinant
XX CC mahogany (mg) proteins (ii); (ii) as a source of antisense, ribozyme or
XX CC triplex-forming therapeutics; (iii) as a source of diagnostic probes and
XX CC primers for detecting expression of mg genes or mutations, regulatory
XX CC defects, in this gene, or for isolation of related sequences; and (iv) in
XX CC (cell-based) gene therapy. (ii) are used to raise specific antibodies
XX CC (Ab); to identify other (extra)cellular products involved in weight
XX CC regulation, and to screen for agents that disrupt interaction between
XX CC (ii) and other macromolecules. The Ab are used to detect abnormal levels
XX CC (or function) of (ii) (for diagnosis, prognosis or monitoring of
XX CC treatment); to evaluate (ii)-expressing cells intended for cell therapy,
XX CC and as therapeutic mg inhibitors. Cells that express the mg gene (or
XX CC contain the mg polypeptide) are used to identify agents (A) that modulate
XX CC mg activity. (A) are potentially useful for the treatment of body weight
XX CC disorders, particularly obesity, cachexia or anorexia, or other
XX CC conditions associated with the mg gene such as hyperpigmentation,
XX CC hyperphagia and disorders that result in increased metabolic rate
XX SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACC 21
Db 10 CTGTGTGTCC 1

RESULT 264
AAH18978
ID AAH18978 standard; DNA; 10 BP.
XX AC AAH18978;
XX XX
XX DT 21-JUN-2001 (first entry)
XX XX
XX DE UCP3 polymorphism detection allele specific primer #91.
XX XX
XX KW UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.
XX OS Homo sapiens.
XX PN W0200118232-A2.
XX PD 15-MAR-2001.
XX XX
XX PF 08-SEP-2000; 2000WO-US024784.

```


XX New haplotypes of the FKBP8-binding protein 8 gene, useful for genotyping
PT that gene in individual and to design new therapy for associated disease
PT such as immunosuppression and cancer.
XX
XX Claim 16; Page 15; 98pp; English.
XX
XX The invention relates to haplotyping the FKBP8-binding protein 8 (38kD)
CC (FKBP8) gene in an individual. The method involves determining the
CC identity of the nucleotide pair at one or more polymorphic sites selected
CC from PI to P26 (described in the specification). The invention is useful
CC to improve the efficiency and reliability of several steps in the
CC discovery and development of drugs for treating diseases associated with
CC FKBP8 activity, for example immunosuppression and cancer. Sequences
CC AA167352-403 represent oligonucleotide primers for detecting FKBP8 gene
CC polymorphisms by primer extension techniques
XX
XX Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
SQ

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

Qy 15 TGTGACCTGG 24
Db 1 TGTGACCTGG 10
|||||

RESULT 267
AAH63201
ID AAH63201 standard; cDNA; 10 BP.
XX
XX AC AAH63201;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human colon epithelium specific transcriptome sequence SEQ ID NO: 41.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 1; Page 39; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
SQ

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

Qy 15 TGTGACCTGG 24
Db 1 TGTGACCTGG 10
|||||

RESULT 267
AAH63201
ID AAH63201 standard; cDNA; 10 BP.
XX
XX AC AAH63201;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human colon epithelium specific transcriptome sequence SEQ ID NO: 41.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 1; Page 39; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
SQ

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

Qy 12 CTGTGTGACC 21
Db 1 CTGTGTGACC 10
|||||

RESULT 268
AAH63192
ID AAH63192 standard; cDNA; 10 BP.
XX
XX AC AAH63192;
XX
XX 20-SEP-2001 (first entry)
XX
XX Human colon epithelium specific transcriptome sequence SEQ ID NO: 32.
XX
XX Human; transcriptome; gene expression pattern; cancer; drug screening;
XX cancer diagnosis; cell specific gene expression; ss.
XX
XX Homo sapiens.
OS
XX WO200138577-A2.
XX
XX 31-MAY-2001.
XX
XX 21-NOV-2000; 2000WO-US031922.
XX
XX 24-NOV-1999; 99US-00448480.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX WPI; 2001-367706/38.
XX
XX New isolated polynucleotides, useful for identifying specific cell type,
XX such as cancer cell, comprises transcriptomes expressed in particular
XX cell types.
XX
XX Claim 1; Page 39; 94pp; English.
XX
XX The present invention describes a method of identifying the type of cell
XX in a sample, involving determining which of the sequences AAH63161-
XX AAH64724 is expressed by the cell. The transcriptomes described in the
XX invention are cell-type specific, cancer specific or ubiquitously
XX expressed in humans. They can also be used to screen for drugs, reduce
XX cancer specific gene expression, standardise expression and restore the
XX function of a diseased cell or tissue. The present sequence is one of the
XX transcriptomes described in the exemplification of the invention
XX
XX Sequence 10 BP; 0 A; 4 C; 3 G; 3 T; 0 U; 0 Other;
SQ

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX

Qy 12 CTGTGTGACC 21
Db 1 CTGTGTGACC 10
|||||

RESULT 269
AAH63266
ID AAH63266 standard; cDNA; 10 BP.
XX
XX AC AAH63266;
XX
XX 20-SEP-2001 (first entry)
XX

DE Human colon epithelium specific transcriptome sequence SEQ ID NO: 106.
 XX
 KW Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 PA Velculescu VE, Vogelstein B, Kinzler KW;
 PI
 XX WPI; 2001-367706/38.
 DR
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 XX Claim 13; Page 41; 94pp; English.
 FS
 XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 XX Sequence 10 BP; 0 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 SQ
 Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 12 CTGTGTGACC 21
 DB 1 CTGTGTGTCC 10
 RESULT 270
 AAH63751
 ID AAH63751 standard; cDNA; 10 BP.
 XX
 AC AAH63751;
 XX
 XX 20-SEP-2001 (first entry)
 DT
 XX Human ubiquitously expressed transcriptome sequence SEQ ID NO: 591.
 DE
 XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 DE cancer diagnosis; cell specific gene expression; ss.
 KW
 KW Homo sapiens.
 XX
 OS
 XX WO200138577-A2.
 FN
 XX 31-MAY-2001.
 PD
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 PA Velculescu VE, Vogelstein B, Kinzler KW;
 PI

XX WPI; 2001-367706/38.
 DR
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 XX Claim 13; Page 52; 94pp; English.
 PS
 XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 CTGCTGTGTG 18
 DB 1 CTGCTGTGTG 10
 RESULT 271
 AAH32787
 ID AAH32787 standard; cDNA; 10 BP.
 XX
 AC AAH32787;
 XX
 XX 13-AUG-2001 (first entry)
 DT
 XX LPS activated human monocyte expression gene cDNA tag SEQ:160.
 DE
 XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.
 KW
 OS Homo sapiens.
 XX
 PN JP2001069993-A.
 XX
 XX 21-MAR-2001.
 PD
 XX 28-APR-2000; 2000JP-00131079.
 PF
 XX 08-JUL-1999; 99JP-00195103.
 XX
 PR (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA
 XX WPI; 2001-304369/32.
 XX
 XX LPS activated human monocyte expression gene group.
 PT
 XX Claim 10; Page 31; 52pp; Japanese.
 PS
 XX The present invention describes an lipopolysaccharide (LPS) activated
 CC human monocyte expression gene group consisting of the high-ranking 50
 CC genes of the highest expression among the genes expressed by human
 CC monocyte stimulated by LPS in which the cDNA of each gene has the base
 CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
 CC CATG-3', nearest to the polyA region. The gene group is useful for the
 CC development of new means for the diagnosis and the treatment of various
 CC human diseases in which human monocyte plays an important role. AAH32628
 CC to AAH32943 represent specifically claimed LPS activated human monocyte
 CC expression gene cDNA tags from the present invention. AAH32944 represents
 CC an LPS activated human monocyte expression gene cDNA sequence encoding
 CC AAH98009, which are given in the exemplification of the present invention
 XX


```
SQ Sequence 10 BP; 1 A; 2 C; 3 G; 4 T; 0 U; 0 Other;
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 1 CTGCTATGTG 10

RESULT 272
AAH41694
ID AAH41694 standard; DNA; 10 BP.
XX
AC AAH41694;
XX
DT 28-AUG-2001 (first entry)
XX
XX Anti-PEP gene construction related oligonucleotide S3.
XX
KW Phosphoenolpyruvate carboxylase; PEPCase; seed; acetyl-CoA carboxylase;
KW oilseed; PEP; plant breeding; soya bean; sunflower; rapeseed; peanut;
KW sesame; crop plant; protein content; fatty acid content; anti-PEP; ss.
XX
OS Synthetic.
XX
XX WO200134812-A1.
XX
PD 17-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-CN000418.
XX
PR 09-NOV-1999; 99CN-00124511.
XX
PA (ZHEJ-) ZHEJIANG AGRIC SCI ACAD.
XX
PI Chen J, Lang C, Huang R, Hu Z, Liu Z;
XX
WPI; 2001-335934/35.
XX
Altering protein/fatty acid composition of seeds, useful for producing
e.g. soya bean or sesame seed with high protein/fatty acid content,
comprises introducing antisense gene.
XX
Example 8; Page 8; 25pp; Chinese.
XX
The present invention describes a method for altering the protein/fatty
acid composition of seeds. The method comprises: (1) cloning
phosphoenolpyruvate carboxylase (PEP) or acetyl-CoA carboxylase (ACC)
genes or their fragments; (2) constructing the corresponding antisense
gene of anti-PEP or anti-ACC; and (3) introducing the antisense gene into
the plant cell of a crop. The method is applicable in plant breeding to
give oilseed crops with high oil or protein content like soya bean,
sunflower, rapeseed, peanut and sesame. The produced crop plants have
high yield of oil or protein. The present sequence represents an
oligonucleotide which is used in the construction of an anti-PEP gene in
an example from the present invention
XX
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCCACCTG 11
Db 1 CATCCCCCTG 10

RESULT 273
ABA06109/c
ID ABA06109 standard; cDNA; 10 BP.
XX
AC ABA06109;
XX
DT 10-JAN-2002 (first entry)
XX
DE Human normal hepatocyte expression gene cDNA, SEQ ID NO: 86.
XX
KW Human; hepatocyte; gene expression; hepatopathy; ss.
XX
OS Homo sapiens.
XX
XX JF2001211883-A.
XX
PD 07-AUG-2001.
XX
PF 31-JAN-2000; 2000JP-00023170.
XX
PR 31-JAN-2000; 2000JP-00023170.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-629566/73.
XX
PT Human normal hepatocyte expression gene group.
XX
PS Claim 1; Page 7; 26pp; Japanese.
XX
CC The invention relates to a human normal hepatocyte expression gene group
comprising 200 genes in the human normal hepatocyte. The cDNA of each
gene comprises one of 200 fully defined nucleotide sequences as given in
the specification. The gene group and the cDNAs corresponding to each of
the genes in the group are useful in the diagnosis and treatment of human
hepatopathy. The present sequence is a cDNA corresponding to a gene
expressed by normal human hepatocytes
XX
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGCTGTGTG 17
Db 10 CTGCTGTGTG 1

RESULT 274
AAF69625
ID AAF69625 standard; DNA; 10 BP.
XX
AC AAF69625;
XX
DT 18-APR-2001 (first entry)
XX
DE Human IL4Ralpha gene probe #265.
XX
KW Polymorphism; human; interleukin 4 receptor-alpha; IL4R-alpha;
KW allergic disease; probe; ss.
XX
OS Homo sapiens.
XX
XX WO200104270-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019094.
XX
PR 13-JUL-1999; 99US-0143435P.
XX
PA (GENA-) GENAISANCE PHARM INC.
XX
PI Chew A, Denton RE, Duda A, Nandabalan K, Stephens JC;
PI Windemuth AK;
```

XX WPI; 2001-103078/11.

XX New isolated polynucleotide useful for the identification of therapeutics

PT in allergic diseases is new.

XX

XX Disclosure; Page 46; 188pp; English.

XX The present invention relates to polymorphisms of the human interleukin 4

CC receptor-alpha gene (IL4R-alpha; see AAF57718 for the reference

CC sequence). Polynucleotides comprising polymorphic gene variants are

CC useful for therapeutic purposes. For example, where a patient may benefit

CC from expression of a particular IL4Ralpha protein isoform, an expression

CC vector encoding the isoform may be administered to the patient. It may

CC desirable to decrease or block expression of a particular IL4Ralpha

CC isogene, which may be done by turning off by transforming a targeted

CC organ, tissue or cell population with an expression vector that expresses

CC high levels of untranslatable mRNA for the isogene. Specific therapeutics

CC identified by these methods may be useful for allergic diseases. The

CC present sequence is a probe for human IL4R-alpha

XX

SQ Sequence 10 BP; 3 A; 4 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12

Db 1 ATACACCTGC 10

RESULT 275

AAF34164/C

XX AAF34164 standard; DNA; 10 BP.

XX

AC AAF34164;

XX

DT 23-MAR-2001 (first entry)

XX

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:903.

DE

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

PF 14-JUN-2000; 2000WO-US016223.

XX

PR 16-JUN-1999; 99US-00335032.

XX

PA (UYJO) UNIV JOHNS HOPKINS.

XX

XX Velulescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX

DR Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX

XX Example; Page 32; 419pp; English.

XX

PS The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC described are: (1) a method (M1) of using NORF genes to affect the cell

CC cycle comprising administering a NORF gene whose expression varies by at

CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate

CC antifungal drugs comprising: (a) contacting a test substance with a yeast

CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of

CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for

CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10

CC contiguous nucleotides of a NORF gene whose expression varies as in M1;

CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a

CC yeast cell comprising contacting a yeast cell with a candidate drug and

CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used

CC to study, monitor and affect phases of the cell cycle, the differentially

CC expressed genes may be used as markers of phases of the cell cycle. The

CC methods may be used to identify candidate drugs which affect the cell

CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064

CC represent SAGE tags used in the exemplification of the present invention.

CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE

CC method, in the exemplification of the present invention

XX

SQ Sequence 10 BP; 2 A; 2 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAA 28

Db 10 AACTGGTAAA 1

RESULT 276

AAF35667

ID AAF35667 standard; DNA; 10 BP.

XX

AC AAF35667;

XX

DT 23-MAR-2001 (first entry)

XX

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2406.

DE

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;

KW nor previously assigned open reading frame; nonannotated ORF; SAGE;

KW serial analysis of gene expression; antifungal; tag; identification;

KW linker; PCR primer; ds.

XX

OS Saccharomyces cerevisiae.

XX

PN WO200077214-A2.

XX

PD 21-DEC-2000.

XX

PF 14-JUN-2000; 2000WO-US016223.

XX

PR 16-JUN-1999; 99US-00335032.

XX

XX (UYJO) UNIV JOHNS HOPKINS.

PA

XX Velulescu V, Vogelstein B, Kinzler K;

PI WPI; 2001-061874/07.

XX

DR Yeast gene coding sequences comprising NORF genes with serial analysis of

PT gene expression (SAGE) tags, useful for studying, monitoring and

PT affecting phases of the cell cycle.

XX

XX Example; Page 85; 419pp; English.

XX

PS The present invention describes an isolated DNA molecule comprising a

CC coding sequence of a yeast gene selected from a group of 745 NORF (not

CC previously assigned open reading frame; or nonannotated ORF) genes

CC comprising a SAGE (serial analysis of gene expression) tag. Also

CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCACCTGCT 13

Db 1 TCACCTACT 10

RESULT 277

AAF35804/c

ID AAF35804 standard; DNA; 10 BP.

XX AAF35804;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2543.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

XX WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

XX 16-JUN-1999; 99US-00335032.

PR (UYJO) UNIV JOHNS HOPKINS.

PA Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX

PS Example; Page 90; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCT 22

Db 10 TGTCTGACCT 1

RESULT 278

AAF44017/c

ID AAF44017 standard; DNA; 10 BP.

XX AAF44017;

XX 23-MAR-2001 (first entry)

DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12156.

XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

PN WO200077214-A2.

XX 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PR 16-JUN-1999; 99US-00335032.

PA (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of

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PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 384; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACTCGTAA 28
Db 10 ACCTGGAAAA 1

RESULT 279
AAF43467/c
ID AAF43467 standard; DNA; 10 BP.
AC AAF43467;
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11606.
DE
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW Serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX

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DR WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
XX Example; Page 364; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GACCTGGTAA 27
Db 10 GACTTGGTAA 1

RESULT 280
AAF34829
ID AAF34829 standard; DNA; 10 BP.
XX
XX AAF34829;
AC
XX
XX 23-MAR-2001 (first entry)
XX
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1568.
DE
DE Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW Serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US016223.
XX
XX 16-JUN-1999; 99US-00335032.
XX
XX (UYJO ) UNIV JOHNS HOPKINS.
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XX PF 14-JUN-2000; 2000WO-US016223.
XX PR 16-JUN-1999; 99US-00335032.
XX PR (UYJO) UNIV JOHNS HOPKINS.
XX PA Velculescu V, Vogelstein B, Kinzler K;
XX FI WPI; 2001-061874/07.
XX DR
XX XX
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis of
XX PT gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle.
XX PS Example; Page 79; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a yeast
XX CC cell; and (b) monitoring expression of a NORF gene whose expression
XX CC varies as in M1, where a test substance which modifies the expression of
XX CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
XX CC identifying human genes which are involved in cell cycle progression
XX CC comprising contacting human DNA with a probe which comprises at least 10
XX CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
XX CC and (4) a method (M4) for identifying a candidate drug as a member of a
XX CC class of drugs having a characteristic effect on gene expression in a
XX CC yeast cell comprising contacting a yeast cell with a candidate drug and
XX CC monitoring expression in the yeast cell of at least 1 NORF gene whose
XX CC expression is affected by the class of drugs. The NORF genes may be used
XX CC to study, monitor and affect phases of the cell cycle, the differentially
XX CC expressed genes may be used as markers of phases of the cell cycle. The
XX CC methods may be used to identify candidate drugs which affect the cell
XX CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
XX CC represent SAGE tags used in the exemplification of the present invention.
XX CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
XX CC method, in the exemplification of the present invention
XX SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCCCACT 10
DB 10 CCATCACT 1
RESULT 283
ABL42879
ID ABL42879 standard; cDNA; 10 BP.
XX AC ABL42879;
XX DT 12-APR-2002 (first entry)
XX DE Human maturation/activation dendritic cell expression gene tag #253.
XX KW Human; maturation/activation dendritic cell expression gene; tag;
XX KW maturation; activation; dendritic cell; ss.
XX OS Homo sapiens.
XX PN JP2001327293-A.
XX DR
XX PT
XX PS
XX CC The present invention describes a human maturation/activation dendritic
XX CC cell (DC) expression gene group consisting of 100 genes which show the
XX CC highest expression among the genes expressed in human maturation/
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC human maturation/activation DC expression gene; (2) an antibody against
XX CC the protein; and (3) an antagonist against the expression of each gene
XX CC belonging to the above gene group. The gene group is useful for the
XX CC treatment and the diagnosis of various human diseases related to human
XX CC DC. ABL42627 to ABL42926 represent specifically claimed human
XX CC maturation/activation DC expression gene tags from the present invention
XX SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CTCTGTGACC 21
DB 1 CTCTGAGACC 10
RESULT 284
ABL42726
ID ABL42726 standard; cDNA; 10 BP.
XX AC ABL42726;
XX DT 12-APR-2002 (first entry)
XX DE Human maturation/activation dendritic cell expression gene tag #100.
XX KW Human; maturation/activation dendritic cell expression gene; tag;
XX KW maturation; activation; dendritic cell; ss.
XX OS Homo sapiens.
XX PN JP2001327293-A.
XX DR 27-NOV-2001.
XX PF 22-MAY-2000; 2000JP-00150562.
XX PR 22-MAY-2000; 2000JP-00150562.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-127070/17.
XX PT Human maturation/activation dendritic cell expression gene group.
XX PS Claim 1; Page 10; 41pp; Japanese.
XX CC The present invention describes a human maturation/activation dendritic
XX CC cell (DC) expression gene group consisting of 100 genes which show the
XX CC highest expression among the genes expressed in human maturation/
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC human maturation/activation DC expression gene; (2) an antibody against
XX CC the protein; and (3) an antagonist against the expression of each gene

PD 27-NOV-2001.
XX PF 22-MAY-2000; 2000JP-00150562.
XX PR 22-MAY-2000; 2000JP-00150562.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-127070/17.
XX PT Human maturation/activation dendritic cell expression gene group.
XX PS Claim 19; Page 16; 41pp; Japanese.
XX CC The present invention describes a human maturation/activation dendritic
XX CC cell (DC) expression gene group consisting of 100 genes which show the
XX CC highest expression among the genes expressed in human maturation/
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC human maturation/activation DC expression gene; (2) an antibody against
XX CC the protein; and (3) an antagonist against the expression of each gene
XX CC belonging to the above gene group. The gene group is useful for the
XX CC treatment and the diagnosis of various human diseases related to human
XX CC DC. ABL42627 to ABL42926 represent specifically claimed human
XX CC maturation/activation DC expression gene tags from the present invention
XX SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CTCTGTGACC 21
DB 1 CTCTGAGACC 10
RESULT 284
ABL42726
ID ABL42726 standard; cDNA; 10 BP.
XX AC ABL42726;
XX DT 12-APR-2002 (first entry)
XX DE Human maturation/activation dendritic cell expression gene tag #100.
XX KW Human; maturation/activation dendritic cell expression gene; tag;
XX KW maturation; activation; dendritic cell; ss.
XX OS Homo sapiens.
XX PN JP2001327293-A.
XX DR 27-NOV-2001.
XX PF 22-MAY-2000; 2000JP-00150562.
XX PR 22-MAY-2000; 2000JP-00150562.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 2002-127070/17.
XX PT Human maturation/activation dendritic cell expression gene group.
XX PS Claim 1; Page 10; 41pp; Japanese.
XX CC The present invention describes a human maturation/activation dendritic
XX CC cell (DC) expression gene group consisting of 100 genes which show the
XX CC highest expression among the genes expressed in human maturation/
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC activation DC. Also described are: (1) a protein expressed by the above
XX CC human maturation/activation DC expression gene; (2) an antibody against
XX CC the protein; and (3) an antagonist against the expression of each gene

CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABL42627 to ABL42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAA 28
|||||
Db 1 ACCTGGCAAA 10

RESULT 285

ABL42777
ID ABL42777 standard; cDNA; 10 BP.

XX AC

XX ABL42777;

DT 12-APR-2002 (first entry)

DE Human maturation/activation dendritic cell expression gene tag #151.

XX Human; maturation/activation dendritic cell expression gene; tag;

XX maturation; activation; dendritic cell; ss.

XX Homo sapiens.

XX JP2001327293-A.

XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-00150562.

XX 22-MAY-2000; 2000JP-00150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group.

XX Claim 10; Page 13; 41pp; Japanese.

XX The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABL42627 to ABL42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention
XX
SQ Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAA 28
|||||
Db 1 ACCTGGCAAA 10

RESULT 286

ABL42899
ID ABL42899 standard; cDNA; 10 BP.

XX

AC ABL42899;
XX 12-APR-2002 (first entry)
DT
DE Human maturation/activation dendritic cell expression gene tag #273.
XX
XX Human; maturation/activation dendritic cell expression gene; tag;
KW maturation; activation; dendritic cell; ss.
XX
XX Homo sapiens.

XX JP2001327293-A.

XX 27-NOV-2001.

XX 22-MAY-2000; 2000JP-00150562.

XX 22-MAY-2000; 2000JP-00150562.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX WPI; 2002-127070/17.

XX Human maturation/activation dendritic cell expression gene group.

XX Claim 19; Page 17; 41pp; Japanese.

XX The present invention describes a human maturation/activation dendritic
CC cell (DC) expression gene group consisting of 100 genes which show the
CC highest expression among the genes expressed in human maturation/
CC activation DC. Also described are: (1) a protein expressed by the above
CC human maturation/activation DC expression gene; (2) an antibody against
CC the protein; and (3) an antagonist against the expression of each gene
CC belonging to the above gene group. The gene group is useful for the
CC treatment and the diagnosis of various human diseases related to human
CC DC. ABL42627 to ABL42926 represent specifically claimed human
CC maturation/activation DC expression gene tags from the present invention
XX
SQ Sequence 10 BP; 1 A; 1 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCT 22

|||||

Db 1 TGTGTGACCT 10

RESULT 287

ABL39528/c

ID ABL39528 standard; DNA; 10 BP.

XX

AC ABL39528;

XX

DT 22-APR-2002 (first entry)

XX Human ETPB primer-extension oligonucleotide 34.

XX Human; electron-transfer flavoprotein beta polypeptide; ETPB;
KW electron acceptor; mitochondrial matrix; glutaric acidemia type II;
KW novel polymorphic site; novel polymorphism; ETPB genotype; ss; GAI1;
KW ETPB haplotype; transgenic animal; primer; probe; chromosome 19q13;
KW primer-extension oligonucleotide; single nucleotide polymorphism; SNP.

XX Homo sapiens.

XX WO200202580-A2.

XX 10-JAN-2002.

XX 05-JUL-2001; 2001WO-US021306.

XX

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PR 05-JUL-2000; 2000US-0215984P.
XX
FA (GENA-) GENAISSANCE PHARM INC.
XX
PT Bentivegna SC, Bieglecki KM, Kazemi A, Koshy B;
XX
XX WPI; 2002-154722/20.
XX
XX Novel isolated human electron-transfer-flavoprotein, beta polynucleotide,
PT useful for therapeutic purposes, for studying the expression and function
PT of the polynucleotide, and for expressing the flavoprotein.
XX
XX Claim 19; Page 15; 143pp; English.
XX
XX The invention comprises DNA, cDNA and protein sequences of the human
CC electron-transfer flavoprotein, beta polypeptide (ETFB) gene (located on
CC chromosome 19q13.3-13.4). The invention specifically relates to the
CC identification of 27 novel polymorphic sites within the ETFB gene.
XX Electron-transfer flavoprotein (ETFB) is an obligatory electron acceptor
CC for nine primary flavoprotein dehydrogenases and is located in the
CC mitochondrial matrix. ETF is composed of an alpha (ETFA) and a beta
CC (ETFB) subunit. Electrons accepted by ETF are transferred to the
CC mitochondrial respiratory chain by ETF dehydrogenases (ETFDHs).
CC Deficiency of ETF or ETFDH leads to glutaric acidemia type II (GAI1).
CC Therefore ETFB is a pharmaceutically-important gene in the treatment of
CC GAI1. The novel ETFB polymorphisms identified in the invention are useful
CC for genotyping and haplotyping the ETFB gene of an individual. The ETFB
CC protein and nucleic acids of the invention are useful for studying the
CC expression and function of ETFB in vivo. The ETFB protein and nucleic
CC acids are also useful for testing the efficacy of therapeutic agents and
CC compounds for glutaric acidemia type II. The nucleic acids of the
CC invention are useful in the production of a transgenic animal expressing
CC the ETFB gene. Nucleic acids ABL39414-ABL39440 represent claimed ETFB
CC allele-specific probes. Nucleic acids ABL39441-ABL39494 represent claimed
CC ETFB allele-specific PCR primers. Nucleic acids ABL39495-ABL39548
CC represent claimed ETFB primer-extension oligonucleotides
XX
SQ Sequence 10 BP; 2 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTG 16
Db 10 ACCTGCTGAG 1

RESULT 288
ABV84850/C
ID ABV84850 standard; cDNA; 10 BP.
XX
AC ABV84850;
XX
DT 12-DEC-2002 (first entry)
XX
DE Human mitochondrial 16S rRNA SAGE tag #660.
XX
XX SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
XX CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
XX expression pattern; ss.
XX
XX Homo sapiens.
XX
OS JP2002209591-A.
XX
XX 30-JUL-2002.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX 19-JAN-2001; 2001JP-00012328.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX

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XX WPI; 2002-631294/68.
XX
XX Human chronic hepatitis C tissue expression exasperating gene group
PT comprises 100 high-ranking genes.
XX
XX Claim 55; Page 29; 139pp; Japanese.
XX
XX The invention relates to SAGE (serial analysis of gene expression) tags
CC representing groups of genes which are differentially expressed in human
CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
CC polyA region of cDNAs derived from a variety of genes. These tags serve
CC to uniquely identify each transcript and can thus be used to analyse the
CC pattern of gene expression in particular cell types. The invention also
CC relates to proteins encoded by the genes expressed in chronic hepatitis C
CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
CC the expression of groups of genes that are overexpressed in chronic
CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
CC treatment of these diseases. Such genes, inhibitors of their expression
CC or activity, and antibodies against the gene products may be used in the
CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
CC ABV84791-ABV84890 are SAGE tags representing 100 genes which are highly
CC expressed in chronic hepatitis C liver tissue
XX
SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
Db 10 CTTGCTGTGT 1

RESULT 289
ABK09446/C
ID ABK09446 standard; DNA; 10 BP.
XX
AC ABK09446;
XX
XX 14-MAR-2002 (first entry)
XX
DE Human NPR1 gene allele-specific oligonucleotide PCR primer #26.
XX
XX Human; natriuretic peptide receptor A/guanylate cyclase A; NPR1; ss;
XX atrionatriuretic peptide receptor A; haplotyping; cytosolic; genotyping;
XX haplotype pair; single nucleotide polymorphism; gene therapy; PCR primer;
XX drug screening; hypertension; hypotensive; sequencing primer; probe.
XX
XX Homo sapiens.
XX
XX WO200179231-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US012300.
XX
XX 14-APR-2000; 2000US-0197330P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bentivegna SC, Choi JY, Kliem SE, Nandabalan K;
XX
XX WPI; 2002-066340/09.
XX
XX Genotyping human natriuretic peptide receptor A/guanylate cyclase gene of
PT an individual, involves determining identity of nucleotide pair at
PT specific polymorphic sites for two copies of the gene.
PT

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XX Claim 17; Page 15; 96pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene

CC encoding the human natriuretic peptide receptor A/guanylate cyclase A

CC (atriuretic peptide receptor A) or NPRI polypeptide. A method for

CC haplotyping the NPRI gene in an individual comprises identifying the

CC nucleotide at one or more polymorphic sites and determining whether one

CC of the copies of the gene is defined by one of the NPRI haplotypes given

CC in the specification or whether both copies are defined by a haplotype

CC pair. This method is useful in genotyping, whereby all possible haplotype

CC pairs can be assigned to specific genotypes. An association between a

CC trait and a haplotype or haplotype pair of the NPRI gene can be

CC identified by comparing the frequency of the haplotype or haplotype pair

CC in a population exhibiting the trait with the frequency of the haplotype

CC or haplotype pair in a reference population, where a higher haplotype

CC frequency in the trait population indicates the trait is associated with

CC the haplotype or haplotype pair. NPRI and its corresponding DNA are used

CC for studying the expression and function of NPRI, for use in screening

CC for candidate drugs to treat diseases related to NPRI activity, such as

CC hypertension. The sequences are also useful for studying the effect of

CC variation on the biological activity of NPRI as well as on the binding

CC affinity of candidate drugs targeting NPRI. Sequences AAS99959-AAS99990

CC and ABK09390-ABK09462 represent probes, sequencing primers and PCR

CC primers used to detect NPRI gene polymorphisms

XX

XX Sequence 10 BP; 4 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 TGTGACCTGG 24

Db | | | | | | | |

10 TGTGACCTGG 1

RESULT 290

ABK09921/c

ID ABK09921 standard; DNA; 10 BP.

XX

AC ABK09921;

XX

DT 14-MAR-2002 (first entry)

XX

DE P2RY1 gene allele-specific oligonucleotide #72.

XX

KW Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;

KW coagulant; platelet aggregation; haplotyping; drug screening;

KW transgenic animal; human; allele-specific oligonucleotide; ss.

XX

OS Homo sapiens.

XX

PN WO200190117-A2.

XX

PD 29-NOV-2001.

XX

PF 21-MAY-2001; 2001WO-US016432.

XX

PR 19-MAY-2000; 2000US-0205996P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Kazemi A, Koshiy B, Tanguay DA;

XX

DR WPI; 2002-083074/11.

XX

PT New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic

PT variants, useful e.g. in studying the expression and function of P2RY1

PT and screening candidate drugs for treating diseases related to P2RY1

PT activity.

XX

PS Claim 18; Page 14; 79pp; English.

XX The invention relates to a novel isolated polypeptide comprising a

CC sequence which is a polymorphic variant of a reference sequence for the

CC purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its

CC fragment. The polymorphic variant comprises one or more variant amino

CC acids selected from valine at a position 34 and glycine at a position

CC 262. The polymorphic variants are useful in studying the expression and

CC function of P2RY1, in expressing P2RY1 protein for use in screening for

CC candidate drugs to treat diseases related to P2RY1 activity, in studying

CC the effect of the variation on the biological activity of P2RY1, and the

CC binding affinity of candidate drugs targeting P2RY1 for the treatment of

CC disorders related to platelet aggregation. The haplotyping methods are

CC useful in validating P2RY1 as a candidate target for treating a specific

CC condition or disease predicted to be associated with P2RY1 activity, or

CC in the design of clinical trials of candidate drugs for treating a

CC specific condition or disease associated with P2RY1 activity. The

CC transgenic animals are useful for studying expression of the P2RY1

CC isogenes in vivo, for in vivo screening and testing of drugs targeted

CC against P2RY1 protein, and for testing the efficacy of therapeutic agents

CC and compounds for disorders related to platelet aggregation in a

CC biological system. ABK09950-ABK09924 represent human purinergic receptor

CC P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of

CC the invention

XX

XX Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;

Best Local Similarity 90.0%; Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAA 28

Db | | | | | | | |

10 ACCAGGTAAA 1

RESULT 291

ABK09919/c

ID ABK09919 standard; DNA; 10 BP.

XX

AC ABK09919;

XX

DT 14-MAR-2002 (first entry)

XX

DE P2RY1 gene allele-specific oligonucleotide #70.

XX

KW Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;

KW coagulant; platelet aggregation; haplotyping; drug screening;

KW transgenic animal; human; allele-specific oligonucleotide; ss.

XX

OS Homo sapiens.

XX

PN WO200190117-A2.

XX

PD 29-NOV-2001.

XX

PF 21-MAY-2001; 2001WO-US016432.

XX

PR 19-MAY-2000; 2000US-0205996P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Kazemi A, Koshiy B, Tanguay DA;

XX

DR WPI; 2002-083074/11.

XX

PT New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic

PT variants, useful e.g. in studying the expression and function of P2RY1

PT and screening candidate drugs for treating diseases related to P2RY1

PT activity.

XX

PS Claim 18; Page 14; 79pp; English.

XX

CC The invention relates to a novel isolated polypeptide comprising a

sequence which is a polymorphic variant of a reference sequence for the purinergic receptor P2Y₁, G-protein coupled, 1 (P2RY1) protein or its fragment. The polymorphic variant comprises one or more variant amino acids selected from valine at a position 34 and glycine at a position 262. The polymorphic variants are useful in studying the expression and function of P2RY1, in expressing P2RY1 protein for use in screening for candidate drugs to treat diseases related to P2RY1 activity, in studying the effect of the variation on the biological activity of P2RY1, and the binding affinity of candidate drugs targeting P2RY1 for the treatment of disorders related to platelet aggregation. The haplotyping methods are useful in validating P2RY1 as a candidate target for treating a specific condition or disease predicted to be associated with P2RY1 activity, or in the design of clinical trials of candidate drugs for treating a specific condition or disease associated with P2RY1 activity. The transgenic animals are useful for studying expression of the P2RY1 isogenes in vivo, for in vivo screening and testing of drugs targeted against P2RY1 protein, and for testing the efficacy of therapeutic agents and compounds for disorders related to platelet aggregation in a biological system. ABK09950-ABK09924 represent human purinergic receptor P2Y₁, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of the invention

XX
SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 20 CCTGGTAAAT 29
DB 10 CCAGGTAAAT 1

RESULT 292
ABS64264
ID ABS64264 standard; DNA; 10 BP.
AC ABS64264;
XX
DT 15-NOV-2002 (first entry)
DE Tachykinin receptor gene TACR2, primer extension oligo #18.
XX Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;
KW tachykinin receptor.
XX Homo sapiens.
XX WO200263046-A1.
XX 15-AUG-2002.
XX 09-NOV-2001; 2001WO-US047394.
XX 09-NOV-2000; 2000US-0247649P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Cappola G, Chew A, Gilson CR, Koshy B;
XX WPI; 2002-636600/68.
XX New genetic variants having polymorphisms in the Tachykinin receptor (TACR2) protein, useful for studying the function of TACR2, and for treating disorders associated with abnormal expression or function of TACR2 isogene.
XX Claim 16; Page 15; 139pp; English.

The invention relates to an isolated polypeptide comprising a polymeric variant of a reference sequence for the Tachykinin receptor (TACR2) protein. Also described is a method for: (1) haplotyping or genotyping the TACR2 gene of an individual; (2) predicting a haplotype pair for the

CC TACR2 gene of an individual; (3) identifying an association between a trait and at least one haplotype or haplotype pair of the TACR2 gene; and
CC (4) isolated oligonucleotide for detecting a single nucleotide polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene are useful in studying the expression and biological function of TACR2, and in identifying drugs targeting TACR2 protein for treating disorders associated with abnormal expression or function of TACR2, e.g. asthma or breast cancer. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or increased expression of a particular TACR2 protein isoform, or an expression vector encoding the isoform may be administered to the patient. Haplotype information is useful in improving the efficiency and output of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. Information on polymorphisms may be applied in studying biological functions of TACR2 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. ABS64163-ABS64302 represent human TACR2 gene allele-specific oligonucleotide probes and primers used to detect haplotypes of the TACR2 gene of the invention

XX
SQ Sequence 10 BP; 2 A; 1 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGA 19
DB 1 TGCTGTGTAA 10

RESULT 293
ABS64271/C
ID ABS64271 standard; DNA; 10 BP.
AC ABS64271;
XX
DT 15-NOV-2002 (first entry)
DE Tachykinin receptor gene TACR2, primer extension oligo #25.
XX Human; single nucleotide polymorphism; SNP; TACR2; primer; probe; ss;
KW tachykinin receptor.
XX Homo sapiens.
XX WO200263046-A1.
XX 15-AUG-2002.
XX 09-NOV-2001; 2001WO-US047394.
XX 09-NOV-2000; 2000US-0247649P.
XX (GENA-) GENAISSANCE PHARM INC.
XX Cappola G, Chew A, Gilson CR, Koshy B;
XX WPI; 2002-636600/68.
XX New genetic variants having polymorphisms in the Tachykinin receptor (TACR2) protein, useful for studying the function of TACR2, and for treating disorders associated with abnormal expression or function of TACR2 isogene.
XX Claim 16; Page 15; 139pp; English.

The invention relates to an isolated polypeptide comprising a polymeric variant of a reference sequence for the Tachykinin receptor (TACR2) protein. Also described is a method for: (1) haplotyping or genotyping the TACR2 gene of an individual; (2) predicting a haplotype pair for the TACR2 gene of an individual; (3) identifying an association between a

CC trait and at least one haplotype or haplotype pair of the TACR2 gene; and
 CC (4) isolated oligonucleotide for detecting a single nucleotide
 CC polymorphism in the TACR2 gene. Polymorphic variants of the TACR2 gene
 CC are useful in studying the expression and biological function of TACR2,
 CC and in identifying drugs targeting TACR2 protein for treating disorders
 CC associated with abnormal expression or function of TACR2, e.g. asthma or
 CC breast cancer. Polynucleotides comprising a polymorphic gene variant or
 CC fragment may be used for therapeutic purposes, where a patient could
 CC benefit from expression or increased expression of a particular TACR2
 CC protein isoform, or an expression vector encoding the isoform may be
 CC administered to the patient. Haplotype information is useful in improving
 CC the efficiency and output of several steps in drug discovery and
 CC development process, including target validation, identifying lead
 CC compounds, and early phase clinical trials. Information on polymorphisms
 CC may be applied in studying biological functions of TACR2 as well as in
 CC identifying drugs targeting this protein for the treatment of disorders
 CC related to its abnormal expression or function. ABS64163-ABS64302
 CC represent human TACR2 gene allele-specific oligonucleotide probes and
 CC primers used to detect haplotypes of the TACR2 gene of the invention
 XX
 SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTG 11
 |||||
 Db 10 CACCCACCTG 1

RESULT 294
 AAS99384
 ID AAS99384 standard; DNA; 10 BP.
 XX
 AC AAS99384;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #77.
 XX
 KW Aldehyde dehydrogenase 5 family member A1; ALDH5A1;
 KW succinate-semialdehyde dehydrogenase; gene therapy; primer;
 KW antisense technology; primer extension oligonucleotide;
 KW 4-hydroxybutyric aciduria; metabolic disease; transgenic animal; ss.
 XX
 OS Synthetic.

XX WO200190119-A2.
 XX
 XX 29-NOV-2001.
 XX
 XX 21-MAY-2001; 2001WO-US016558.
 XX
 XX 19-MAY-2000; 2000US-0205849P.
 XX
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Kliem SE, Koshy B, Tanguay DA;
 XX WPI; 2002-089912/12.
 XX
 XX New genetic variants of human aldehyde dehydrogenase 5 family, member A1,
 XX ALDH5A1 gene for treating metabolic diseases and for expressing ALDH5A1
 XX protein useful in identifying drugs to treat 4-hydroxybutyric aciduria.
 XX
 XX Claim 18; Page 14; 151pp; English.

XX The invention describes an isolated polynucleotide comprising a
 XX nucleotide sequence which is a polymorphic variant of a reference
 XX sequence for the aldehyde dehydrogenase 5 family, member A1 (succinate-
 XX semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment. The
 XX polypeptide is useful for screening for drugs targeting it by contacting

CC the ALDH5A1 polymorphic variant with a candidate agent and assaying for
 CC binding activity. The polypeptide and haplotypes are useful for
 CC identifying an association between a trait such as a clinical response to
 CC a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene. Transgenic animals
 CC are also useful for studying expression of the ALDH5A1 isogenes in vivo,
 CC for in vivo screening and testing of drugs against ALDH5A1 protein and
 CC for testing the efficacy of therapeutic agents and compounds for 4-
 CC hydroxybutyric aciduria and metabolic diseases in a biological system.
 CC Antibodies are useful for diagnostic and prognostic formats and
 CC therapeutic methods, for immunoprecipitating the polypeptide from
 CC solution, for detecting ALDH5A1 protein isoforms in biological samples,
 CC frozen tissue sections, for use in immunocytochemical, and
 CC immunohistochemical and immunofluorescence techniques. The polynucleotide
 CC is useful for gene therapy and antisense gene therapy. This sequence is a
 CC primer extension oligonucleotide used to detect polymorphisms in the
 CC ALDH5A1 gene described in the method of the invention
 XX
 SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
 |||||
 Db 1 ATGCACCTGC 10

RESULT 295
 AAD47793
 ID AAD47793 standard; DNA; 10 BP.
 XX
 AC AAD47793;

DT 24-FEB-2003 (first entry)
 XX
 DE Human GNB3 gene polymorphisms detecting primer #13.

XX Human; guanine nucleotide binding protein beta polypeptide 3; G protein;
 KW GNB3; polymorphism; obesity; left ventricular hypertrophy; hypertension;
 KW drug discovery; cardiovascular; development process; asthma; anorectic;
 KW gene therapy; primer; ss.

XX Homo sapiens.

XX WO200277284-A1.

XX 03-OCT-2002.

XX 21-MAR-2001; 2001WO-US008961.

XX 21-MAR-2001; 2001WO-US008961.

XX (GENA-) GENAISSANCE PHARM INC.

XX Bentivegna SC, Choi JY, Kliem SE, Koshy B;

XX WPI; 2003-018947/01.

XX New genetic variants having polymorphisms in the G protein, GNB3 gene,
 XX useful for treating disorders with abnormal expression or function of the
 XX GNB3 gene, such as asthma, obesity, hypertension and left ventricular
 XX hypertrophy.

XX Claim 18; Page 15; 89pp; English.

XX The invention relates to an isolated polypeptide which comprises a first
 XX nucleotide sequence which is a polymorphic variant of a reference
 XX sequence for the guanine nucleotide binding protein (G protein), beta
 XX polypeptide 3 (GNB3) gene or fragment. Polymorphic variants of the GNB3
 XX gene are useful in studying the expression and biological function of
 XX GNB3 and in identifying drugs targeting GNB3 protein for treating
 XX disorders associated with abnormal expression or function of GNB3, e.g.

CC hypertension, obesity, asthma and left ventricular hypertrophy.
CC Polynucleotides comprising a polymorphic gene variant or fragment may be
CC used for therapeutic purposes, where a patient could benefit from
CC expression or increased expression of a particular GNB3 gene isoform or
CC an expression vector encoding the isoform may be administered to the
CC patient. Haplotype information is useful in improving the efficiency and
CC output of several steps in drug discovery and development process,
CC including target validation, identifying lead compounds and early phase
CC clinical trials. The invention is used in gene therapy. The present
CC sequence is human GNB3 gene polymorphisms detecting primer
XX
XX SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
Db 1 CCACCTGCTG 10

RESULT 296
ID ACC69006 standard; DNA; 10 BP.
XX
XX AC ACC69006;
XX
XX DT 10-JUL-2003 (first entry)
XX
XX DE AMP protocol HpaII oligonucleotide PCR primer SEQ ID NO:3.
XX
XX KW Amplified DNA methylation polymorphism protocol; AMP protocol;
XX KW methylation profile; functional genomics; identification; mapping;
XX KW diagnosis; forensic; genomic; PCR primer; ss.
XX OS Synthetic.
XX
XX PN WO2003025215-A1.
XX
XX PD 27-MAR-2003.
XX
XX PF 13-SEP-2002; 2002WO-AU001362.
XX
XX PR 14-SEP-2001; 2001AU-00007685.
XX
XX PA (UYQU) UNIV QUEENSLAND.
XX
XX PI Carroll BJ, Harrison DK, Aung HT;
XX
XX DR WPI; 2003-371826/35.
XX
XX PT Determining DNA methylation profile within the genome of a eukaryotic
XX PT cell comprises the exposure of genomic or transgenic DNA to a methylation
XX PT -sensitive enzyme, e.g. HpaII, and subjecting the DNA to an amplification
XX PT reaction.
XX
XX PS Example 1; Page 40; 88pp; English.
XX
XX CC The present invention describes a method for determining the methylation
XX CC profile of one or more nucleotides at one or more sites within the genome
XX CC of a eukaryotic cell or group of cell comprising the exposure of genomic
XX CC or transgenic DNA to a methylation-sensitive enzyme and subjecting the
XX CC DNA to an amplification reaction. The method is useful in detecting DNA
XX CC methylation, in functional genomics, and in the design of therapeutic and
XX CC trait-modifying protocols for animals and plants. The method may also be
XX CC used in identifying and mapping functions between methylated and
XX CC unmethylated DNA, in identifying DNA methylation polymorphisms that can
XX CC be used in diagnosis and forensics, and in monitoring the aging process
XX CC of particular cells of an animal, including humans, or plants. The
XX CC present sequence represents a PCR primer which is used in an example from
XX CC the present invention for an amplified DNA methylation polymorphism (AMP)
XX CC protocol

XX
XX SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 GTGACCTGGT 25
Db 10 GTGACCGGTT 1

RESULT 297
ID ABE114241 standard; DNA; 10 BP.
XX
XX AC ABE114241;
XX
XX DT 20-FEB-2003 (first entry)
XX
XX DE Nucleic acid PCR amplification method-related RAPD PCR primer #11.
XX
XX KW Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;
XX KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.
XX OS Unidentified.
XX
XX PN WO200281743-A2.
XX
XX PD 17-OCT-2002.
XX
XX PF 28-MAR-2002; 2002WO-GB001489.
XX
XX PR 02-APR-2001; 2001GB-00008182.
XX
XX PA (HAMI/) HAMILL B.
XX
XX PI Hamill B;
XX
XX DR WPI; 2003-075484/07.
XX
XX PT Amplification of nucleotide sequences from polynucleotides by chain
XX PT extension of oligonucleotide primers, comprises 2 oligonucleotides in
XX PT solution, 2 attached to supports and both share complementary sequences.
XX
XX PS Disclosure; Fig 17; 60pp; English.
XX
XX CC The invention comprises a method for the PCR amplification of nucleic
XX CC acids. The method involves a set of primers, where two of the primers are
XX CC in solution and at least two other primers are attached to a solid
XX CC support. The method of the invention can be used for the analysis of a
XX CC nucleic acid or a mixture of nucleic acids, including: single-stranded
XX CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The
XX CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)
XX CC PCR primer of the invention
XX
XX SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCCACCTG 11
Db 1 CATCCACCTG 10

RESULT 298
ID ABE14194 standard; DNA; 10 BP.
XX
XX AC ABE14194;
XX

KW cytosstatic; gene therapy; microarray; gene expression characteristic;
 KW haematopoietic cell; haematopoiesis; myeloid leukaemia; probe;
 KW CD15+ myeloid cell; ss.
 XX Homo sapiens.
 OS
 XX
 XX US2003165949-A1.
 PN
 XX
 XX 04-SEP-2003.
 PD
 XX
 XX 23-DEC-2002; 2002US-00329465.
 PF
 XX
 XX 27-DEC-2001; 2001US-0343826P.
 PR
 XX
 XX (WANG/) WANG S M.
 PA (LEES/) LEE S.
 PA (CHEN/) CHEN J.
 PA (ZHOU/) ZHOU G.
 PA (ROWL/) ROWLEY J D.
 XX
 XX Wang SM, Lee S, Chen J, Zhou G, Rowley JD;
 PI WPI; 2003-863699/80.
 DR
 XX
 XX New microarray for measuring gene expression characteristics of
 PT hematopoietic cells, useful for preparing a composition for diagnosing or
 PT treating myeloid leukemia.
 XX
 XX Claim 1; SEQ ID NO 244; 32pp; English.
 PS
 XX The invention describes a microarray for measuring gene expression
 CC characteristics of haematopoietic cells comprising at least 5
 CC polynucleotides having distinct sequences. Also described are: a method
 CC of diagnosing or treating an abnormality associated with haematopoiesis;
 CC and diagnosing myeloid leukaemia in a patient. The microarray is useful
 CC for preparing a composition for diagnosing or treating myeloid leukaemia.
 CC This sequence represents a polynucleotide probe comprising a portion of
 CC an expressed gene isolated from a population of CD15+ myeloid cells and
 CC suitable for use in the microarray of the invention.
 XX
 XX Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 8 CCTGCTGTGT 17
 Db 10 CTTGCTGTGT 1
 RESULT 301
 ADG13687/C
 ID ADG13687 standard; RNA; 10 BP.
 AC
 XX
 XX ADG13687;
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX
 XX Human EGFR Amberzyme target sequence #19.
 DE
 KW Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
 KW HER4; hammerhead ribozyme; inozyme; zinzyme; DNAzyme; amberzyme; cancer;
 KW brain tumour; cytosstatic; short interfering RNA; siRNA; RNA interference;
 KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
 KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
 KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
 KW multidrug resistant cancer.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003186909-A1.
 PN
 XX

PD 02-OCT-2003.
 XX
 PF 21-OCT-2002; 2002US-00277494.
 XX
 XX 27-JAN-1997; 97US-0036749P.
 PR 04-DEC-1997; 97US-00985162.
 PR 22-SEP-1999; 99US-00401063.
 PR 03-MAY-2001; 2001US-00848754.
 PR 25-JUL-2001; 2001US-00916466.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Mcswiggen J;
 PI WPI; 2004-032029/03.
 DR
 XX
 XX New double stranded short interfering ribonucleic acid molecule for
 PT inhibiting expression of epidermal growth factor receptor gene.
 XX
 XX Claim 7; SEQ ID NO 114; 113pp; English.
 PS
 XX The invention relates to a double stranded short interfering RNA (siRNA)
 CC molecule that inhibits expression of epidermal growth factor receptor
 CC (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
 CC expression vector comprising a nucleic acid sequence encoding siRNA
 CC molecule(s) in a manner that allows expression of the nucleic acid
 CC molecule. The siRNA molecules comprise hammerhead ribozymes, inozymes,
 CC amberzymes zinzymes and DNAzymes. The invention is used for inhibiting
 CC expression of EGFR. It can be used for treatment of cancer, prostate
 CC cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
 CC cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
 CC cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
 CC cancer or a brain tumour. The invention has enhanced shelf-life, half-
 CC life in vitro, stability, and ease of introduction of oligonucleotide to
 CC target site. The present sequence is an EGFR/HER1-4 target sequence for
 CC an siRNA of the invention.
 XX
 XX Sequence 10 BP; 3 A; 0 C; 5 G; 0 T; 2 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 10 CCATCCACTT 1
 RESULT 302
 ADH14437
 ID ADH14437 standard; DNA; 10 BP.
 AC
 XX
 XX ADH14437;
 XX
 XX 11-MAR-2004 (first entry)
 DT
 XX
 XX Human retinoblastoma 1 (RB1CC1) genomic DNA 3' border of intron 19.
 DE
 XX
 XX cell nucleus; transcription; gene expression; retinoblastoma-1; RB1CC1;
 KW diagnosis; cancer; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO2003102028-A1.
 PN
 XX
 XX 11-DEC-2003.
 PD
 XX
 XX 30-JAN-2003; 2003WO-JP000882.
 PF
 XX
 XX 03-JUN-2002; 2002JP-00161400.
 PR 24-JUL-2002; 2002JP-00214978.
 XX
 XX (OKAB/) OKABE H.
 PA

PA (IKEG/) IKEGAWA S.
 PA (CHAN/) CHANO T.
 PI Chano T;
 XX WPI; 2004-081932/08.
 DR
 XX Protein in the nuclei of human and animal cells associated with
 PT expression of retinoblastoma-1 gene for diagnosis of cancer.
 PT
 XX Disclosure; Page 11; 113pp; Japanese.
 PS
 XX The invention relates to a protein or polypeptide found in the nuclei of
 CC human and animal cells that are associated with transcription and/or
 CC induction of expression of retinoblastoma-1 gene (RB1CC1). The detection
 CC of RB1CC1 gene and its protein is useful for the diagnosis of cancer. The
 CC human RB1CC1 cDNA is 6.6 kb containing a 4782 bp ORF, encoding a 180 kD
 CC 1594 amino acid protein. This sequence corresponds to the sequence at the
 CC junction between an intron and an exon in the human RB1CC1 genomic
 CC sequence.
 XX
 SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 CCACCTGCTG 14
 DB 1 CCACCTGCAG 10
 ADK12825;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Human glioma endothelial marker (GEM) standard tag SEQ ID NO:3.
 DE
 XX glioma; brain tissue; neoplastic; glioma endothelial marker; GEM;
 KW anticancer; antiglioma; immune response; cytostatic;
 KW multi-drug sensitive glioma; human; standard tag; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX WO2004016758-A2.
 PN
 XX 26-FEB-2004.
 PD
 XX 15-AUG-2003; 2003WO-US025614.
 PF
 XX 15-AUG-2002; 2002US-0403390P.
 PR
 XX 01-APR-2003; 2003US-0458978P.
 PR
 XX (GENZ) GENZYME CORP.
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Madden SI, Wang CJ, Cook BP, Lattera J, Walter K;
 PI WPI; 2004-247973/23.
 XX
 XX Diagnosing glioma by detecting expression product of any one of 255
 PT genes, glioma endothelial markers, in brain tissue sample suspected of
 PT being neoplastic, and comparing the expression with expression in normal
 PT brain tissue sample.
 XX
 XX Claim 36; SEQ ID NO 3; 114pp; English.
 PS
 XX The present invention describes a method (M1) for aiding in the diagnosis

CC of glioma. (M1) involves detecting an expression product of at least one
 CC gene (I) in a first brain tissue sample (T) suspected of being
 CC neoplastic, where (I) is chosen from any one of 255 genes (glioma
 CC endothelial markers (GEMs)) as given in specification, and comparing the
 CC expression of (I) in (T) with expression of (I) in a second normal brain
 CC tissue sample (R), where increased expression of (I) in (T) relative to
 CC (R), identifies (T) as likely to be neoplastic. Also described: (1)
 CC treating (M2) glioma involves contacting cells of the glioma with an
 CC antibody that specifically binds to an extracellular epitope; (2)
 CC identifying (M3) a test compound as potential anticancer or anti-glioma
 CC drug involves contacting a test compound with the cell which expresses
 CC (I), monitoring an expression product of the at least one gene and
 CC identifying test compound as a potential anticancer drug if it decreases
 CC the expression of at least one gene; (3) identifying (M4) a test compound
 CC as potential anticancer or anti-glioma drug involves contacting a test
 CC compound with the cell which expresses mRNA of at least one gene
 CC identified by a tag as described above, monitoring mRNA of the gene, and
 CC identifying the test compound as a potential anticancer drug if it
 CC decreases the expression of at least one gene; and (4) inducing (M5) an
 CC immune response to glioma involves administering to a mammal, a protein
 CC or (I). (I) have cytostatic activities, and can be used to trigger immune
 CC destruction of glioma cells, and as immune response inducers. (M1) is
 CC useful for aiding in diagnosing glioma. (M2) is useful for treating multi
 CC -drug sensitive glioma in a human. (M5) is useful for inducing an immune
 CC response to a glioma in a mammal having glioma or in a mammal who has had
 CC a glioma surgically removed. The present sequence represents a human GEM
 CC standard tag oligonucleotide, which is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 10 BP; 5 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CCTGCTGTGT 17
 DB 10 CTTGCTGTGT 1
 RESULT 304
 ADK27959/c
 ID ADK27959 standard; DNA; 10 BP.
 XX
 AC ADK27959;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Murine VE-statin exon 7 3' oligonucleotide.
 XX
 KW Cytostatic; Ophthalmological; Vasotropic; Antiarteriosclerotic;
 KW VE-statin; endothelium; perivascular smooth muscle cell; angiogenesis;
 KW cancer; retinopathy; atherosclerosis; restenosis; gene therapy; mouse;
 KW ds.
 XX
 OS Mus musculus.
 XX
 PN FR2851249-A1.
 XX
 XX 20-AUG-2004.
 PD
 XX 17-FEB-2003; 2003FR-00001875.
 PF
 XX 17-FEB-2003; 2003FR-00001875.
 PR
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA
 XX Soncin F, Mattot V;
 PI
 XX WPI; 2004-618122/60.
 DR
 XX Using VE-statins to inhibit recruitment of perivascular smooth muscle
 PT cells, for treating e.g. cancer and retinopathy, also new VE-statins,

```

PT related nucleic acids and antibodies.
PS Example 3; Page 11; 63pp; French.
XX
CC The present invention relates to a method for preparing a composition for
CC inhibiting recruitment of perivascular cells of smooth muscle type using
CC a VE-statin protein (I; ADR27861-ADR27863 and ADR27902). VE-statins,
CC soluble factors secreted by endothelial cells of the blood vessels, block
CC recruitment of perivascular smooth muscle cells (but do not affect their
CC proliferation), so inhibit angiogenesis. VE-statins, also their peptide
CC fragments, nucleic acids encoding them and vectors containing this
CC nucleic acid, are used for treating cancer, retinopathy, atherosclerosis
CC and restenosis, including in gene therapy. The VE-statin nucleic acids
CC can also be used to produce transgenic animals (for studying the VE-
CC statin proteins and genes); the VE-statins are used to screen for
CC specific (ant)agonists, and antibodies specific for VE-statins can be
CC used to determine expression profiles, particularly for diagnosis of
CC diseases associated with VE-statins. The present sequence was used to
CC illustrate the structure of the murine VE-statin gene.
XX
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18
DB 10 CTGCTGTGGG 1

RESULT 305
ADS78008/c
ID ADS78008 standard; DNA; 10 BP.
XX
AC ADS78008;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #1790.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
PI PI; 2004-728732/71.
XX
DR Diagnosing breast cancer comprises determining expression levels of a
DR gene selected from those differentially expressed in normal or cancerous
DR cells of a breast tissue sample including interleukin 1, thrombospondin 1
DR and cystatin C.
XX
PS Example 2; SEQ ID NO 17; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
DB 10 CTGCTGTGT 1

RESULT 306
ADS76235/c
ID ADS76235 standard; DNA; 10 BP.
XX
AC ADS76235;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #17.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
PI PI; 2004-728732/71.
XX
DR Diagnosing breast cancer comprises determining expression levels of a
DR gene selected from those differentially expressed in normal or cancerous
DR cells of a breast tissue sample including interleukin 1, thrombospondin 1
DR and cystatin C.
XX
PS Example 2; SEQ ID NO 17; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
CC specification, and (c) if the gene is expressed in the test sample at a
CC lower level than in a control normal breast tissue sample, diagnosing the
CC test sample as containing cancer cells. The method is used for diagnosing
CC breast cancer. This sequence corresponds to an oligonucleotide primer
CC used in the method of the invention.
XX
SQ Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
DB 10 CTGCTGTGT 1

RESULT 306
ADS76235/c
ID ADS76235 standard; DNA; 10 BP.
XX
AC ADS76235;
XX
DT 30-DEC-2004 (first entry)
XX
DE Breast cancer detection oligonucleotide #17.
XX
KW ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
KW cathepsin L inhibitor; cathepsin F inhibitor;
KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
OS Homo sapiens.
XX
PN WO2004085621-A2.
XX
PD 07-OCT-2004.
XX
PF 22-MAR-2004; 2004WO-US008866.
XX
PR 20-MAR-2003; 2003US-0456735P.
XX
PA (DAND ) DANA FARBER CANCER INST INC.
XX
PI Polyak K, Porter D, Allinen M;
XX
PI PI; 2004-728732/71.
XX
DR Diagnosing breast cancer comprises determining expression levels of a
DR gene selected from those differentially expressed in normal or cancerous
DR cells of a breast tissue sample including interleukin 1, thrombospondin 1
DR and cystatin C.
XX
PS Example 2; SEQ ID NO 17; 149pp; English.
XX
CC The invention relates to a method of diagnosis (M1) comprising: (a)
CC providing a test sample of breast tissue; (b) determining the level of
CC expression in the test sample of a gene (e.g. interleukin-8, superoxide

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Query Match 29.0%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACTGCG 12
 Db 10 AACCACTGCG 1

RESULT 312
 AAV55915
 ID AAV55915 standard; DNA; 11 BP.
 XX
 AC AAV55915;
 XX
 DT 02-DEC-1998 (first entry)
 XX
 DE CYP1B1 gene exon II 5' splice donor sequence.
 XX
 KW CYP1B1; human; cytochrome P4501B1; glaucoma; mutation; 8q24 gene;
 KW 10p1 gene; glaucoma-associated gene; primary open-angle glaucoma;
 KW primary congenital glaucoma; PCG; gene therapy; optical nerve; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9836098-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 12-FEB-1998; 98WO-US002851.
 XX
 PR 13-FEB-1997; 97US-00800036.
 PR 10-SEP-1997; 97US-00926492.
 XX
 PA (UYCO-) UNIV CONNECTICUT.
 XX
 PI Sarfarazi M;
 XX
 WPI; 1998-506317/43.
 XX
 DR
 XX
 PT Diagnosis of glaucoma by detecting mutations in, or altered expression
 PT from, specific genes - also treatment with non-mutant nucleic acid or
 PT proteins, or antibodies against mutant protein.
 XX
 PS Example; Page 30; 61pp; English.
 XX
 CC Sequences shown in AAV55913 to AAV55916 represent splice donor and
 CC acceptor sequences of the exons of the human cytochrome P4501B1 (CYP1B1)
 CC gene. The invention provides a method for the diagnosis of glaucoma which
 CC comprises detecting a mutation in a glaucoma-associated gene or by
 CC detecting altered expression of the protein encoded by the gene. The
 CC method is specifically used to diagnose primary open-angle glaucoma,
 CC associated with genes at 8q24 or 10p1 and primary congenital glaucoma
 CC (PCG), associated with gene CYP1B1, but more generally for any form of
 CC the disease having a genetic cause. Glaucoma can be treated with non-
 CC mutant forms of the glaucoma-associated protein (or its mimics) and the
 CC encoding gene, or antibodies or correction of a mutation by heterologous
 CC recombination. Gene therapy methods can be applied in vivo or cells are
 CC transfected ex vivo and then returned to the patient. The method allows
 CC diagnosis, and treatment, at an early stage, before significant damage to
 CC the optical nerve has occurred. Identification of particular mutations
 CC allows optimisation of treatment

Qy 19 ACCTGGTAAA 28
 Db 1 ACCAGGTAAA 10

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTCCTGTGTG 18
 Db 1 CTCCTGTGTG 10

RESULT 314
 AAZ18803
 ID AAZ18803 standard; DNA; 11 BP.
 XX
 AC AAZ18803;

RESULT 313
 AAZ18975
 ID AAZ18975 standard; DNA; 11 BP.
 XX
 AC AAZ18975;
 XX
 DT 22-OCT-1999 (first entry)
 XX
 DE Murine MRL SAGE tag 1998778.
 XX
 KW Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
 KW healing response; microsatellite marker; treatment; central nerve;
 KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
 XX
 OS Mus sp.
 XX
 PN WO9941364-A2.
 XX
 PD 19-AUG-1999.
 XX
 PF 12-FEB-1999; 99WO-US002962.
 XX
 PR 13-FEB-1998; 98US-0074737P.
 PR 26-AUG-1998; 98US-0097937P.
 PR 28-SEP-1998; 98US-0102051P.
 XX
 PA (WIST-) WISTAR INST.
 XX
 PI Heber-Katz E;
 XX
 WPI; 1999-494533/41.
 XX
 DR New mammalian model for enhanced wound healing - useful for identifying
 PT enhanced wound healing genes.
 XX
 PS Claim 13; Page 73; 136pp; English.
 XX
 CC This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.
 CC The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AAZ18691-219036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention

Qy Sequence 11 BP; 0 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
 Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTCCTGTGTG 18
 Db 1 CTCCTGTGTG 10

RESULT 314
 AAZ18803
 ID AAZ18803 standard; DNA; 11 BP.
 XX
 AC AAZ18803;

XX 22-OCT-1999 (first entry)
 XX Murine C57BL/6 SAGE tag 1998778.
 DE Wound healing; non-MRL healer mouse; quantitative trait locus; QTL;
 KW healing response; microsatellite marker; treatment; central nerve;
 KW peripheral nerve; nerve injury; SAGE tag; murine; ss.
 XX Mus sp.
 OS WO9941364-A2.
 XX 19-AUG-1999.
 FD 12-FEB-1999; 99WO-US002962.
 XX 13-FEB-1998; 98US-0074737P.
 PR 26-AUG-1998; 98US-0097937P.
 PR 28-SEP-1998; 98US-0102051P.
 XX (WIST-) WISTAR INST.
 PA Heber-Katz E;
 XX WPI; 1999-494533/41.
 DR New mammalian model for enhanced wound healing - useful for identifying
 XX enhanced wound healing genes.
 XX Claim 13; Page 57; 136pp; English.
 XX This invention describes a novel non-MRL healer mouse (M) having at least
 CC one quantitative trait locus selected from those given in the
 CC specification, exhibiting an enhanced healing response to a wound
 CC compared to mice (m) without the locus. The invention describes a novel
 CC method of identifying a gene involved in enhanced wound healing by
 CC identifying DNA microsatellite markers which can distinguish healer mice
 CC from non-healer mice and identifying microsatellite markers which
 CC segregate with enhanced wound healing in progeny of the mice, where a
 CC chromosomal locus containing at least one enhanced wound healing gene is
 CC identified. A method of treating a wound in a mammal is also disclosed.
 CC The new methods are useful for treating wounds, especially central and
 CC peripheral nerve wound. The methods of the invention are useful for
 CC restoring function after nerve injury in a mammal. (M) is useful as a
 CC mammalian model of enhanced wound healing, useful for identifying genes
 CC and gene products involved in enhanced wound healing, and to provide
 CC methods for wound healing. AA218691-219036 represent murine SAGE tags
 CC from C57BL/6 and MRL mice which are used to illustrate the method of the
 CC invention
 XX SQ Sequence 11 BP; 0 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 CTGCTGTGTG 18
 Db 1 CTGCTTTGTG 10
 RESULT 315
 AAA16608/c
 ID AAA16608 standard; DNA; 11 BP.
 XX AAA16608;
 AC 16-JUN-2000 (first entry)
 XX Human MN gene 3' acceptor consensus splice sequence SEQ ID NO:86.
 DE Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
 XX

KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
 KW MN/CA IX isoenzyme; ds.
 XX Homo sapiens.
 XX US6027887-A.
 XX 22-FEB-2000.
 XX 24-JAN-1997; 97US-00787739.
 XX 21-OCT-1992; 92US-00964589.
 PR 30-DEC-1993; 93US-00177093.
 PR 15-JUN-1994; 94US-00260190.
 PR 07-JUN-1995; 95US-00477504.
 PR 07-JUN-1995; 95US-00481658.
 PR 07-JUN-1995; 95US-00485049.
 PR 07-JUN-1995; 95US-00485862.
 PR 07-JUN-1995; 95US-00485863.
 PR 07-JUN-1995; 95US-00486756.
 PR 07-JUN-1995; 95US-00487077.
 XX (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
 PA Pastorek J, Zavada J, Pastorekova S;
 PI WPI; 2000-194827/17.
 DR Nucleic acid based assay for diagnosing a wide variety of
 XX preneoplastic/neoplastic disease comprises screening for the presence of
 PT abnormal MN gene expression in a vertebrate.
 XX Disclosure; Col 16; 87pp; English.
 XX The present invention describes a method of screening for
 CC preneoplastic/neoplastic disease. The method comprises: (1) determining
 CC whether abnormal MN gene expression is present in a vertebrate; and (2)
 CC if abnormal MN gene expression is determined to be present in the
 CC vertebrate, determining that the vertebrate has a significant risk of
 CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and
 CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
 CC protein is a tumour associated carbonic anhydrase isoenzyme. The method
 CC is used for detecting a wide variety of preneoplastic/neoplastic diseases
 CC in a vertebrate, preferably a human. The disease detected is mammary,
 CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
 CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
 CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,
 CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
 CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
 CC mucosa, pancreatic duct epithelium or liver duct epithelium
 CC preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AA53228 to
 CC AA53245 represent sequences used in the exemplification of the present
 CC invention
 XX SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CCTGCTGTGT 17
 Db 10 CCTCTGTGT 1
 RESULT 316
 AAA52527/c
 ID AAA52527 standard; DNA; 11 BP.
 XX AAA52527;
 AC 25-SEP-2000 (first entry)
 XX

DE Human MN gene intron 10 splice acceptor sequence.

XX MN protein; tumour associated cell adhesion molecule; oncoprotein;

XX proteoglycan domain; PG domain; carbonic anhydrase; CA domain;

KW abnormal expression; neoplastic disease; cancer; gene therapy; ds.

XX Homo sapiens.

OS

XX WO200024913-A2.

XX

XX 04-MAY-2000.

XX

XX 22-OCT-1999; 99WO-US024879.

XX

XX 23-OCT-1998; 98US-00177776.

XX

XX 23-OCT-1998; 98US-00178115.

XX

XX (FARB) BAYER CORP.

PA (VIRO-) INST VIROLOGY.

XX

XX Zavada J, Pastorekova S, Pastorek J;

XX

XX WPI; 2000-350752/30.

XX

XX A molecule which specifically binds to a site on MN protein (oncoprotein)

PT and prevents adhesion of vertebrate cells to the protein, useful for

PT treating preneoplastic or neoplastic diseases such as cancer.

XX

XX Disclosure; Page 26; 154pp; English.

XX

XX The invention relates to the inhibition of cell adhesion mediated by the

CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250

CC protein). The MN protein is a tumour-associated adhesion molecule which

CC comprises a proteoglycan-like (PG) domain (AA803017) which contains the

CC protein's binding site, and a carbonic anhydrase (CA) domain (AA803018).

CC Abnormal expression of the MN protein is associated with tumorigenicity.

CC The invention encompasses molecules (e.g., proteins and peptides) which

CC which specifically bind to a site on the MN protein, thereby preventing

CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It

CC also encompasses MN proteins or MN protein fragments which can be added

CC to the extracellular environment to prevent the adhesion of vertebrate

CC cells to each other. The invention also relates to the identification of

CC the binding site of the MN protein and to a method of identifying a site

CC on an MN protein to which cells adhere, comprising testing a series of

CC overlapping peptides from the protein in a cell adhesion assay. The

CC invention encompasses a vector comprising an expression control sequence

CC operatively linked to a nucleic acid encoding the variable domains of a

CC MN-specific antibody, where the domains are separated by a flexible

CC linker peptide (AA803035) and the vector inhibits the growth of a

CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN

CC protein. The invention also encompasses a vector comprising a nucleic

CC acid encoding a cytotoxic protein or peptide operatively linked to the MN

CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or

CC neoplastic cell. Also claimed is a repressor complex that binds to the MN

CC gene promoter (AA52473). MN proteins and peptides, MN-binding proteins

CC and peptides, and expression vectors encoding such proteins and peptides

CC are useful for treating patients with preneoplastic or neoplastic disease

CC (e.g., cancers) associated with or characterised by abnormal MN

CC expression. The present sequence represents a fragment of the human MN

CC gene (AA52462) specified in the invention

XX

SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.8e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17

Db 10 CCTTCTGTGT 1

RESULT 317

AAF75228

ID AAF75228 standard; DNA; 11 BP.

XX

AC AAF75228;

XX

DT 09-MAY-2001 (first entry)

XX

DE Human RXR binding element, SEQ ID NO: 28.

XX

XX Human; peroxisome proliferator-activator receptor delta; PPARGdelta; RXR;

KW cytosolic; neotropic; neuroprotective; anti-HIV; cardiant;

KW cerebroprotective; vasotropic; antitumor; immunosuppressive;

KW nephrotropic; antibacterial; antiviral; antifungal; protozoacide;

KW non-steroidal anti-inflammatory disease; NSAID; infection;

KW Alzheimer's disease; AIDS; muscle wasting disease; autoimmune disease;

XX binding element; ds.

XX

OS Homo sapiens.

XX

XX WO200112858-A1.

XX

XX 22-FEB-2001.

PD

XX

XX 16-AUG-2000; 2000WO-US022411.

PF

XX

XX 16-AUG-1999; 99US-0148701P.

PR

PR 15-AUG-2000; 2000US-00638623.

XX

XX (UYJO) UNIV JOHNS HOPKINS.

PA

XX

XX He T, Kinzler KW, Vogelstein B;

PI

XX WPI; 2001-211236/21.

DR

XX

PT Novel subgenomic polynucleotide having peroxisome proliferator-activator

PT receptor proliferator (PPAR-delta) and RXR binding elements used to

PT identify downregulators of PPAR-delta transcriptional activity.

XX

XX Claim 1; Fig 3A; 70pp; English.

XX

CC The present sequence is provided in a specification relating to an

CC isolated subgenomic polynucleotide comprising a peroxisome proliferator-

CC activator receptor (PPAR)delta binding element and an RXR binding

CC element. The polynucleotide is useful for identifying potential

CC therapeutic agents for cancer treatment and for ameliorating negative

CC side effects of non-steroidal anti-inflammatory diseases (NSAIDs). Test

CC compounds which increase transcription of PPARGdelta protein, PPARGdelta

CC protein binding to a PPARGdelta binding element, or expression of a

CC reporter gene which is under the control of a PPARGdelta binding element,

CC are identified. These are candidates for use in encouraging cell

CC proliferation or preventing cell apoptosis in a disease state such as

CC Alzheimer's disease, AIDS, muscular dystrophy, amyotrophic lateral

CC sclerosis, or other muscle wasting diseases, autoimmune diseases, heart

CC attack, stroke, ischaemic heart disease, kidney failure, septic shock, or

CC a disease in which the cell is infected with a pathogen, such as a virus,

CC bacterium, fungus, mycoplasma, or protozoan, to promote healing of the

CC stomach or intestines, or to ameliorate negative side effects of NSAIDs,

CC such as gastric and intestinal ulceration

XX

SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 1.8e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAAT 29

Db 1 CCTGGTCAAT 10

RESULT 318

ABQ86838/c

ID ABQ86838 standard; cDNA; 11 BP.

```
XX AC ABQ86838;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 593.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
XX PS Claim 8; Page 61; 325pp; German.
XX
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACTGTC 12
DB 10 ATCCAACCTGC 1
|||||
|||||

RESULT 319
ABQ86763/C
ID ABQ86763 standard; cDNA; 11 BP.
XX
XX AC ABQ86763;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 518.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACTGTC 12
DB 10 ATCCAACCTGC 1
|||||
|||||

RESULT 319
ABQ86763/C
ID ABQ86763 standard; cDNA; 11 BP.
XX
XX AC ABQ86990;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 745.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
XX PS Claim 8; Page 68; 325pp; German.
XX
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
```

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XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
XX PS Claim 8; Page 58; 325pp; German.
XX
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
CC or animals, are important for skin ageing and/or skin stress by serial
CC analysis of gene expression between mixtures of transcribed and
CC optionally translated, genetically encoded factors (A) obtained from
CC young and aged skin, to identify that genes that show strong differential
CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
CC useful for: identifying markers of skin ageing and/or stress; determining
CC skin ageing and/or stress; and identifying or determining the effects of
CC pharmaceutical or cosmetic agents for control of skin ageing. The present
CC sequence is one of a group of human skin ageing/stress related expressed
CC sequence tags (ABQ86246-ABQ87680) of the invention
XX
XX SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
DB 11 CCTCCTGTGT 2
|||||
|||||

RESULT 320
ABQ86990
ID ABQ86990 standard; cDNA; 11 BP.
XX
XX AC ABQ86990;
XX
XX DT 10-SEP-2002 (first entry)
XX
XX DE Human skin stress/ageing related EST SEQ ID NO 745.
XX
XX KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200253773-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-EP015178.
XX
XX PR 03-JAN-2001; 2001DE-01000121.
XX
XX PA (HENK ) HENKEL KGAA.
XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX
XX DR WPI; 2002-528865/56.
XX
XX PT Identifying genes involved in skin stress and aging, useful e.g. in
PT screening for cosmetic or therapeutic agents, based on differential gene
PT expression.
XX
XX PS Claim 8; Page 68; 325pp; German.
XX
XX CC The invention relates to identifying (M1) genes in vitro that, in humans
```

CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 XX
 SQ Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 ATCCACCTGC 12
 Db 1 ATCCGCCTGC 10
 |||||
 |||||

RESULT 321
 ABQ87167/C
 ID ABQ87167 standard; cDNA; 11 BP.
 XX
 AC ABQ87167;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 922.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 FN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.

Claim 8; Page 75; 325pp; German.
 XX
 PS The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 6 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 16 GTGACCTGGT 25
 Db 10 GTGGCCTGGT 1
 |||||
 |||||

RESULT 322
 ABQ87430
 ID ABQ87430 standard; cDNA; 11 BP.
 XX
 AC ABQ87430;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 1185.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 FN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX

Identifying genes involved in skin stress and aging, useful e.g. in
 screening for cosmetic or therapeutic agents, based on differential gene
 expression.
 PS Claim 8; Page 86; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 TCACCTGGT 13
 Db 2 TCACGCTGGT 11
 |||||
 |||||

RESULT 323
 ABQ86674
 ID ABQ86674 standard; cDNA; 11 BP.
 XX
 AC ABQ86674;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 429.
 XX

KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253773-A2.
 FN 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000121.
 XX (HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-528865/56.
 XX Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 XX Claim 8; Page 54; 325pp; German.
 XX The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present
 CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX Sequence 11 BP; 2 A; 7 C; 1 G; 1 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ATCCACCTGC 12
 DB 1 ATCCACCTGC 10
 RESULT 324
 ABV63315
 ID ABV63315 standard; cDNA; 11 BP.
 AC ABV63315;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 1101.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 FN 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 130; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ATCCACCTGC 12
 DB 1 ATCCACCTGC 10
 RESULT 325
 ABV66003/C
 ID ABV66003 standard; cDNA; 11 BP.
 AC ABV66003;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 3789.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 FN 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 130; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)

PI Petersohn D, Conradt M, Hofmann K;
 XX WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 55; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX Sequence 11 BP; 1 A; 6 C; 2 G; 2 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ATCCACCTGC 12
 DB 1 ATCCACCTGC 10
 RESULT 325
 ABV66003/C
 ID ABV66003 standard; cDNA; 11 BP.
 AC ABV66003;
 XX 21-OCT-2002 (first entry)
 DT Human skin EST 3789.
 DE Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX Homo sapiens.
 OS WO200253774-A2.
 FN 11-JUL-2002.
 XX 20-DEC-2001; 2001WO-EP015179.
 XX 03-JAN-2001; 2001DE-01000127.
 XX (HENKEL KGAA.
 PA Petersohn D, Conradt M, Hofmann K;
 PI WPI; 2002-590638/63.
 XX In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX Disclosure; Page 130; 1345pp; German.
 XX The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)

PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 40; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 TCCACCTGCT 13
 DB 11 TCCACCTCCT 2
 |||||
 RESULT 331
 ABV62815/c
 ID ABV62815 standard; cDNA; 11 BP.
 XX
 AC ABV62815;
 XX
 XX Human skin EST 601.
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 601.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 601.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 XX WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 42; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;

CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CCTGCTGTGT 17
 DB 11 CCTCCTGTGT 2
 |||||
 RESULT 332
 ABV69214
 ID ABV69214 standard; cDNA; 11 BP.
 XX
 AC ABV69214;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 7000.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 XX WPI; 2002-590638/63.
 XX
 In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 220; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 TCGTGTGTCA 19
 |||||

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Db      2 TGCTGCTGTA 11

RESULT 333
ABV70185/c
ID      ABV70185 standard; cDNA; 11 BP.
XX
AC      ABV70185;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 7971.
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
PN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX
PA      (HENK ) HENKEL KGAA.
XX
PI      Petersohn D, Conradt M, Hofmann K;
XX
WPI; 2002-590638/63.
XX
In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
PS      Claim 24; Page 254; 1345pp; German.
XX
CC      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
SQ      Sequence 11 BP; 4 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TCCACCTGCT 13
Db      11 TCCACCTCCT 2

RESULT 334
ABV70837/c
ID      ABV70837 standard; cDNA; 11 BP.
XX
AC      ABV70837;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 8623.
XX

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KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
PN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX
PA      (HENK ) HENKEL KGAA.
XX
PI      Petersohn D, Conradt M, Hofmann K;
XX
WPI; 2002-590638/63.
XX
In vitro identification of skin-expressed genes, useful for determining
PT      homeostasis and identifying cosmetic or pharmaceutical agents against
PT      e.g. skin cancer.
XX
PS      Claim 24; Page 276; 1345pp; German.
XX
CC      The invention relates to in vitro identification (M1) of genes expressed
CC      in the skin of humans or animals by subjecting a mixture of genetically
CC      encoded factors from skin, to serial analysis of gene expression (SAGE)
CC      so as to identify skin-expressed genes and quantify their expression.
CC      (M1) is useful for identifying genes involved in skin homeostasis; to
CC      determine skin homeostasis and to test agent (A) that maintains or
CC      promotes skin homeostasis or that can be used for treating skin
CC      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
CC      ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
CC      rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
CC      skin. The present sequence is that of a human expressed sequence tag
CC      (EST) of the invention
XX
SQ      Sequence 11 BP; 6 A; 3 C; 2 G; 0 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGCTG 17
Db      10 CTTGCTGCTG 1

RESULT 335
ABV65404
ID      ABV65404 standard; cDNA; 11 BP.
XX
AC      ABV65404;
XX
DT      21-OCT-2002 (first entry)
XX
DE      Human skin EST 3190.
XX
KW      Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
KW      immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW      psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
OS      Homo sapiens.
XX
PN      WO200253774-A2.
XX
PD      11-JUL-2002.
XX
PF      20-DEC-2001; 2001WO-EP015179.
XX
PR      03-JAN-2001; 2001DE-01000127.
XX

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RESULT 339
ABV70736

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XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 168; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 1.8e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4 TCCACCTGGT 13
XX DB 11 TCCACCTGGT 2
XX
XX RESULT 342
XX ABV67423
XX ID ABV67423 standard; cDNA; 11 BP.
XX AC ABV67423;
XX XX
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 5209.
XX XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200253774-A2.
XX XX
XX PD 11-JUL-2002.
XX XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX XX
XX PA (HENKEL KGAA.
XX XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX
XX DR WPI; 2002-590638/63.
XX XX
XX PT In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 169; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 0 A; 2 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 1.8e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 9 CTGCTGTGTG 18
XX DB 1 CTCTGTGTG 10
XX
XX RESULT 341
XX ABV67400/C
XX ID ABV67400 standard; cDNA; 11 BP.
XX AC ABV67400;
XX XX
XX DT 21-OCT-2002 (first entry)
XX DE Human skin EST 5186.
XX XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
XX KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX XX
XX PN WO200253774-A2.
XX XX
XX PD 11-JUL-2002.
XX XX
XX PF 20-DEC-2001; 2001WO-EP015179.
XX XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX XX
XX PA (HENKEL KGAA.
XX XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX

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CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 TCCACCTGCT 13
 Db 2 TCCACCTGCT 11
 |||||
 |||||
 RESULT 343
 ABV70236/C
 ID ABV70236 standard; cDNA; 11 BP.
 XX
 AC ABV70236;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 8022.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Claim 24; Page 255; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
 |||||
 Db 11 CCTCCTGTGT 2
 |||||
 |||||
 RESULT 344
 ABV63416/C
 ID ABV63416 standard; cDNA; 11 BP.
 XX
 AC ABV63416;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 1202.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhaeic;
 KW immunosuppressive; antinflammatory; cytosatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 58; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 6 A; 3 C; 2 G; 0 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 8 CCTGCTGTGT 17
 |||||
 Db 10 CTTCCTGTGT 1
 |||||
 |||||
 RESULT 345
 ABV64243/C
 ID ABV64243 standard; cDNA; 11 BP.
 XX
 AC ABV64243;
 XX
 DT 21-OCT-2002 (first entry)


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XX DE Human skin EST 2029.
XX DE
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antinflammatory; cystostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Conradt M, Hofmann K;
XX DR WPI; 2002-590638/63.
XX XX
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 81; 1345pp; German.
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 1.8e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 3 ATCCACCTGC 12
DB 10 ATCCAACTGC 1
|||||
|

RESULT 346
ABV67475/c
ID ABV67475 standard; cDNA; 11 BP.
XX
XX AC ABV67475;
XX XX
XX DT 21-OCT-2002 (first entry)
XX XX
XX DE Human skin EST 5261.
XX XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antinflammatory; cystostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX XX

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PF 20-DEC-2001; 2001WO-EP015179.
XX XX
XX PR 03-JAN-2001; 2001DE-01000127.
XX XX
XX PA (HENK ) HENKEL KGAA.
XX XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX
XX DR WPI; 2002-590638/63.
XX XX
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.
XX PS Disclosure; Page 170; 1345pp; German.
XX XX
XX CC The invention relates to in vitro identification (M1) of genes expressed
XX CC in the skin of humans or animals by subjecting a mixture of genetically
XX CC encoded factors from skin, to serial analysis of gene expression (SAGE)
XX CC so as to identify skin-expressed genes and quantify their expression.
XX CC (M1) is useful for identifying genes involved in skin homeostasis; to
XX CC determine skin homeostasis and to test agent (A) that maintains or
XX CC promotes skin homeostasis or that can be used for treating skin
XX CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX CC skin. The present sequence is that of a human expressed sequence tag
XX CC (EST) of the invention
XX SQ Sequence 11 BP; 2 A; 5 C; 2 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 11;
XX Best Local Similarity 90.0%; Pred. No. 1.8e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 17 TGACCTGGTA 26
DB 11 TGACCTGGGA 2
|||||
|

RESULT 347
ABV71664/c
ID ABV71664 standard; cDNA; 11 BP.
XX
XX AC ABV71664;
XX XX
XX DT 21-OCT-2002 (first entry)
XX XX
XX DE Human skin EST 9450.
XX XX
XX KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrhoeic;
XX KW immunosuppressive; antinflammatory; cystostatic; SAGE; neurodermatitis;
XX KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX OS Homo sapiens.
XX PN WO200253774-A2.
XX PD 11-JUL-2002.
XX PF 20-DEC-2001; 2001WO-EP015179.
XX PR 03-JAN-2001; 2001DE-01000127.
XX XX
XX PA (HENK ) HENKEL KGAA.
XX XX
XX PI Petersohn D, Conradt M, Hofmann K;
XX XX
XX DR WPI; 2002-590638/63.
XX XX
XX XX In vitro identification of skin-expressed genes, useful for determining
XX PT homeostasis and identifying cosmetic or pharmaceutical agents against
XX PT e.g. skin cancer.

```

XX Claim 24; Page 305; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

 Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 3 ATCCACCTGC 12
 Db 10 ATCCAACTGC 1
 ||||| ||||

 RESULT 348
 ABV67586
 ID ABV67586 standard; cDNA; 11 BP.
 AC
 AC ABV67586;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 5372.
 XX
 KW Human; skin; dermatological; vulnary; antipsoriatic; antiseborrhoeic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Disclosure; Page 173; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the

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RESULT 350
AAD40434
ID AAD40434 standard; DNA; 11 BP.
XX AC
XX AC AAD40434;
XX DT
XX DT 22-OCT-2002 (first entry)
XX DE
XX DE Bovine DGAT1 gene fragment #11.
XX KW
XX KW Bovine, diacylglycerol acyltransferase; genotyping; milk production;
XX KW DGAT1; polymorphism; farming industry; transgenic; ds.
XX OS
XX OS Bos taurus.
XX PN
XX PN WO200236824-A1.
XX PD
XX PD 10-MAY-2002.
XX PF
XX PF 31-OCT-2001; 2001WO-NZ000245.
XX PR
XX PR 31-OCT-2000; 2000NZ-00507888.
XX PR 06-DEC-2000; 2000NZ-00508662.
XX PA
XX PA (GEOR/) GEORGES M A J.
XX PA (COPP/) COPPIETERS W H R.
XX PA (GRIS/) GRISART B M J.
XX PA (SNEL/) SNELL R G.
XX PA (REID/) REID S J.
XX PA (FORD/) FORD C A.
XX PA (SPEL/) SPELMAN R J.
XX PI
XX PI Georges MAJ, Coppieters WHR, Grisart BMJ, Snell RG, Reid SJ;
XX PI Ford CA, Spelman RJ;
XX DR
XX DR WPI; 2002-500128/53.
XX PT
XX PT Determining genetic merit of a bovine with respect to milk composition
XX PT and volume for improved milk production, comprises determining the
XX PT diacylglycerol acyltransferase gene genotypic state of the bovine.
XX PS
XX PS Claim 4; Page 8; 128pp; English.
XX CC
XX CC The invention relates to a method of genotyping bovine for improved milk
XX CC production traits which comprises determining the diacylglycerol
XX CC acyltransferase (DGAT1) genotypic state of the bovine, wherein the DGAT1
XX CC gene and polymorphisms have been found to be associated with such
XX CC improved milk production traits. The method is useful for selecting a
XX CC bovine having a desired DGAT1 genotypic state. It is also useful for the
XX CC identification and selection of a bovine having one of the polymorphisms
XX CC in its DGAT1 gene. Milk produced from selected bovine which is useful for
XX CC making a dairy product provides a beneficial health effect. An antibody
XX CC to the protein having DGAT1 activity is useful for inhibiting the
XX CC activity of bovine DGAT1 in a lactating bovine so as to modulate milk
XX CC production and/or milk solids content. DGAT1 nucleic acid and its
XX CC fragments are useful in the farming industry. They are also useful to
XX CC generate transgenic animals which are useful to investigate the molecular
XX CC basis of DGAT1 action and to test a substance for the ability to prevent,
XX CC slow or enhance DGAT1 activity. The present sequence is bovine DGAT1 gene
XX CC fragment. This sequence is used to illustrate the method of the invention
XX SQ
XX SQ Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 GTGTGACCTG 23
DB 1 GAGTGACCTG 10
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RESULT 351
ABV78654
ID ABV78654 standard; DNA; 11 BP.
XX AC
XX AC ABV78654;
XX DT
XX DT 26-NOV-2002 (first entry)
XX DE
XX DE RXR binding site from clone X9TOP.
XX KW
XX KW PPARdelta; peroxisome proliferator-activated receptor delta; nootropic;
XX KW neuroprotective; anti-HIV; cardiant; cytostatic; antiinflammatory;
XX KW immunosuppressive; cerebroprotective; gene therapy; inflammation; cancer;
XX KW Alzheimer's disease; AIDS; muscular dystrophy; autoimmune disease;
XX KW heart attack; stroke; fecundity; RXR; ds.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200268386-A2.
XX PD
XX PD 06-SEP-2002.
XX PF
XX PF 27-FEB-2002; 2002WO-US003408.
XX PR
XX PR 27-FEB-2001; 2001US-0271412P.
XX PA
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI
XX PI Park BH, Kinzler KW, Vogelstein B;
XX DR
XX DR WPI; 2002-691649/74.
XX PT
XX PT Homozygous PPAR gene-defective cell line, useful for treating
XX PT inflammation and cancer and disorders associated with premature cell
XX PT death such as Alzheimer's disease, AIDS, muscular dystrophy, autoimmune
XX PT diseases and heart attacks.
XX PS
XX PS Example 2; Fig 6; 33pp; English.
XX CC
XX CC The invention relates to a novel homoygous peroxisome proliferator-
XX CC activated receptor delta (PPARdelta) gene-defective cell line. The
XX CC compositions of the invention have nootropic, neuroprotective, anti-HIV,
XX CC cardiant, cytostatic, antiinflammatory, immunosuppressive, and
XX CC cerebroprotective activity. The cell lines may have a use in gene
XX CC therapy. The methods and compositions are useful for treating
XX CC inflammation and cancer and other disorders with increased cell
XX CC proliferation or in which cells are dying prematurely such as Alzheimer's
XX CC disease, AIDS, muscular dystrophy, autoimmune diseases, heart attack and
XX CC stroke, improving fecundity and/or ameliorating toxic effects of non-
XX CC steroidal antiinflammatory drugs. The sequence represents a PCR product
XX CC of an oligonucleotide template that bound a fusion protein containing the
XX CC DNA binding domain of RXR
XX SQ
XX SQ Sequence 11 BP; 2 A; 3 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 20 CCTGGTAAAT 29
DB 1 CCTGGTCAAT 10
```

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RESULT 352
ADG13667/c
ID ADG13667 standard; RNA; 11 BP.
XX AC
XX AC ADG13667;
XX DT
XX DT 26-FEB-2004 (first entry)
XX DE
XX DE Human EGFR Amberzyme target sequence #15.
```

XX Human; ss; EGFR; epidermal growth factor receptor; HER1; HER2; HER3;
KW HER4; hammerhead ribozyme; inozyme; zinzyme; DNazyme; amberyzyme; cancer;
KW brain tumour; cytostatic; short interfering RNA; siRNA; RNA interference;
KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
KW multidrug resistant cancer.
XX Homo sapiens.
XX US2003186909-A1.
XX 02-OCT-2003.
XX 21-OCT-2002; 2002US-00277494.
XX 27-JAN-1997; 97US-0036749P.
XX 04-DEC-1997; 97US-00985162.
XX 22-SEP-1999; 99US-00401063.
XX 03-MAY-2001; 2001US-00848754.
XX 25-JUL-2001; 2001US-00916466.
XX (RIBO-) RIBOZYME PHARM INC.
XX Mswiggen J;
XX WPI; 2004-032029/03.
XX New double stranded short interfering ribonucleic acid molecule for
PT inhibiting expression of epidermal growth factor receptor gene.
XX Claim 7; SEQ ID NO 94; 113pp; English.
XX The invention relates to a double stranded short interfering RNA (siRNA)
CC molecule that inhibits expression of epidermal growth factor receptor
CC (EGFR) gene (e.g. HER1-4) by RNA interference is new. Also included is an
CC expression vector comprising a nucleic acid sequence encoding siRNA
CC molecule(s) in a manner that allows expression of the nucleic acid
CC amberyzymes zinzymes and DNazymes. The invention is used for inhibiting
CC expression of EGFR. It can be used for treatment of cancer, prostate
CC cancer, colorectal cancer, brain cancer, oesophageal cancer, stomach
CC cancer, bladder cancer, pancreatic cancer, cervical cancer, head and neck
CC cancer, ovarian cancer, melanoma, lymphoma, glioma, multidrug resistant
CC cancer or a brain tumour. The invention has enhanced shelf-life, half-
CC life in vitro, stability, and ease of introduction of oligonucleotide to
CC target site. The present sequence is an EGFR/HER1-4 target sequence for
CC an siRNA of the invention.
XX
XX Sequence 11 BP; 3 A; 1 C; 5 G; 0 T; 2 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCATCCCACT 10
Db 10 CCATCCCACT 1
RESULT 353
ADK41836/c
ID ADK41836 standard; DNA; 11 BP.
XX
XX ADR41836;
XX 06-MAY-2004 (first entry)
XX Human MN gene intron-exon boundary sequence SeqID65.
XX carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
XX human; vertebrate; cytostatic; vaccine; gene therapy;
KW

KW renal cell carcinoma; breast cancer; colorectal cancer; splice acceptor;
KW ds.
XX Homo sapiens.
XX WO2004005348-A1.
XX 15-JAN-2004.
XX 22-FEB-2003; 2003WO-US005137.
XX 23-MAY-2002; 2002US-0383068P.
XX 05-DEC-2002; 2002US-0431499P.
XX (FARB) BAYER CORP.
XX (VIRO-) INST VIROLOGY.
XX Zavada J, Pastorekova S, Pastorek J, Zavadvova Z;
XX WPI; 2004-083500/08.
XX New soluble form of the carbonic anhydrase IX (CA IX) protein for
PT screening, diagnosing or prognosing diseases associated with abnormal
PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
PT colorectal cancer.
XX Disclosure; SEQ ID NO 65; 159pp; English.
XX This invention relates to a novel soluble form of the carbonic anhydrase
CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
CC precancerous and/or cancerous cells of a vertebrate into a body fluid.
CC The invention may be useful for the development of compounds with a
CC cyostatic activity or a vaccine whilst the disclosed sequences may be
CC used for gene therapy. The protein and method are useful for screening,
CC diagnosing or prognosing diseases associated with abnormal expression of
CC carbonic anhydrase IX protein, such as precancerous and cancerous
CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.
CC The monoclonal antibody may also be used for treating or preventing
CC precancerous and cancerous diseases. The present sequence is that of a
CC splice acceptor site from a human MN gene intron-exon boundary which is
CC related to the invention.
XX
XX Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CCTGCTGTGT 17
Db 10 CCTGCTGTGT 1
RESULT 354
ADQ35801/c
ID ADQ35801 standard; DNA; 11 BP.
XX
XX ADQ35801;
XX 23-SEP-2004 (first entry)
XX Human hair-bearing skin-associated DNA fragment SEQ ID NO 618.
XX hair-bearing skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX Homo sapiens.
XX DE10260931-A1.
XX 08-JUL-2004.
XX 20-DEC-2002; 2002DE-01060931.
XX

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XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PT Conradt M, Hofmann K;
XX PT WPI; 2004-518857/50.
XX PS Claim 5; SEQ ID NO 618; 250pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for hair-bearing skin in humans. The method
XX CC comprises recovering, from hair-bearing skin, a first mixture of
XX CC genetically expressed (transcribed and optionally translated) factors
XX CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
XX CC mixture from skin on which hair does not grow and subjecting both
XX CC mixtures to serial analysis of gene expression (SAGE) to identify those
XX CC genes for which expression is markedly different between the two types of
XX CC skin. The invention also describes in vitro methods for determining
XX CC homeostasis of human hair-bearing skin and for determining activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
XX CC a test kit comprising a solid support (flexible or rigid) with
XX CC immobilised probes are also described for determining homeostasis. The
XX CC hair-bearing skin is from the scalp and the other skin is from the face.
XX CC The method allows identification of as many as possible of the genes
XX CC important for hair-bearing skin, and therefore, of a very wide range of
XX CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
XX CC human DNA Tag fragments used to identify genes associated with hair-
XX CC bearing skin.
XX SQ Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
    Query Match      29.0%; Score 8.4; DB 1; Length 11;
    Best Local Similarity 90.0%; Pred. No. 1.8e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 TCCACCTGCT 13
Db 11 TCCACCTGGT 2

RESULT 355
ADQ35910
ID ADQ35910 standard; DNA; 11 BP.
XX AC ADQ35910;
XX DT 23-SEP-2004 (first entry)
XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 727.
XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX OS Homo sapiens.
XX PN DE10260931-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060931.
XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PT Conradt M, Hofmann K;
XX PT WPI; 2004-518857/50.

XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PT Conradt M, Hofmann K;
XX PT WPI; 2004-518857/50.
XX PS Claim 5; SEQ ID NO 727; 250pp; German.
XX CC This invention describes a novel in vitro method for identifying genes
XX CC that are significant for hair-bearing skin in humans. The method
XX CC comprises recovering, from hair-bearing skin, a first mixture of
XX CC genetically expressed (transcribed and optionally translated) factors
XX CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
XX CC mixture from skin on which hair does not grow and subjecting both
XX CC mixtures to serial analysis of gene expression (SAGE) to identify those
XX CC genes for which expression is markedly different between the two types of
XX CC skin. The invention also describes in vitro methods for determining
XX CC homeostasis of human hair-bearing skin and for determining activity of
XX CC cosmetic and pharmaceutical agents for use against disorders or
XX CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
XX CC a test kit comprising a solid support (flexible or rigid) with
XX CC immobilised probes are also described for determining homeostasis. The
XX CC hair-bearing skin is from the scalp and the other skin is from the face.
XX CC The method allows identification of as many as possible of the genes
XX CC important for hair-bearing skin, and therefore, of a very wide range of
XX CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
XX CC human DNA Tag fragments used to identify genes associated with hair-
XX CC bearing skin.
XX SQ Sequence 11 BP; 3 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
    Query Match      29.0%; Score 8.4; DB 1; Length 11;
    Best Local Similarity 90.0%; Pred. No. 1.8e+02;
    Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ATCCACCTGC 12
Db 1 ACCCAGCTGC 10

RESULT 356
ADQ35843/C
ID ADQ35843 standard; DNA; 11 BP.
XX AC ADQ35843;
XX DT 23-SEP-2004 (first entry)
XX DE Human hair-bearing skin-associated DNA fragment SEQ ID NO 660.
XX KW hair-bearing skin; human; serial analysis of gene expression; SAGE;
XX KW homeostasis; cosmetic; pharmaceutical; biochip; ds.
XX OS Homo sapiens.
XX PN DE10260931-A1.
XX PD 08-JUL-2004.
XX PF 20-DEC-2002; 2002DE-01060931.
XX PR 20-DEC-2002; 2002DE-01060931.
XX PA (HENK ) HENKEL KGAA.
XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX PT Conradt M, Hofmann K;
XX PT WPI; 2004-518857/50.

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PT In vitro identification of genes important for hair-bearing skin, useful
PT for assessing homeostasis and in screening for pharmaceutical or cosmetic
XX agents, based on differential expression analysis.

PS Claim 5; SEQ ID NO 660; 250pp; German.

XX This invention describes a novel in vitro method for identifying genes
CC that are significant for hair-bearing skin in humans. The method
CC comprises recovering, from hair-bearing skin, a first mixture of
CC genetically expressed (transcribed and optionally translated) factors
CC (i.e. proteins, mRNA or their fragments), recovering a second, similar
CC mixture from skin on which hair does not grow and subjecting both
CC mixtures to serial analysis of gene expression (SAGE) to identify those
CC genes for which expression is markedly different between the two types of
CC skin. The invention also describes in vitro methods for determining
CC homeostasis of human hair-bearing skin and for determining activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human hair-bearing skin. A biochip and
CC a test kit comprising a solid support (flexible or rigid) with
CC immobilised probes are also described for determining homeostasis. The
CC hair-bearing skin is from the scalp and the other skin is from the face.
CC The method allows identification of as many as possible of the genes
CC important for hair-bearing skin, and therefore, of a very wide range of
CC potential therapeutic and cosmetic agents. ADQ35184-ADQ36518 represent
CC human DNA Tag fragments used to identify genes associated with hair-
CC bearing skin.

XX Sequence 11 BP; 3 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
DB 11 ATCCACCTTC 2

RESULT 357

ADQ33204

ID ADQ33204 standard; DNA; 11 BP.

XX ADQ33204;

XX 23-SEP-2004 (first entry)

DE Human facial skin-associated DNA fragment SEQ ID NO 1294.

XX facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.

XX Homo sapiens.

XX DE10260928-A1.

XX 08-JUL-2004.

XX 20-DEC-2002; 2002DE-01060928.

XX 20-DEC-2002; 2002DE-01060928.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;

XX WPI; 2004-518955/50.

XX In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.

PS Claim 5; SEQ ID NO 1294; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed
CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
CC their fragments), recovering a second, similar mixture from some other
CC human tissue, preferably skin from a protected area, especially from the
CC breast and subjecting the mixtures to serial analysis of gene expression
CC (SAGE) to identify those genes for which expression is markedly different
CC between facial skin and the other tissue. The invention also describes an
CC in vitro method for determining homeostasis of human facial skin; a test
CC kit which comprises a solid support (flexible or rigid) on which are
CC immobilised probes that bind specifically to the factors of interest and
CC a biochip for determining homeostasis of human facial skin. The products
CC of the invention are also used in a method which determines activity of
CC cosmetic and pharmaceutical agents for use against disorders or
CC disturbances of the homeostasis of human skin and a screening method for
CC identifying cosmetic and pharmaceutical agents. The method allows
CC identification of as many as possible of the genes important for facial
CC skin and thus of a very wide range of potential therapeutic and cosmetic
CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
CC identify the facial skin-associated genes described in the invention.

XX Sequence 11 BP; 2 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
DB 1 ATCCACCCGC 10

RESULT 358

ADQ33521/c

ID ADQ33521 standard; DNA; 11 BP.

XX ADQ33521;

XX 23-SEP-2004 (first entry)

DE Human facial skin-associated DNA fragment SEQ ID NO 1611.

XX facial skin; human; serial analysis of gene expression; SAGE;
KW homeostasis; biochip; cosmetic; pharmaceutical; ds.

XX Homo sapiens.

XX DE10260928-A1.

XX 08-JUL-2004.

XX 20-DEC-2002; 2002DE-01060928.

XX 20-DEC-2002; 2002DE-01060928.

XX (HENK) HENKEL KGAA.

XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
PI Conradt M, Hofmann K;

XX WPI; 2004-518955/50.

XX In vitro identification of genes important for facial skin, useful for
PT assessing homeostasis and in screening for pharmaceutical or cosmetic
PT agents, based on differential expression analysis.

PS Claim 5; SEQ ID NO 1611; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
CC that are significant for facial skin in humans. The method comprises
CC recovering, from facial skin, a first mixture of genetically expressed

CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.

XX
 SQ Sequence 11 BP; 5 A; 3 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTG 18
 DB 10 CTGCTTGTG 1

RESULT 359
 ADQ33660/c
 ID ADQ33660 standard; DNA; 11 BP.
 XX
 AC ADQ33660;
 DT 23-SEP-2004 (first entry)
 DE Human facial skin-associated DNA fragment SEQ ID NO 1750.
 XX facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX Homo sapiens.
 XX DE10260928-A1.
 XX 08-JUL-2004.
 XX 20-DEC-2002; 2002DE-01060928.
 XX 20-DEC-2002; 2002DE-01060928.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX WPI; 2004-518855/50.
 XX
 PT In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 5; SEQ ID NO 1750; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression

CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.

SQ Sequence 11 BP; 4 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
 DB 11 TCCACCTTCT 2

RESULT 360
 ADQ33652
 ID ADQ33652 standard; DNA; 11 BP.
 XX
 AC ADQ33652;
 DT 23-SEP-2004 (first entry)
 DE Human facial skin-associated DNA fragment SEQ ID NO 1742.
 XX facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX Homo sapiens.
 XX DE10260928-A1.
 XX 08-JUL-2004.
 XX 20-DEC-2002; 2002DE-01060928.
 XX 20-DEC-2002; 2002DE-01060928.
 XX (HENK) HENKEL KGAA.
 XX Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX WPI; 2004-518855/50.
 XX
 PT In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 5; SEQ ID NO 1742; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are

CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.
 XX
 SQ Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACTGCTGT 15
 DB 2 CACTGCTGT 11
 |||||

RESULT 361
 ADQ34937/c
 ID ADQ34937 standard; DNA; 11 BP.

XX AC ADQ34937;
 XX DT 23-SEP-2004 (first entry)
 XX DE Human facial skin-associated DNA fragment SEQ ID NO 3027.
 XX KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX OS Homo sapiens.

XX PN DE10260928-A1.
 XX PD 08-JUL-2004.
 XX PF 20-DEC-2002; 2002DE-01060928.
 XX PR 20-DEC-2002; 2002DE-01060928.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX WPI; 2004-518855/50.

In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 4; SEQ ID NO 3027; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or

CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.
 XX
 SQ Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCACCTGCT 13
 DB 11 TCACCTGCT 2
 |||||

RESULT 362
 ADQ32556/c
 ID ADQ32556 standard; DNA; 11 BP.

XX AC ADQ32556;
 XX DT 23-SEP-2004 (first entry)
 XX DE Human facial skin-associated DNA fragment SEQ ID NO 646.
 XX KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX OS Homo sapiens.

XX PN DE10260928-A1.
 XX PD 08-JUL-2004.
 XX PF 20-DEC-2002; 2002DE-01060928.
 XX PR 20-DEC-2002; 2002DE-01060928.
 XX PA (HENK) HENKEL KGAA.
 XX PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX WPI; 2004-518855/50.

In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 6; SEQ ID NO 646; 577pp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic

CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.
 CC
 SQ Sequence 11 BP; 5 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
 |||||
 Db 11 CCTCCTGTGT 2

RESULT 363
 ADQ33878
 ID ADQ33878 standard; DNA; 11 BP.
 XX
 AC ADQ33878;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human facial skin-associated DNA fragment SEQ ID NO 1968.
 XX
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10260928-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002DE-01060928.
 XX
 PR 20-DEC-2002; 2002DE-01060928.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX
 DR WPI; 2004-518855/50.
 XX

In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 5; SEQ ID NO 1968; 577bp; German.
 XX
 CC This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.

XX Sequence 11 BP; 1 A; 5 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCT 13
 |||||
 Db 2 TCCACCTGCT 11

RESULT 364
 ADQ32289
 ID ADQ32289 standard; DNA; 11 BP.
 XX
 AC ADQ32289;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human facial skin-associated DNA fragment SEQ ID NO 379.
 XX
 KW facial skin; human; serial analysis of gene expression; SAGE;
 KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
 XX
 OS Homo sapiens.
 XX
 PN DE10260928-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002DE-01060928.
 XX
 PR 20-DEC-2002; 2002DE-01060928.
 XX
 PA (HENK) HENKEL KGAA.
 XX
 PI Petersohn D, Schlottmann K, Gassenmeier T, Holtkoetter O;
 PI Conradt M, Hofmann K;
 XX
 DR WPI; 2004-518855/50.
 XX

In vitro identification of genes important for facial skin, useful for
 PT assessing homeostasis and in screening for pharmaceutical or cosmetic
 PT agents, based on differential expression analysis.

XX Claim 8; SEQ ID NO 379; 577bp; German.

XX This invention describes a novel in vitro method for identifying genes
 CC that are significant for facial skin in humans. The method comprises
 CC recovering, from facial skin, a first mixture of genetically expressed
 CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
 CC their fragments), recovering a second, similar mixture from some other
 CC human tissue, preferably skin from a protected area, especially from the
 CC breast and subjecting the mixtures to serial analysis of gene expression
 CC (SAGE) to identify those genes for which expression is markedly different
 CC between facial skin and the other tissue. The invention also describes an
 CC in vitro method for determining homeostasis of human facial skin; a test
 CC kit which comprises a solid support (flexible or rigid) on which are
 CC immobilised probes that bind specifically to the factors of interest and
 CC a biochip for determining homeostasis of human facial skin. The products
 CC of the invention are also used in a method which determines activity of
 CC cosmetic and pharmaceutical agents for use against disorders or
 CC disturbances of the homeostasis of human skin and a screening method for
 CC identifying cosmetic and pharmaceutical agents. The method allows
 CC identification of as many as possible of the genes important for facial
 CC skin and thus of a very wide range of potential therapeutic and cosmetic
 CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
 CC identify the facial skin-associated genes described in the invention.

XX Sequence 11 BP; 2 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 11;
 Best Local Similarity 90.0%; Pred. No. 1.8e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy      14 GTGTGACCTG 23
Db      ||| |||||
        2 GTGAGACCTG 11

RESULT 365
ADQ32669
ID      ADQ32669 standard; DNA; 11 BP.
XX      AC
XX      AC ADQ32669;
XX      DT
XX      DT 23-SEP-2004 (first entry)
XX      DE
XX      DE Human facial skin-associated DNA fragment SEQ ID NO 759.
XX      KW facial skin; human; serial analysis of gene expression; SAGE;
XX      KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX      OS Homo sapiens.
XX      PN DE10260928-A1.
XX      PD 08-JUL-2004.
XX      PF 20-DEC-2002; 2002DE-01060928.
XX      PR 20-DEC-2002; 2002DE-01060928.
XX      PR (HENK ) HENKEL KGAA.
XX      PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX      PI Conradt M, Hofmann K;
XX      PA WPI; 2004-518855/50.
XX      PT In vitro identification of genes important for facial skin, useful for
XX      PT assessing homeostasis and in screening for pharmaceutical or cosmetic
XX      PT agents, based on differential expression analysis.
XX      PS Claim 5; SEQ ID NO 759; 577bp; German.
XX      CC This invention describes a novel in vitro method for identifying genes
XX      CC that are significant for facial skin in humans. The method comprises
XX      CC recovering, from facial skin, a first mixture of genetically expressed
XX      CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX      CC their fragments), recovering a second, similar mixture from some other
XX      CC human tissue, preferably skin from a protected area, especially from the
XX      CC breast and subjecting the mixtures to serial analysis of gene expression
XX      CC (SAGE) to identify those genes for which expression is markedly different
XX      CC between facial skin and the other tissue. The invention also describes an
XX      CC kit which comprises a solid support (flexible or rigid) on which are
XX      CC immobilised probes that bind specifically to the factors of interest and
XX      CC a biochip for determining homeostasis of human facial skin. The products
XX      CC of the invention are also used in a method which determines activity of
XX      CC cosmetic and pharmaceutical agents for use against disorders or
XX      CC disturbances of the homeostasis of human skin and a screening method for
XX      CC identifying cosmetic and pharmaceutical agents. The method allows
XX      CC identification of as many as possible of the genes important for facial
XX      CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX      CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
XX      CC identify the facial skin-associated genes described in the invention.
XX      SQ Sequence 11 BP; 2 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      2 CATCCACCTG 11
Db      ||||| |||
        1 CATCCATCTG 10

RESULT 366
ADQ34474/c
ID      ADQ34474 standard; DNA; 11 BP.
XX      AC
XX      AC ADQ34474;
XX      DT
XX      DT 23-SEP-2004 (first entry)
XX      DE
XX      DE Human facial skin-associated DNA fragment SEQ ID NO 2564.
XX      KW facial skin; human; serial analysis of gene expression; SAGE;
XX      KW homeostasis; biochip; cosmetic; pharmaceutical; ds.
XX      OS Homo sapiens.
XX      PN DE10260928-A1.
XX      PD 08-JUL-2004.
XX      PF 20-DEC-2002; 2002DE-01060928.
XX      PR 20-DEC-2002; 2002DE-01060928.
XX      PR (HENK ) HENKEL KGAA.
XX      PI Petersohn D, Schlotmann K, Gassenmeier T, Holtkoetter O;
XX      PI Conradt M, Hofmann K;
XX      PA WPI; 2004-518855/50.
XX      PT In vitro identification of genes important for facial skin, useful for
XX      PT assessing homeostasis and in screening for pharmaceutical or cosmetic
XX      PT agents, based on differential expression analysis.
XX      PS Claim 4; SEQ ID NO 2564; 577bp; German.
XX      CC This invention describes a novel in vitro method for identifying genes
XX      CC that are significant for facial skin in humans. The method comprises
XX      CC recovering, from facial skin, a first mixture of genetically expressed
XX      CC (transcribed and optionally translated) factors (i.e. proteins, mRNA or
XX      CC their fragments), recovering a second, similar mixture from some other
XX      CC human tissue, preferably skin from a protected area, especially from the
XX      CC breast and subjecting the mixtures to serial analysis of gene expression
XX      CC (SAGE) to identify those genes for which expression is markedly different
XX      CC between facial skin and the other tissue. The invention also describes an
XX      CC kit which comprises a solid support (flexible or rigid) on which are
XX      CC immobilised probes that bind specifically to the factors of interest and
XX      CC a biochip for determining homeostasis of human facial skin. The products
XX      CC of the invention are also used in a method which determines activity of
XX      CC cosmetic and pharmaceutical agents for use against disorders or
XX      CC disturbances of the homeostasis of human skin and a screening method for
XX      CC identifying cosmetic and pharmaceutical agents. The method allows
XX      CC identification of as many as possible of the genes important for facial
XX      CC skin and thus of a very wide range of potential therapeutic and cosmetic
XX      CC agents. ADQ31911-ADQ35111 represent human DNA Tag fragments used to
XX      CC identify the facial skin-associated genes described in the invention.
XX      SQ Sequence 11 BP; 3 A; 0 C; 7 G; 1 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      4 TCCACCTGCT 13
Db      ||||| |||
        11 TCCACCTCCT 2

RESULT 367
AAQ52115/c

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ID AAQ52115 standard; RNA; 12 BP.
XX AC
XX AAQ52115;
XX 25-MAR-2003 (revised)
XX 26-MAY-1994 (first entry)
XX DE
XX DE Breast cancer specific mRNA ribozyme cleavable nucleotide (2833).
XX KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
XX KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
XX KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
XX KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
XX KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
XX KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
XX KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
XX KW hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.
XX OS
XX OS Homo sapiens.
XX PN WO9323057-A1.
XX PN
XX PD 25-NOV-1993.
XX PF 13-MAY-1993; 93WO-US004573.
XX PR 14-MAY-1992; 92US-00882822.
XX PR 14-MAY-1992; 92US-00882885.
XX PR 26-AUG-1992; 92US-00936110.
XX PR 26-AUG-1992; 92US-00936421.
XX PR 26-AUG-1992; 92US-00936422.
XX PR 26-AUG-1992; 92US-00936531.
XX PR 26-AUG-1992; 92US-00936532.
XX PR 07-DEC-1992; 92US-00987131.
XX PR 19-JAN-1993; 93US-00006122.
XX PR 19-JAN-1993; 93US-00008910.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI
XX PI Thompson JD, Draper KG;
XX DR WPI; 1993-386203/48.
XX DR
XX DR New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
XX PT with tumours or mRNA expressed from gene encoding multiple drug
XX PT resistance.
XX PS Claim 3; Fig 8; 69pp; English.
XX CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are
XX CC associated with development or maintenance of chronic myelogenous
XX CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
XX CC lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
XX CC leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
XX CC The full length mRNAs containing these target sequences, encode aberrant
XX CC cellular proteins which are able to control cellular proliferation and
XX CC are directly linked to a leukemic phenotype. These target sequences are
XX CC identified by the ribozyme of the invention. The ribozymes are formed in a
XX CC hammerhead motif, but may also be formed in the motif of a hairpin,
XX CC hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
XX CC may be used to inhibit the development or expression of a transformed
XX CC phenotype in man and other animals by modulating expression of the
XX CC corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
XX CC and transformed cells elicits inhibition of the transformed state.
XX CC Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
XX CC mechanism of drug resistance used by transformed cells and thus enhances
XX CC drug therapies for tumours. The ribozymes may also be used to study
XX CC genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
XX CC correct PN field.)
XX SQ Sequence 12 BP; 3 A; 1 C; 6 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CCATCCACCT 10
XX DB |||||
XX 10 CCATCCACTT 1
XX
XX RESULT 368
XX AAV32307/c
XX ID AAV32307 standard; DNA; 12 BP.
XX AC
XX AC AAV32307;
XX DT 18-AUG-1998 (first entry)
XX DE Random primed reverse transcription PCR primer 139.
XX DE RT-PCR; primer; amplification; reverse transcription; RNA fingerprinting;
XX KW differential gene expression; ss.
XX OS
XX OS Synthetic.
XX PN WO9813521-A1.
XX PN
XX PD 02-APR-1998.
XX PF 26-SEP-1997; 97WO-EP005290.
XX PR 27-SEP-1996; 96GB-00020216.
XX PA (SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
XX PI
XX PI Consalez G, Pesce R;
XX DR WPI; 1998-230725/20.
XX DR
XX PT Differential screening of gene expression by reverse transcription
XX PT polymerase chain reaction - uses random priming with primers selected for
XX PT high efficiency and selectivity by computer screening of database(s).
XX PS Claim 9; Page 24; 37pp; English.
XX CC The invention provides a method for the differential screening of gene
XX CC expression by random primed reverse transcription PCR (RT-PCR). The
XX CC primer sequences are generated by stimulating PCR reactions on non-
XX CC redundant mammalian nucleotide sequence databank entries containing at
XX CC least 1,000 bp of coding region. The primers selected, such as the
XX CC present one, had to meet various criteria such as having an efficiency
XX CC index between 2-10, having a selectivity index higher than 1, being 12 bp
XX CC long i.e. 8 C or G and 4 T or A, and each primer differed from the others
XX CC in at least 5 of the 8 bases at the 3'-end. The invention claims the
XX CC selected primers make it possible to use internally primed, PCR-based RNA
XX CC fingerprinting for simple, exhaustive and systematic analysis of
XX CC differential gene expression as an advantageous alternative to
XX CC differential display. The method can also be useful for isolating new
XX CC coding sequences and to compare known and new genes
XX SQ Sequence 12 BP; 1 A; 0 C; 7 G; 3 T; 0 U; 1 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 CCATCCACCT 10
XX DB |||||
XX 10 CCACCCACCT 1
XX
XX RESULT 369
XX AAV32258/c
XX ID AAV32258 standard; DNA; 12 BP.
XX

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XX
PI Inoue T;
XX WPI; 1999-592157/51.
DR
XX Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
XX Example 1; Page 22; 78pp; German.
XX
CC This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AA241640-241855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTG 14
DB 11 CCACCTGCTG 2

RESULT 372
AAZ41780
ID AAZ41780 standard; DNA; 12 BP.
XX
AC AAZ41780;
XX
XX 20-MAR-2003 (revised)
DT 21-JAN-2000 (first entry)
XX
XX Organic material detecting primer 141.
XX
XX Amplification; polymerase chain reaction; PCR; microorganism; compost;
KW detection; pollutant; soil; food; agricultural chemical; polymer;
KW organochlorine; primer; ss.
XX
OS Synthetic.
XX
XX DE19914461-Al.
PN
XX 21-OCT-1999.
PD
XX
XX 30-MAR-1999; 99DE-01014461.
XX
XX 31-MAR-1998; 98JP-00087651.
PR
XX 16-MAR-1999; 99JP-00069694.
XX
XX (SAOL ) SANYO ELECTRIC CO LTD.
PA (NORQ ) SOC TECHNO-INNOVATION AGRIC FORESTV & FI.
XX
PI Inoue T;
XX
XX WPI; 1999-592157/51.
DR
XX Novel polymerase chain reaction method, for differentiating between
PT microorganisms and for detecting contaminants.
XX
XX Example 1; Page 20; 78pp; German.
XX

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```

CC This invention describes a novel method for the amplification of DNA
CC comprising (i) preparing many primers (P) with different probabilities of
CC amplification and (ii) simultaneous polymerase chain reaction (PCR) of
CC many different DNA using these primers. The method is used (i) to
CC differentiate between different microorganisms in a mixed population and
CC (ii) to determine presence/absence of an impurity (pollutant), or its
CC concentration, in e.g. soil, foods, compost etc., typically metals,
CC agricultural chemicals, polymers, organochlorine compounds etc. A
CC particular use is monitoring composting of organic material.
CC Amplification with many primers produces a lot of information, so
CC reliability of the test is improved, and many samples may be tested
CC quickly. AA241640-241855 represent the primers described in the method of
CC the invention. (Updated on 20-MAR-2003 to correct PR field.)
XX
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 CACCTGCTGT 15
DB 1 CTCCTGCTGT 10

RESULT 373
AAZ41564
ID AAZ41564 standard; DNA; 12 BP.
XX
AC AAZ41564;
XX
XX 19-JAN-2000 (first entry)
DT
XX
DE Microbe detection in organic waste arbitrarily primed PCR primer #141.
XX
XX Microbe; detection; organic waste; arbitrarily primer PCR;
KW random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
OS Synthetic.
XX
XX JP11276176-A.
PN
XX 12-OCT-1999.
PD
XX
XX 31-MAR-1998; 98JP-00087652.
PR
XX 31-MAR-1998; 98JP-00087652.
XX
XX (SAOL ) SANYO ELECTRIC CO LTD.
PA (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
XX
XX WPI; 1999-626940/54.
DR
XX Amplification of a DNA fragment - in order to establish the state of
PT existence of a microbe.
PT
XX
XX Example; Page 9; 40pp; Japanese.
PS
XX
XX A method has been developed for the amplification of a DNA fragment in
CC which amplification is carried out on the DNA fragments of a number of
CC different DNAs. The method comprises a PCR reaction repeatedly carrying
CC out a heat-denaturing step, a primer annealing step and a polymerase
CC extending step, to amplify the DNA fragments of a plural of different
CC DNAs. The method can detect the existence of a microbe in organic waste.
CC AA241424 to AA241639 represent PCR primers used in random amplified
CC polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC organic waste
XX
XX
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy      6 CACCTGCTGT 15
Db      1 CTCCTGCTGT 10

RESULT 374
AAZ41614/C
ID  AAZ41614 standard; DNA; 12 BP.
XX
XX  AAZ41614;
AC
XX
XX  19-JAN-2000 (first entry)
DT
XX
XX  Microbe detection in organic waste arbitrarily primed PCR primer #191.
DE
XX
XX  Microbe; detection; organic waste; arbitrarily primer PCR;
KW
XX  random amplified polymorphic DNA; amplification; PCR primer; ss.
XX
XX  Synthetic.
OS
XX
XX  JPI1276176-A.
XX
XX  12-OCT-1999.
PD
XX
XX  31-MAR-1998; 98JP-00087652.
PF
XX
XX  31-MAR-1998; 98JP-00087652.
PR
XX
XX  (SAOL ) SANYO ELECTRIC CO LTD.
PA
XX  (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
PA
XX
XX  WPI; 1999-626940/54.
DR
XX
XX  Amplification of a DNA fragment - in order to establish the state of
PT  existence of a microbe.
PT
XX
XX  Example; Page 10; 40pp; Japanese.
PS
XX
XX  A method has been developed for the amplification of a DNA fragment in
CC  which amplification is carried out on the DNA fragments of a number of
CC  different DNAs. The method comprises a PCR reaction repeatedly carrying
CC  out a heat-denaturing step, a primer annealing step and a polymerase
CC  extending step, to amplify the DNA fragments of a plural of different
CC  DNAs. The method can detect the existence of a microbe in organic waste.
CC  AAZ41424 to AAZ41639 represent PCR primers used in random amplified
CC  polymorphic DNA arbitrarily primed PCR, for the detection of microbes in
CC  organic waste
XX
XX  Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      5 CCACCTGCTG 14
Db      11 CCACCTGCTG 2

RESULT 375
AAF74730/C
ID  AAF74730 standard; DNA; 12 BP.
XX
XX  AAF74730;
AC
XX
XX  17-MAY-2001 (first entry)
DT
XX
XX  Human smoothelin variant intron-exon splice recognition sequence #26.
DE
XX
XX  Human; smoothelin; smoothelin B gene; smooth muscle cell promoter;
KW  vascular contractile smooth muscle cell; gene therapy; PCR primer;
KW  visceral contractile smooth muscle cell; cardiovascular; ss.

```

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XX
OS  Homo sapiens.
XX
XX  EP1083231-A1.
PN
XX
XX  14-MAR-2001.
PD
XX
XX  09-SEP-1999; 99EP-00202943.
PF
XX
XX  09-SEP-1999; 99EP-00202943.
PR
XX
XX  (INTR-) INTROGENE BV.
PA
XX
XX  WPI; 2001-236858/25.
DR
XX
XX  Nucleic acids encoding smooth muscle cell specific promoters, useful e.g.
PT  for treating cardiovascular diseases or in targeting transgene expression
PT  to smooth muscle cells expressing endogenous smoothelin proteins.
PT
XX
XX  Example 3; Page 16; 51pp; English.
PS
XX
XX  The present invention describes a nucleic acid delivery vehicle (I)
CC  comprising a nucleic acid capable of expressing specifically in a
CC  contractile smooth muscle cell, preferably a vascular contractile smooth
CC  muscle cell and/or a visceral contractile smooth muscle cell. Also
CC  described are smooth muscle cell specific promoters which can be
CC  incorporated into a nucleic acid delivery vehicle, where the nucleic acid
CC  delivery vehicle preferably comprises a virus-like particle such as an
CC  adenovirus particle, an adeno-associated virus particle or a retrovirus
CC  particle. (I) has cardiovascular activity and can be used in gene
CC  therapy. The nucleic acid delivery vehicle is useful for the preparation
CC  of a pharmaceutical for the treatment of a cardiovascular disease. The
CC  promoter of the smoothelin gene (a smooth muscle cell specific promoter)
CC  is useful for providing a particular nucleic acid with the capacity to
CC  express proteins specifically in contractile smooth muscle cells. The
CC  promoter may also be used in targeting transgene expression to smooth
CC  muscle cells that express endogenous smoothelin protein, in
CC  distinguishing subsets of smooth muscle cells, and in expressing foreign
CC  genetic material specifically in contractile smooth muscle cells.
CC  AAF74719 to AAF74756 represent human smoothelin variant intron-exon
CC  splice recognition sites, which are used in an example from the present
CC  invention
XX
XX  Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
SQ
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      3 ATCCACCTGC 12
Db      12 ATCCACCTGC 3

RESULT 376
AAS01805/C
ID  AAS01805 standard; DNA; 12 BP.
XX
XX  AAS01805;
AC
XX
XX  12-SEP-2001 (first entry)
DT
XX
XX  Human smoothelin gene intron-exon splice recognition sequence #12.
DE
XX
XX  Human; smoothelin; promoter; nucleic acid delivery vehicle; restenosis;
KW  contractile smooth muscle cell; pharmaceutical; cardiovascular disease;
KW  hypertension; atherosclerosis; transgene expression; oligo linker; ds;
KW  percutaneous transluminal coronary angioplasty.
XX
XX  Homo sapiens.
OS
XX
XX  WO200118048-A2.
PN
XX

```

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PD 15-MAR-2001.
XX
XX 08-SEP-2000; 2000WO-NL000638.
XX
XX 09-SEP-1999; 99EP-00202943.
XX
XX 09-SEP-1999; 99US-0153284P.
XX
XX (INTR-) INTROGENE BV.
XX
XX Van Eijls GJJM, Hateboer G, Havenga MJE;
XX
XX WPI; 2001-244559/25.
XX
XX New nucleic acids encoding smooth muscle cell specific promoters, useful
XX for treating a cardiovascular disease or in targeting transgene
XX expression to smooth muscle cells expressing endogenous smoothelin
XX protein.
XX
XX Example 3; Page 45; 60pp; English.
XX
XX The sequence represents an intron-exon splice recognition sequence of the
XX human smoothelin gene. The smoothelin gene promoter, or its functional
XX part, derivative and/or analogue, can be used as part of a nucleic acid
XX delivery vehicle, comprising a nucleic acid capable of expressing
XX specifically in a contractile smooth muscle cell. The nucleic acid
XX delivery vehicle is useful for the preparation of a pharmaceutical for
XX the treatment of cardiovascular diseases, such as hypertension,
XX atherosclerosis and restenosis after percutaneous transluminal coronary
XX angioplasty. The promoter of a smoothelin gene is useful for providing a
XX particular nucleic acid with the capacity to express foreign genetic
XX material specifically in a contractile smooth muscle cell. The promoter
XX may also be used in targeting transgene expression to smooth muscle cells
XX that express endogenous smoothelin protein, in distinguishing subsets of
XX smooth muscle cells, and in expressing foreign genetic material
XX specifically in contractile smooth muscle cells
XX
XX Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 3 ATCCACCTGC 12
Db 12 ATCCAGCTGC 3
XX
RESULT 377
AAC97965/C
ID AAC97965 standard; DNA; 12 BP.
XX
XX AAC97965;
AC
XX
XX 28-FEB-2001 (first entry)
DT
XX
XX Primer used to illustrate DNA amplification method SEQ ID 191.
DE
XX
XX Primer; amplification; selective; ss.
KW
XX
XX Synthetic.
OS
XX
XX JP2000270867-A.
PN
XX
XX 03-OCT-2000.
PD
XX
XX 19-MAR-1999; 99JP-00076844.
PF
XX
XX 19-MAR-1999; 99JP-00076844.
PR
XX
XX (SAOL) SANYO ELECTRIC CO LTD.
PA
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
PA
XX
XX WPI; 2001-011047/02.
DR
XX
XX Amplification of a DNA fragment and its apparatus.
PT
XX
XX Example 1; Page 10; 32pp; Japanese.
PS
XX
XX This invention relates to a method for amplifying a DNA fragment. The
XX method comprises successive repetitions of heat-denaturing, annealing of
XX a primer and an extending step using a DNA polymerase. The method makes
XX use of a cDNA pool in which the primer is one primer or a pair of primer
XX sets and has an amplification probability which allows it to amplify a
XX DNA fragment from a limited number of the cDNAs among the DNA pool (where
XX the limited number is in the range of 1 to 25). Also included in the
XX invention are apparatus used for carrying out the method, a primer and a
XX DNA polymerase and a kit used for amplifying a DNA fragment. The method
XX can be used to amplify a limited number of cDNAs from a pool in which a
XX wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
XX represent primers used in an example illustrating the method of the
XX
XX Amplification of a DNA fragment and its apparatus.
XX
XX Example 1; Page 11; 32pp; Japanese.
XX
XX This invention relates to a method for amplifying a DNA fragment. The
XX method comprises successive repetitions of heat-denaturing, annealing of
XX a primer and an extending step using a DNA polymerase. The method makes
XX use of a cDNA pool in which the primer is one primer or a pair of primer
XX sets and has an amplification probability which allows it to amplify a
XX DNA fragment from a limited number of the cDNAs among the DNA pool (where
XX the limited number is in the range of 1 to 25). Also included in the
XX invention are apparatus used for carrying out the method, a primer and a
XX DNA polymerase and a kit used for amplifying a DNA fragment. The method
XX can be used to amplify a limited number of cDNAs from a pool in which a
XX wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
XX represent primers used in an example illustrating the method of the
XX
XX Sequence 12 BP; 2 A; 2 C; 6 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2
XX
RESULT 378
AAC97915
ID AAC97915 standard; DNA; 12 BP.
XX
XX AAC97915;
AC
XX
XX 28-FEB-2001 (first entry)
DT
XX
XX Primer used to illustrate DNA amplification method SEQ ID 141.
DE
XX
XX Primer; amplification; selective; ss.
KW
XX
XX Synthetic.
OS
XX
XX JP2000270867-A.
PN
XX
XX 03-OCT-2000.
PD
XX
XX 19-MAR-1999; 99JP-00076844.
PF
XX
XX 19-MAR-1999; 99JP-00076844.
PR
XX
XX (SAOL) SANYO ELECTRIC CO LTD.
PA
XX (NORI-) ZH NORIN SUISAN SENTAN GIJUTSU SANGYO.
PA
XX
XX WPI; 2001-011047/02.
DR
XX
XX Amplification of a DNA fragment and its apparatus.
PT
XX
XX Example 1; Page 10; 32pp; Japanese.
PS
XX
XX This invention relates to a method for amplifying a DNA fragment. The
XX method comprises successive repetitions of heat-denaturing, annealing of
XX a primer and an extending step using a DNA polymerase. The method makes
XX use of a cDNA pool in which the primer is one primer or a pair of primer
XX sets and has an amplification probability which allows it to amplify a
XX DNA fragment from a limited number of the cDNAs among the DNA pool (where
XX the limited number is in the range of 1 to 25). Also included in the
XX invention are apparatus used for carrying out the method, a primer and a
XX DNA polymerase and a kit used for amplifying a DNA fragment. The method
XX can be used to amplify a limited number of cDNAs from a pool in which a
XX wide variety of cDNAs are present. Oligonucleotides AAC97775 - AAC97990
XX represent primers used in an example illustrating the method of the
XX

```

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CC invention
XX
SQ Sequence 12 BP; 0 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10
   |||||
   |||||

RESULT 379
ABI29917
ID ABI29917 standard; DNA; 12 BP.
XX
AC ABI29917;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 329890 for detecting SNP TSC0035228.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 329890; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19
Db 3 TGTGTGTGA 12
   |||||
   |||||

RESULT 380
ABH85587/C
ID ABH85587 standard; DNA; 12 BP.
XX
AC ABH85587;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 285580 for detecting SNP TSC0012360.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PS WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 285580; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other;

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19
Db 10 TGTGTGTGA 1
   |||||
   |||||

RESULT 381
ABI59162/C
ID ABI59162 standard; DNA; 12 BP.
XX
AC ABI59162;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 359135 for detecting SNP TSC0051475.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

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XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 359135; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 1 A; 0 C; 8 G; 3 T; 0 U; 0 Other;
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CCATCCACCT 10
Db 10 CCACCCACCT 1
RESULT 382
ABH74750/c
ID ABH74750 standard; DNA; 12 BP.
XX AC ABH74750;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 274735 for detecting SNP TSC0003662.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 274735; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 0 C; 7 G; 2 T; 0 U; 0 Other;
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 CCATCCACCT 10
Db 11 CCACCCACCT 2
RESULT 383
ABH75922
ID ABH75922 standard; DNA; 12 BP.
XX AC ABH75922;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 275915 for detecting SNP TSC0004038.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN W0200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 275915; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The

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```
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCCACT 10
Db 1 CCATCCCACT 10
|||||

RESULT 384
ABI26643
ID ABI26643 standard; DNA; 12 BP.
XX
AC ABI26643;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 326616 for detecting SNP TSC0033176.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 326616; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCCACT 10
Db 1 CCATCCCACT 10
|||||

RESULT 386
ABI59024
ID ABI59024 standard; DNA; 12 BP.
XX
AC ABI59024;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCCACT 10
Db 1 CCATCCCACT 10
|||||

RESULT 388
ABI53560
ID ABI53560 standard; DNA; 12 BP.
XX
AC ABI53560;
XX
DT 22-FEB-2002 (first entry)
DE Oligonucleotide primer SEQ ID NO 353533 for detecting SNP TSC0048564.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 353533; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 0 Other;

Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCCACT 10
Db 1 CCATCCCACT 10
|||||

RESULT 386
ABI59024
ID ABI59024 standard; DNA; 12 BP.
XX
AC ABI59024;
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XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 358997 for detecting SNP TSC0010504.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 358997; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 1 A; 8 C; 0 G; 3 T; 0 U; 0 Other;
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCCACCT 10
DB 3 CCATCCCCCT 12
RESULT 387
ABI60693/C
ID ABI60693 standard; DNA; 12 BP.
XX AC ABI60693;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 360666 for detecting SNP TSC0052209.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.

```

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PD 18-OCT-2001.
XX 06-APR-2001; 2001WO-IB000713.
XX 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 360666; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 12 BP; 2 A; 0 C; 8 G; 2 T; 0 U; 0 Other;
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCCACCT 10
DB 11 CCATCCACCT 2
RESULT 388
ABI18617
ID ABI18617 standard; DNA; 12 BP.
XX AC ABI18617;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 318590 for detecting SNP TSC0028751.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX (EPiG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cell typing, is

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PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PS Claim 1; SEQ ID NO 318590; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCCACCT 10
Db 2 CCTTCCACCT 11
||| |||||
RESULT 389
ABH71661
ID ABH71661 standard; DNA; 12 BP.
XX
AC ABH71661;
XX
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 271638 for detecting SNP TSC0002575.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 271638; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCCACCT 10
Db 2 CCTTCCACCT 11
||| |||||
RESULT 389
ABH71661
ID ABH71661 standard; DNA; 12 BP.
XX
AC ABH71661;
XX
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 271638 for detecting SNP TSC0004433.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 277305; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCATCCACCT 10
Db 3 CCTTCCACCT 12
||| |||||
RESULT 390
ABH77312
ID ABH77312 standard; DNA; 12 BP.
XX
AC ABH77312;
XX
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 277305 for detecting SNP TSC0004433.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 277305; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;
SQ
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TCCACCTGCT 13
||| |||||
```


XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX Claim 1; SEQ ID NO 369132; 29pp + Sequence Listing; German.
XX XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX SQ Sequence 12 BP; 2 A; 0 C; 6 G; 4 T; 0 U; 0 Other;
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 3 ATCCACCTGC 12
XX Db 11 ATCCACCTAC 2
XX |||||
XX
XX RESULT 394
XX ABH81976/c
XX ID ABH81976 standard; DNA; 12 BP.
XX AC ABH81976;
XX XX 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 281969 for detecting SNP TSC0010212.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX Claim 1; SEQ ID NO 281969; 29pp + Sequence Listing; German.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX Claim 1; SEQ ID NO 369130; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX SQ Sequence 12 BP; 1 A; 0 C; 9 G; 2 T; 0 U; 0 Other;
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 CCATCCACCT 10
XX Db 11 CCACCCACCT 2
XX |||||
XX
XX RESULT 395
XX ABI69157/c
XX ID ABI69157 standard; DNA; 12 BP.
XX AC ABI69157;
XX XX 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 369130 for detecting SNP TSC0057462.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX XX WO200177384-A2.
XX PN 18-OCT-2001.
XX PD 06-APR-2001; 2001WO-IB000713.
XX PF 07-APR-2000; 2000DE-01019173.
XX PR (EPIG-) EPIGENOMICS AG.
XX PA Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX Claim 1; SEQ ID NO 369130; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX SQ Sequence 12 BP; 1 A; 0 C; 9 G; 2 T; 0 U; 0 Other;

```

SQ Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACTGCT 12
Db 10 ATCCACTCT 1

RESULT 396
ABI80903/c
ID ABI80903 standard; DNA; 12 BP.
XX
AC ABI80903;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 380876 for detecting SNP TSC0064024.
XX
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
DR Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 380876; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
PS Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 10 CCATCCATCT 1

RESULT 397
ABH97813/c
ID ABH97813 standard; DNA; 12 BP.
XX
AC ABH97813;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 293466 for detecting SNP TSC0015629.
XX
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.

```


CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 7 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 TCCACCTGCT 13
 Db 2 TCCACCTCCT 11
 RESULT 401
 ABI05466
 ID ABI05466 standard; DNA; 12 BP.
 XX
 AC ABI05466;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 305439 for detecting SNP TSC0021446.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 305439; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
 Db 2 CCCTCCACCT 11
 RESULT 402
 ABI13967
 ID ABI13967 standard; DNA; 12 BP.
 XX
 AC ABI13967;
 XX
 XX 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 313940 for detecting SNP TSC0026041.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 313940; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 4 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db 1 CCACCCACCT 10
 RESULT 403
 ABI16340/c
 ID ABI16340 standard; DNA; 12 BP.
 XX
 AC ABI16340;
 XX
 XX 22-FEB-2002 (first entry)

XX Oligonucleotide primer SEQ ID NO 316313 for detecting SNP TSC0027391.
DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 316313; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 5 G; 4 T; 0 U; 0 Other;
SQ

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTCGTAAA 28
Db |||||
12 ACCTCGTAAA 3

RESULT 404
ABH69681
ID ABH69681 standard; DNA; 12 BP.
XX
XX AC ABH69681;
XX
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 269658 for detecting SNP TSC0001842.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX

PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 269658; 29pp + Sequence Listing; German.
PS
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
SQ

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
Db |||||
3 CCACCCACCT 12

RESULT 405
ABI37541
ID ABI37541 standard; DNA; 12 BP.
XX
XX AC ABI37541;
XX
XX 22-FEB-2002 (first entry)
DT
XX Oligonucleotide primer SEQ ID NO 337514 for detecting SNP TSC0039905.
DE
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
OS
XX WO200177384-A2.
PN
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX 07-APR-2000; 2000DE-01019173.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K;
PI
XX WPI; 2001-657177/75.
DR
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX

XX PS Claim 1; SEQ ID NO 337514; 29pp + Sequence Listing; German.

XX CC This invention describes novel oligonucleotide primers or peptide nucleic

XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX CC and cytosine methylation status in chemically pretreated genomic DNA. The

XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX CC range of diseases including immune system, gastrointestinal, respiratory,

XX CC central nervous system, cardiovascular and metabolic disorders. The

XX CC oligomers are also used for detecting cell type differentiation. ABC00010

XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX CC represent the oligomers described in the invention. NOTE: The sequence

XX CC data for this patent did not form part of the printed specification, but

XX CC was obtained in electronic format from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 10 TGCTGTGTGA 19

Db 2 TGATGTGTGA 11

RESULT 406

ABH77664/C

ID ABH77664 standard; DNA; 12 BP.

XX AC ABH77664;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 277657 for detecting SNP TSC0004662.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 277657; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 2 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 18 GACCTCGTAA 27

Db 11 GACCTCGTAA 2

RESULT 407

ABH86388

ID ABH86388 standard; DNA; 12 BP.

XX AC ABH86388;

XX DT 22-FEB-2002 (first entry)

XX DE Oligonucleotide primer SEQ ID NO 286381 for detecting SNP TSC0012703.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX OS Homo sapiens.

XX PN WO200177384-A2.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-IB000713.

XX PR 07-APR-2000; 2000DE-01019173.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 286381; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 2e+02;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCATCCACCT 10

Db 2 CCCTCCACCT 11

```

RESULT 408
ABH74692/c
ID ABH74692 standard; DNA; 12 BP.
XX
XX AC ABH74692;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 274677 for detecting SNP TSC0003635.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX PS Claim 1; SEQ ID NO 302245; 29pp + Sequence Listing; German.
XX
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACTTCG 12
Db 12 ATCCACTTAC 3

RESULT 409
ABI02272
ID ABI02272 standard; DNA; 12 BP.
XX
XX AC ABI02272;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 302245 for detecting SNP TSC0019886.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.

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XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 377361; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC000010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 0 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGA 19
Db 1 TGTGTGTGA 10
||| |||||
Oligonucleotide primer SEQ ID NO 297604 for detecting SNP TSC0017656.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 297604; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC000010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences

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CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC000010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACCT 10
Db 12 CCATCTACCT 3
||||| |||||
Oligonucleotide primer SEQ ID NO 284017 for detecting SNP TSC0011628.
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
central nervous system; gastrointestinal; respiratory; immune; metabolic.
Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 284017; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC000010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI02073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

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Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
Db 1 ATCCACCTAC 10
|||||
|

RESULT 413
ABH85692/C
ID ABH85692 standard; DNA; 12 BP.
XX
XX
AC ABH85692;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 285685 for detecting SNP TSC0012400.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
PD
XX
XX 06-APR-2001; 2001WO-IB000713.
PF
XX
XX 07-APR-2000; 2000DE-01019173.
PR
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 353779; 29pp + Sequence Listing; German.
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
PS
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABF99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 12 BP; 2 A; 1 C; 6 G; 3 T; 0 U; 0 Other;
SQ
XX
XX Query Match          29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
Db 10 ATCCACCTGC 1
|||||
|

RESULT 414
ABI53806/C
ID ABI53806 standard; DNA; 12 BP.
XX
XX
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 319359 for detecting SNP TSC0029177.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN

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XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 319359; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 CCATCCACCT 10
Db 1 CCACCCACCT 10
|||||
RESULT 416
ABH69682
ID ABH69682 standard; DNA; 12 BP.
XX
XX AC ABH69682;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 269659 for detecting SNP TSC0001842.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 319359; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 3 A; 7 C; 0 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 1 CCATCCACCT 10
Db 1 CCACCCACCT 10
|||||
RESULT 417
ABI29310
ID ABI29310 standard; DNA; 12 BP.
XX
XX AC ABI29310;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 329283 for detecting SNP TSC0034861.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 329283; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 3 ATCCACCTGC 12
Db 1 ATCCACCTGC 10
|||||
RESULT 417
ABI29310
ID ABI29310 standard; DNA; 12 BP.
XX
XX AC ABI29310;
XX
XX DT 22-FEB-2002 (first entry)
XX
XX DE Oligonucleotide primer SEQ ID NO 329283 for detecting SNP TSC0034861.
XX
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 06-APR-2001; 2001WO-IB000713.
XX
XX PR 07-APR-2000; 2000DE-01019173.
XX
XX PA (EPiG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX Claim 1; SEQ ID NO 329283; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 2 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 3 ATCCACCTGC 12
Db 1 ATCCACCTGC 10
|||||

```


XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 359791; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 12 BP; 2 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCATCCACCT 10
 Db |||||
 10 CCAACCACCT 1
 RESULT 421
 ABK72569
 ID ABK72569 standard; DNA; 12 BP.
 XX AC ABK72569;
 XX 13-AUG-2002 (first entry)
 XX Human OP1 gene, exon/intron junction #36.
 XX Human; ophthalmological; OP1; autosomal dominant optic atrophy; ADOA;
 KW gene; ds.
 XX Homo sapiens.
 XX WO200227022-A2.
 XX 04-APR-2002.
 XX 26-SEP-2001; 2001WO-GB004284.
 XX 26-SEP-2000; 2000GB-00023555.
 XX (UNLO) UNIV COLLEGE LONDON.
 XX (UYEY-) UNIV EYE HOSPITAL.
 XX Bhattacharya S, Wissing B, Alexander C, Votruba M;
 XX WPI; 2002-416484/44.
 XX Novel human normal or mutant OP1 (the predominant locus for autosomal
 PT dominant optic atrophy (ADOA)) polypeptides and the OP1 gene, useful in
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
 XX Disclosure; Fig 12; 75pp; English.
 XX The invention relates to an isolated human normal or mutant OP1 (the
 CC predominant locus for autosomal dominant optic atrophy (ADOA))
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa, DNA
 CC and substantially free of other human proteins. Also described is the
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OP1
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC and antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OP1 gene or gene product. ABK72533-ABK72593
 CC represent the human OP1 gene and intron/exon splice junctions
 XX Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 18 GACCTGGTAA 27
 Db |||||
 1 GACCGGTAA 10
 RESULT 422
 ABK72535
 ID ABK72535 standard; DNA; 12 BP.
 XX AC ABK72535;
 XX 13-AUG-2002 (first entry)
 XX Human OP1 gene, exon/intron junction #2.
 XX Human; ophthalmological; OP1; autosomal dominant optic atrophy; ADOA;
 KW gene; ds.
 XX Homo sapiens.
 XX WO200227022-A2.
 XX 04-APR-2002.
 XX 26-SEP-2001; 2001WO-GB004284.
 XX 26-SEP-2000; 2000GB-00023555.
 XX (UNLO) UNIV COLLEGE LONDON.
 XX (UYEY-) UNIV EYE HOSPITAL.
 XX Bhattacharya S, Wissing B, Alexander C, Votruba M;
 XX WPI; 2002-416484/44.
 XX Novel human normal or mutant OP1 (the predominant locus for autosomal
 PT dominant optic atrophy (ADOA)) polypeptides and the OP1 gene, useful in
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
 XX Disclosure; Fig 12; 75pp; English.
 XX The invention relates to an isolated human normal or mutant OP1 (the
 CC predominant locus for autosomal dominant optic atrophy (ADOA))
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa, DNA
 CC and substantially free of other human proteins. Also described is the
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OP1
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC and antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OP1 gene or gene product. ABK72533-ABK72593
 CC represent the human OP1 gene and intron/exon splice junctions
 XX Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 18 GACCTGGTAA 27
 Db |||||
 1 GACCGGTAA 10

XX (UNLO) UNIV COLLEGE LONDON.
 PA (UYEY-) UNIV EYE HOSPITAL.
 XX Bhattacharya S, Wissing B, Alexander C, Votruba M;
 XX WPI; 2002-416484/44.
 XX Novel human normal or mutant OP1 (the predominant locus for autosomal
 PT dominant optic atrophy (ADOA)) polypeptides and the OP1 gene, useful in
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
 XX Disclosure; Fig 12; 75pp; English.
 XX The invention relates to an isolated human normal or mutant OP1 (the
 CC predominant locus for autosomal dominant optic atrophy (ADOA))
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa, DNA
 CC and substantially free of other human proteins. Also described is the
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OP1
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC and antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OP1 gene or gene product. ABK72533-ABK72593
 CC represent the human OP1 gene and intron/exon splice junctions
 XX Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 18 GACCTGGTAA 27
 Db |||||
 1 GACCGGTAA 10
 RESULT 422
 ABK72535
 ID ABK72535 standard; DNA; 12 BP.
 XX AC ABK72535;
 XX 13-AUG-2002 (first entry)
 XX Human OP1 gene, exon/intron junction #2.
 XX Human; ophthalmological; OP1; autosomal dominant optic atrophy; ADOA;
 KW gene; ds.
 XX Homo sapiens.
 XX WO200227022-A2.
 XX 04-APR-2002.
 XX 26-SEP-2001; 2001WO-GB004284.
 XX 26-SEP-2000; 2000GB-00023555.
 XX (UNLO) UNIV COLLEGE LONDON.
 XX (UYEY-) UNIV EYE HOSPITAL.
 XX Bhattacharya S, Wissing B, Alexander C, Votruba M;
 XX WPI; 2002-416484/44.
 XX Novel human normal or mutant OP1 (the predominant locus for autosomal
 PT dominant optic atrophy (ADOA)) polypeptides and the OP1 gene, useful in
 PT the diagnosis and treatment of autosomal dominant optic atrophy ADOA.
 XX Disclosure; Fig 12; 75pp; English.
 XX The invention relates to an isolated human normal or mutant OP1 (the
 CC predominant locus for autosomal dominant optic atrophy (ADOA))
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa, DNA
 CC and substantially free of other human proteins. Also described is the
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OP1
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC and antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OP1 gene or gene product. ABK72533-ABK72593
 CC represent the human OP1 gene and intron/exon splice junctions
 XX Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 18 GACCTGGTAA 27
 Db |||||
 1 GACCGGTAA 10

CC The invention relates to an isolated human normal or mutant OPA1 (the
 CC predominant locus for autosomal dominant optic atrophy (ADOA))
 CC polypeptide (I), characterised by a molecular weight of about 112 kDa,
 CC and substantially free of other human proteins. Also described is the DNA
 CC (II) encoding (I). (I) and (II) are useful as a medicament, for the
 CC treatment of a medical condition resulting from a defect in the OPA1
 CC gene, which results in autosomal dominant optic atrophy. The nucleic acid
 CC gene, antibodies to (I) are useful in a variety of hybridisation and
 CC immunological assays to screen for, and to detect the presence of, either
 CC a normal or a defective OPA1 gene or gene product. ABK72533-ABK72593
 CC represent the human OPA1 gene and intron/exon splice junctions
 XX
 XX
 SQ Sequence 12 BP; 2 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GACCTGGTAA 27
 Db 1 GGCCTGGTAA 10
 |||||

RESULT 423
 AAL42695/C
 ID AAL42695 standard; DNA; 12 BP.

XX AC AAL42695;

XX DT 08-AUG-2002 (first entry)

XX DE Rice seed bZIP transcription factor-related nucleotide 13.

XX KW Rice seed b-zipper 1; RISB21; ds; rice; b-ZIP transcription factor;
 KW novel plant; transgenic plant; seed production; higher nutrition;
 KW denser protein storage.

XX OS Unidentified.

XX PN WO200231154-A1.

XX PD 18-APR-2002.

XX PF 11-OCT-2001; 2001WO-JP008936.

XX PR 11-OCT-2000; 2000JP-00311295.

XX PA (NORQ) NAT INST AGROBIOLOGICAL SCI.

XX PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

XX PI Takaiwa F, Onodera Y;

XX DR WPI; 2002-372276/40.

XX PT Rice seed-originated bZIP type transcription factors regulating
 PT expression of rice storage protein with binding activity to GCN4 motif,
 PT useful in constructing new breeds of plants to produce seeds with higher
 PT nutrition.

XX PS Example 11; Fig 13; 124pp; Japanese.

XX CC The invention comprises the amino acid and coding sequences of rice seed
 CC b-ZIP type transcription factors (RISB21, RISB24 and RISB25). The DNA and
 CC protein sequences of the rice seed b-ZIP transcription factors are useful
 CC in constructing new breeds of plants (e.g. rice) - to produce seeds with
 CC higher nutrition and denser protein storage. The present DNA sequence is
 CC included in the specification

XX SQ Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACCTGG 24
 Db 12 TGTGACCTGG 3
 |||||

RESULT 424

AAL42645/C

ID AAL42645 standard; DNA; 12 BP.

XX AC AAL42645;

XX DT 08-AUG-2002 (first entry)

XX DE Rice seed bZIP transcription factor PCR primer 1.

XX KW Rice seed b-zipper 1; RISB21; ss; rice; b-ZIP transcription factor;
 KW novel plant; transgenic plant; seed production; higher nutrition;
 KW denser protein storage; PCR; primer.

XX OS Oryza sativa.

XX PN WO200231154-A1.

XX PD 18-APR-2002.

XX PF 11-OCT-2001; 2001WO-JP008936.

XX PR 11-OCT-2000; 2000JP-00311295.

XX PA (NORQ) NAT INST AGROBIOLOGICAL SCI.

XX PA (BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.

XX PI Takaiwa F, Onodera Y;

XX DR WPI; 2002-372276/40.

XX PT Rice seed-originated bZIP type transcription factors regulating
 PT expression of rice storage protein with binding activity to GCN4 motif,
 PT useful in constructing new breeds of plants to produce seeds with higher
 PT nutrition.

XX PS Disclosure; Page 21; 124pp; Japanese.

XX CC The invention comprises the amino acid and coding sequences of rice seed
 CC b-ZIP type transcription factors (RISB21, RISB24 and RISB25). The DNA and
 CC protein sequences of the rice seed b-ZIP transcription factors are useful
 CC in constructing new breeds of plants (e.g. rice) - to produce seeds with
 CC higher nutrition and denser protein storage. DNA sequences AAL42638 -
 CC AAL42682 represent rice seed bZIP transcription factor PCR primers

XX SQ Sequence 12 BP; 4 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACCTGG 24
 Db 12 TGTGACCTGG 3
 |||||

RESULT 425

ABK29928

ID ABK29928 standard; DNA; 12 BP.

XX AC ABK29928;

XX DT 23-APR-2002 (first entry)

XX DE Beta-lactamase promoter wild type sequence for the start site.

XX KW Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;

KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
 KW vanH promoter; androgen receptor promoter; AR promoter;
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;
 KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
 KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KW gene expression modulator; multiple sclerosis; MS;
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KW transgenic; ss.
 XX Escherichia coli.
 OS WO200194600-A2.
 XX PN 13-DEC-2001.
 XX PD 06-JUN-2001; 2001WO-US018343.
 XX PF 06-JUN-2000; 2000US-0209549P.
 XX PR (GENE-) GENELABS TECHNOLOGIES INC.
 XX PA Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
 XX PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
 XX PI Lim MY, Bruice TW;
 XX DR WPI; 2002-130595/17.
 XX New nucleic acid regulatory sequences, which are able to regulate
 PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 PT immunological diseases.
 XX Claim 17; Page 60; 95pp; English.
 XX The invention describes an isolated nucleic acid regulatory sequence for
 CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents a primer used in the invention to
 CC determine the functions of regions within the selected promoters,
 CC described in the method of the invention
 XX Sequence 12 BP; 5 A; 3 C; 1 G; 3 T; 0 U; 0 Other;
 SQ Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 20 CCTGCTAAAT 29
 |||||
 Db 3 CCTGATAAAT 12

RESULT 426
 ABK30092
 ID ABK30092 standard; DNA; 12 BP.
 XX AC ABK30092;
 XX 23-APR-2002 (first entry)
 XX Beta-lactamase promoter, wild type -5 to +7 region.
 XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
 KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
 KW vanH promoter; androgen receptor promoter; AR promoter;
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;
 KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
 KW Enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KW gene expression modulator; multiple sclerosis; MS;
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KW mutant; transgenic; ds.
 XX Escherichia coli.
 OS WO200194600-A2.
 XX PN 13-DEC-2001.
 XX PD 06-JUN-2001; 2001WO-US018343.
 XX PF 06-JUN-2000; 2000US-0209549P.
 XX PR (GENE-) GENELABS TECHNOLOGIES INC.
 XX PA Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EF;
 XX PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
 XX PI Lim MY, Bruice TW;
 XX DR WPI; 2002-130595/17.
 XX New nucleic acid regulatory sequences, which are able to regulate
 PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 PT immunological diseases.
 XX Example 7; Page 57; 95pp; English.
 XX The invention describes an isolated nucleic acid regulatory sequence for
 CC a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents a mutated promoter region used in the
 CC invention to determine the regulatory regions involved in gene

```
CC expression, described in the method of the invention
XX
SQ Sequence 12 BP; 5 A; 3 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAAT 29
   ||||| |||||
Db 3 CCTGATAAAT 12

RESULT 427
ABA91368
ID ABA91368 standard; DNA; 12 BP.
XX
AC ABA91368;
XX
XX
DT 08-APR-2002 (first entry)
XX
DE DNA encoding neuroactive peptide NT-13.
XX
KW Neuroactive peptide; NT-13; hypoxia; ischaemia; therapy; gene; ss.
XX
OS Synthetic.
XX
FN WO200198367-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US019839.
XX
PR 22-JUN-2000; 2000US-0213614P.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Moskal JR, Yamamoto H, Colley PA;
XX
DR WPI; 2002-098225/13.
XX
DR P-PSDB; AAM50692.
XX
PT Use of peptide or amino acid compositions for the treatment of hypoxia
PT and ischemia.
XX
PS Disclosure; Page 13; 41pp; English.
XX
CC The present sequence is that of DNA capable of encoding NT-13 (see
CC AAM50692), a neuroactive peptide that binds to the N-methyl-D-aspartate
CC (NMDA) receptor, and which can be used to treat hypoxia and ischaemia. A
CC method of treating hypoxia by administering a peptide or amino acid
CC composition comprising a neuroactive peptide such as NT-13, a DNA
CC molecule encoding a neuroactive peptide such as NT-13, and a method of
CC treating the effects of hypoxia in the central nervous system by
CC administering a neuroactive peptide, especially NT-13, are claimed. NT-13
CC was shown to be a partial agonist in a pharmacological NMDA-specific
CC function assay, a partial agonist in voltage-clamp experiments in an
CC oocyte expression system, and a partial agonist in a behavioural NMDA-
CC specific function assay
XX
SQ Sequence 12 BP; 3 A; 6 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 90.0%; Pred. No. 2e+02;
  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13
   ||||| |||||
Db 3 TCCACCTACT 12

RESULT 428
ADE85925
ID ADE85925 standard; RNA; 12 BP.
XX
AC ADE85925;
XX
DT 29-JAN-2004 (first entry)
XX
DE Immunostimulatory G,U-containing RNA oligomer from HIV-1.
XX
KW Toll-like receptor; immunostimulant; antimicrobial; antiallergic;
KW cytostatic; vaccine; HIV-1; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO2003086280-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010406.
XX
PR 04-APR-2002; 2002US-0370515P.
PR 29-OCT-2002; 2002US-0421966P.
XX
PA (COLE-) COLEY PHARM GMBH.
XX
PI Lipford G, Bauer S;
XX
DR WPI; 2003-845251/78.
XX
PT New immunostimulatory composition, useful in inducing an immune response
PT against microbial or cancer antigen or allergen.
XX
PS Example 11; SEQ ID NO 2; 220pp; English.
XX
CC The present sequence is that of a G,U-containing RNA oligomer
CC corresponding to nucleotides 112-123 of HIV-1 strain BH10. This is an
CC example of immunostimulatory RNA oligomers of the invention that comprise
CC at least one guanine and at least one uracil. The RNA oligomers are
CC preferably G,U-rich RNA, do not require a CpG dinucleotide, and are at
CC least 50% self-complementary. They are thought to signal through an MyD88
CC -dependent pathway, probably through Toll-like receptor (TLR) 7 or TLR8,
CC and are believed to be ligands of TLR7 or TLR8. Claimed immunostimulatory
CC compositions comprise a G,U-containing RNA oligomer and optionally an
CC antigen, especially an allergen, cancer antigen or microbial antigen.
CC Methods are provided for activating an immune cell, inducing an immune
CC response, stimulating TLR8 or TLR7 signalling, and supplementing a TLR8-
CC or TLR7-mediated immune response. The methods and compositions are useful
CC for activating immune cells in vivo, in vitro and ex vivo, treating
CC infection, treating cancer, identifying a target receptor, and screening
CC for additional immunostimulatory compounds. In an example from the
CC invention, administration of the present RNA oligomer to human peripheral
CC blood mononuclear cells at micromolar concentrations in the presence of
CC DOTAP induced 50-100 ng/ml of tumour necrosis factor and 50-200 ng/ml of
CC interleukin-12 p40.
XX
SQ Sequence 12 BP; 0 A; 1 C; 5 G; 0 T; 6 U; 0 Other;

  Query Match      29.0%; Score 8.4; DB 1; Length 12;
  Best Local Similarity 50.0%; Pred. No. 2e+02;
  Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
   |::|::|::|
Db 3 CUGUUGUGUG 12

RESULT 429
ADF78662/c
ID ADF78662 standard; DNA; 12 BP.
XX
AC ADF78662;
XX
DT 26-FEB-2004 (first entry)
XX
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```

DE  Chromosomal abnormality detection-related PCR primer 243.
XX  chromosomal abnormality; maternal locus; genetic disorder; foetus;
XX  mutation; translocation; transversion; monosomy; trisomy; trisomy 21;
XX  chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;
XX  chromosome addition; chromosome amplification; chromosome translocation;
XX  chromosome rearrangement; single nucleotide polymorphism detection;
XX  SNP detection; pregnant female; PCR; primer; ss.
OS  Homo sapiens.
XX  WO2003074723-A2.
XX  12-SEP-2003.
XX  28-FEB-2003; 2003WO-US006198.
XX  01-MAR-2002; 2002US-0360232P.
XX  11-MAR-2002; 2002US-00093618.
XX  08-MAY-2002; 2002US-0378354P.
XX  (DHALL/) DHALLAN R.
XX  Dhallan R;
XX  WPI; 2003-845073/78.
XX  Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
XX  invasively in a fetus, comprises forming a ratio of amounts of alleles at
XX  a locus of interest and a different heterozygous locus.
XX  Example 11; Page 238; 164pp; English.
XX  This invention relates to a novel method of detecting chromosomal
XX  abnormalities by determining the sequence of alleles of a locus of
XX  interest from template DNA, determining which alleles are present and
XX  comparing to amounts of alleles at a different, selected heterozygous
XX  locus (for example on another chromosome or a maternal locus); relative
XX  amounts are expressed as a ratio indicating presence or absence of the
XX  abnormality. The method is useful for the detection of genetic disorders,
XX  especially in a foetus, including chromosomal abnormalities and
XX  mutations, for example translocations, transversions, monosomies,
XX  trisomies (for example trisomy 21 in which an additional copy of
XX  chromosome 21 results in Down's Syndrome) and other aneuploidies,
XX  deletions, additions, amplifications, translocations and rearrangements.
XX  It can be used to detect any alterations in a gene sequence, especially
XX  single nucleotide polymorphisms (SNPs), and may be used to detect
XX  numerous abnormalities simultaneously, for example if several SNPs are
XX  associated with a particular disease. The method provides a rapid, non-
XX  invasive method for determining the sequence of DNA from a foetus using a
XX  sample from a pregnant female, for example to detect genetic disorders as
XX  above or to determine if a foetus is a carrier of a disease or
XX  predisposed to a disease.
XX  Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
XX  Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX  Best Local Similarity 90.0%; Pred. No. 2e+02;
XX  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  10 TGCTGTGTGA 19
DB  12 TTCTGTGTGA 3

RESULT 430
ADF78486/c
XX  ADF78486 standard; DNA; 12 BP.
XX  AC ADF78486;
XX  26-FEB-2004 (first entry)
XX  DT
XX

DE  Chromosomal abnormality detection-related PCR primer 67.
XX  chromosomal abnormality; maternal locus; genetic disorder; foetus;
XX  mutation; translocation; transversion; monosomy; trisomy; trisomy 21;
XX  chromosome 21; Down's Syndrome; aneuploidies; chromosome deletion;
XX  chromosome addition; chromosome amplification; chromosome translocation;
XX  chromosome rearrangement; single nucleotide polymorphism detection;
XX  SNP detection; pregnant female; PCR; primer; ss.
OS  Homo sapiens.
XX  WO2003074723-A2.
XX  12-SEP-2003.
XX  28-FEB-2003; 2003WO-US006198.
XX  01-MAR-2002; 2002US-0360232P.
XX  11-MAR-2002; 2002US-00093618.
XX  08-MAY-2002; 2002US-0378354P.
XX  (DHALL/) DHALLAN R.
XX  Dhallan R;
XX  WPI; 2003-845073/78.
XX  Detection of chromosomal abnormalities e.g. Down's Syndrome, non-
XX  invasively in a fetus, comprises forming a ratio of amounts of alleles at
XX  a locus of interest and a different heterozygous locus.
XX  Example 11; Page 214; 164pp; English.
XX  This invention relates to a novel method of detecting chromosomal
XX  abnormalities by determining the sequence of alleles of a locus of
XX  interest from template DNA, determining which alleles are present and
XX  comparing to amounts of alleles at a different, selected heterozygous
XX  locus (for example on another chromosome or a maternal locus); relative
XX  amounts are expressed as a ratio indicating presence or absence of the
XX  abnormality. The method is useful for the detection of genetic disorders,
XX  especially in a foetus, including chromosomal abnormalities and
XX  mutations, for example translocations, transversions, monosomies,
XX  trisomies (for example trisomy 21 in which an additional copy of
XX  chromosome 21 results in Down's Syndrome) and other aneuploidies,
XX  deletions, additions, amplifications, translocations and rearrangements.
XX  It can be used to detect any alterations in a gene sequence, especially
XX  single nucleotide polymorphisms (SNPs), and may be used to detect
XX  numerous abnormalities simultaneously, for example if several SNPs are
XX  associated with a particular disease. The method provides a rapid, non-
XX  invasive method for determining the sequence of DNA from a foetus using a
XX  sample from a pregnant female, for example to detect genetic disorders as
XX  above or to determine if a foetus is a carrier of a disease or
XX  predisposed to a disease.
XX  Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
XX  Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX  Best Local Similarity 90.0%; Pred. No. 2e+02;
XX  Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  7 ACCTGCTGTG 16
DB  10 ACCCGCTGTG 1

RESULT 431
ABZ72938
XX  ABZ72938 standard; RNA; 12 BP.
XX  AC ABZ72938;
XX  09-APR-2003 (first entry)
XX  DT
XX

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DE Rod opsin hammerhead ribozyme oligonucleotide.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
XX
PF 01-MAY-2002; 2002WO-US013679.
XX
XX
PR 01-MAY-2001; 2001US-00847601.
XX
XX (UYFL ) UNIV FLORIDA.
XX
XX Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
PS Example 5; Page 73; 115pp; English.
XX
XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, INOS,
XX RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide; or (e) a host cell
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically
XX cleave the mRNA in the cell. (I) has ophthalmological activity, and can
XX be used in gene therapy. (I) can be used for treating a disease or
XX dysfunction of the mammalian eye, such as a retinal disease or retinal
XX degeneration. (I) is also useful for manufacturing a medicament for
XX treating the diseases mentioned above, including autosomal dominant
XX retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
XX for treating, decreasing the severity, or ameliorating the symptoms of a
XX pathological condition, e.g. atrophic or pigmented lesions of the eye,
XX blindness, a reduction in central or peripheral vision, or a reduction in
XX total vision. ABZ72763 to ABZ72953 represent sequences used in the
XX exemplification of the present invention
XX
XX Sequence 12 BP; 2 A; 6 C; 2 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 70.0%; Pred. No. 2e+02;
XX Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 4 TCCACCTGCT 13
XX :|||||
XX Db 1 UCCACCAGCU 10
XX
XX
XX RESULT 432
XX ADM56049
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ID ADM56049 standard; DNA; 12 BP.
XX
AC ADM56049;
XX
XX 03-JUN-2004 (first entry)
XX
DE Antibacterial peptide related PCR primer.
XX
KW antibacterial peptide; bactericidal; antibacterial;
KW solid-phase chemical process; gene engineering expression;
KW Gram-negative bacterium; Gram-positive bacterium; fungal infection;
KW infection; PCR; primer; ss.
XX
OS Synthetic.
XX
XX CN1398897-A.
XX
XX 26-FEB-2003.
XX
XX 02-SEP-2002; 2002CN-00136766.
XX
XX 02-SEP-2002; 2002CN-00136766.
XX
XX (SHAN-) SHANGHAI GAOKO UNION BIOTECHNOLOGY DEV C.
XX
XX Huang Q;
XX
XX WPI; 2003-457919/44.
XX
XX Serial synthetic antibacterial peptide.
XX
XX Example 2; Page 10; 41pp; Chinese.
XX
XX The present invention describes a group of synthetic antibacterial
XX peptides with bactericidal activity stronger than that of a natural
XX antibacterial peptide. The synthetic antibacterial peptide is prepared by
XX the solid-phase chemical process or gene engineering expression. The
XX synthetic antibacterial peptide may be used in preparing medicine for
XX treating diseases caused by Gram-negative bacterium, Gram-positive
XX bacterium and fungus infection. The present sequence represents a PCR
XX primer used in an example from the present invention.
XX
XX Sequence 12 BP; 2 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 5 CCACCTGCTG 14
XX |||||
XX Db 1 CCGCCTGCTG 10
XX
XX
XX RESULT 433
XX ADM56293/C
XX
XX ID ADM56293 standard; DNA; 12 BP.
XX
XX ADM56293;
XX
XX 03-JUN-2004 (first entry)
XX
XX Mouse SLC26A6 anion transporter protein gene splice site #12.
XX
XX SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;
XX splice site; ds; mouse; murine.
XX
XX Mus musculus.
XX
XX WO2003072759-A2.
XX
XX 04-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006469.
```


Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. NO. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCT 10
| | | | | | | | | |
Db 11 CCACCCACT 2

RESULT 436
ADQ30184/c
ID ADQ30184 standard; DNA; 12 BP.
XX
AC ADQ30184;
XX
DT 09-SEP-2004 (first entry)
XX
DE Murine VR1 exon 1d transcription factor binding fragment #76.
XX
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZP1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW hypalgesia; hyperalgesia; neuralgia; myalgia; murine.
XX
OS Mus sp.
XX
FN WO2004053120-A2.
XX
PD 24-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Weihe E, Bieller A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 50; 68pp; German.
XX
CC This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the
CC modulator or the vector into a cell that contains the VR1 gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbant assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VR1 receptor expression includes a
CC binding site for a transcription factor, e.g. MZP1, NFkappaB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VR1
CC receptor. This sequence represents a fragment of murine VR1 exon 1d DNA
CC which is capable of binding to a transcription factor.
XX
SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. NO. 2e+02; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACTGTC 12
| | | | | | | | | |
Db 12 AGCCACTGTC 3

RESULT 437
ADQ30185/c
ID ADQ30185 standard; DNA; 12 BP.
XX
AC ADQ30185;
XX
DT 09-SEP-2004 (first entry)
XX
DE Murine VR1 exon 1d transcription factor binding fragment #77.
XX
KW ds; VR1 receptor; vanilloid receptor type 1; modulator;
KW pain transmission; primary sensory neuron; transcription factor;
KW detection; MZP1; NFkappaB; NFAT; GATA1; sensitivity disorder; analgesia;
KW hypalgesia; hyperalgesia; neuralgia; myalgia; murine.
XX
OS Mus sp.
XX
FN WO2004053120-A2.
XX
PD 24-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-EP013522.
XX
PR 09-DEC-2002; 2002DE-01057421.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Weihe E, Bieller A, Schaefer MKH;
XX
DR WPI; 2004-468868/44.
XX
PT New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX
PS Disclosure; Page 50; 68pp; German.
XX
CC This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridises to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the
CC modulator or the vector into a cell that contains the VR1 gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbant assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VR1 receptor expression includes a
CC binding site for a transcription factor, e.g. MZP1, NFkappaB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hyperalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VR1
CC receptor. This sequence represents a fragment of murine VR1 exon 1d DNA
CC which is capable of binding to a transcription factor.
XX


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SQ Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
   | | | | | | | |
Db 12 AGCCACCTGC 3

RESULT 438
ADQ30343/c
XX ID ADQ30343 standard; DNA; 12 BP.
XX AC ADQ30343;
XX DT 09-SEP-2004 (first entry)
XX DE Human VR1 exon 1d transcription factor binding fragment #62.
XX ds; VR1 receptor; vanilloid receptor type 1; modulator;
XX pain transmission; primary sensory neuron; transcription factor;
XX detection; MZP1, NFKappaB, NFAT; GATA1; sensitivity disorder; analgesia;
XX hypalgesia; hyperalgesia; neuralgia; myalgia; human.
XX OS Homo sapiens.
XX WO2004053120-A2.
XX PD 24-JUN-2004.
XX PF 01-DEC-2003; 2003WO-EP013522.
XX PR 09-DEC-2002; 2002DE-01057421.
XX PA (CHEF ) GRUENENTHAL GMBH.
XX PI Weihe E, Bieller A, Schaefer MKH;
XX WPI; 2004-468868/44.

XX New nucleic acid that modulates expression of the vanilloid receptor-1,
PT useful for control of pain or sensitivity disorders, comprises sequences
PT from control regions of the receptor gene.
XX Disclosure; Page 53; 68pp; German.

XX This invention describes a novel nucleic acid containing a specific
CC segment having at least one region that modulates expression of the VR1
CC (vanilloid receptor type 1) receptor, or a functional derivative, allele
CC or fragment of this region, or a sequence that hybridizes to it under
CC standard conditions. The VR1 modulator is derived from one or more of
CC positions 221931-223344 of GenBank AL670399, 31673-36359 of AL663116, or
CC 44731-43231 or 36616-33151 of AF168787 and is involved in transmission of
CC pain, particularly in primary sensory neurons. The invention also
CC describes a vector that contains the VR1 modulator, host cells containing
CC this vector (other than human germ or embryonal stem cells) and a method
CC for modulating expression of the VR1 receptor by introducing the
CC modulator or the vector into a cell that contains the VR1 gene. The
CC products of the invention are used for detecting a transcription factor
CC from its binding to a regulatory sequence (or a double-stranded
CC oligonucleotide fragment of it), e.g. by Western blotting or enzyme-
CC linked immunosorbant assay, particularly for diagnosis of diseases
CC associated with overexpression or underexpression of the transcription
CC factor. The region that modulates VR1 receptor expression includes a
CC binding site for a transcription factor, e.g. MZP1, NFKappaB, NFAT or
CC GATA1. The nucleic acids of the invention, or vectors containing them,
CC are used for prevention or treatment of pain, also for treating
CC sensitivity disorders, e.g. analgesia, hypalgesia or hyperalgesia, also
CC neuralgia and myalgia, that are associated with activity of the VR1
CC receptor. This sequence represents a fragment of human VR1 exon 1d DNA
CC which is capable of binding to a transcription factor.

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XX SQ Sequence 12 BP; 4 A; 1 C; 5 G; 2 T; 0 U; 0 Other;
Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
   | | | | | | | |
Db 12 ATTCACCTGC 3

RESULT 439
ADR32504
XX ID ADR32504 standard; DNA; 12 BP.
XX AC ADR32504;
XX DT 04-NOV-2004 (first entry)
XX DE Human nicking agent target DNA #45.
XX ss; nicking agent; assay panel; diagnosis; expression pattern;
XX DNA fingerprinting; nosocomial infection; microbiological assay;
XX bacterial contamination; genome mapping; bioremediation.
XX OS Homo sapiens.
XX WO2004067765-A2.
XX PD 12-AUG-2004.
XX PF 29-JAN-2004; 2004WO-US002720.
XX PR 29-JAN-2003; 2003US-0443811P.
XX PA (KECK-) KECK GRADUATE INST.
XX PI Van Ness J, Galas DJ, Van Ness LK;
XX WPI; 2004-581010/56.

XX Identifying nucleic acid sample source, useful for identifying bacterial
PT strains involved in nosocomial infections, comprises treating the nucleic
PT acid sample with components comprising a nicking agent under nicking
PT conditions.
XX Example 1; Page 72; 238pp; English.

XX The invention relates to a method of treating a nucleic acid sample with
CC components under nicking conditions, where the components comprise a
CC nicking agent, and the conditions cause the nicking agent to nick the
CC nucleic acid sample to thus produce a family of initiating
CC oligonucleotide fragments, and subjecting one or more members of the
CC family of initiating oligonucleotide fragments to a characterization
CC process to thus provide results. The method is useful for creating an
CC assay panel of diagnostic oligonucleotides that can identify any organism
CC or individual. The method is useful for characterizing other DNA
CC molecules e.g., cDNA, and for characterizing cDNA expression patterns.
CC The method, kit or composition is useful for identifying the source
CC organism of a nucleic acid sample e.g., bacterium, fungus, virus, plant,
CC non-human animal or human. The method is particularly useful for rapidly
CC fingerprinting DNA to identifying prokaryotic and eukaryotic species. It
CC subspecies, and especially strains or individuals of the subspecies. It
CC is especially useful for identifying different bacterial strains involved
CC in e.g., nosocomial infections. Furthermore, the method is useful for
CC diagnosing bacterial disease in plants and humans, monitoring for
CC bacterial content and/or contamination in the environment, monitoring
CC food for bacterial contamination, monitoring quality assurance/processes for
CC bacterial contamination, monitoring quality assurance/quality control of
CC laboratory tests involving microbiological assays, tracing bacterial
CC contamination and/or outbreaks of bacterial infections, genome mapping,
CC monitoring bioremediation sites, and for monitoring agricultural sites

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CC for test crops, bacteria and recombinant molecules. This sequence
 CC corresponds to nucleic acid used in the method of the invention.
 XX
 SQ Sequence 12 BP; 0 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CTTGCTGTGT 17
 |||||
 Db 3 CTTGCGGTGT 12
 RESULT 440
 ADR98238/c
 ID ADR98238 standard; DNA; 12 BP.
 XX
 AC ADR98238;
 XX 02-DEC-2004 (first entry)
 DT
 DE Human chromosome 21 SNP Set 81 PCR primer #2.
 XX
 KW ss; chromosomal abnormality; detection; foetus; translocation;
 KW transversion; monosomy; trisomy; aneuploidy; deletion; addition;
 KW amplification; prenatal diagnosis; PCR; primer; SNP;
 KW single nucleotide polymorphism; human; chromosome 21.
 XX
 OS Homo sapiens.
 XX
 PN WO2004079011-A1.
 XX
 PD 16-SEP-2004.
 XX
 XX 29-AUG-2003; 2003WO-US027308.
 XX
 PR 28-FEB-2003; 2003WO-US006198.
 XX
 XX (RAVG-) RAVGEN INC.
 XX
 XX Dhallan R;
 XX
 DR WPI; 2004-677127/66.
 XX
 XX Detecting a chromosomal abnormality, e.g. translocations, transversions,
 PT monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises
 PT determining the sequence of alleles of a locus of interest in the sample
 PT from template DNA.
 XX
 XX Example 12; Page 223; 429pp; English.
 XX
 CC This invention describes a novel method for detecting a chromosomal
 CC abnormality in a sample which comprises determining the sequence of
 CC alleles of a locus of interest in a sample from template DNA where
 CC determining the sequence of the alleles comprises amplifying the locus of
 CC interest, hybridising the amplified loci to GeneChip array, washing
 CC GeneChip array, staining the GeneChip array with detectable reagents, and
 CC scanning GeneChip array. The amplification method is self-sustained
 CC sequence reaction, ligase chain reaction, rapid amplification of cDNA
 CC ends, PCR and ligase chain reaction, Q-beta phage amplification, strand
 CC displacement amplification, or splice overlap extension PCR, preferably
 CC PCR. The determination of the sequence of the alleles comprises
 CC fragmenting the locus of interest, fragmenting the amplicon, hybridising
 CC fragmented amplicons to CodeLink Arrays, extension reaction to
 CC incorporate a nucleotide and detecting incorporated nucleotides. The
 CC amplicon fragmentation is by exonuclease digestion. Detecting a
 CC chromosomal abnormality in a sample comprises determining the sequence of
 CC alleles of a locus of interest from template DNA, where determining the
 CC sequence of the alleles comprises using Beadarray Technology. The
 CC determination of the sequence of the alleles may also be done by
 CC amplifying the locus of interest, dephosphorylation of the unused
 CC reagents, in vitro transcription reaction of the products, RNase A

CC cleavage of the products, mixing the products with CleanResin,
 CC transferring products to SpectroCHIP, and analysing the SpectroCHIP. The
 CC dephosphorylation reaction is with shrimp alkaline phosphatase.
 CC Alternatively, the determination of the sequence of the alleles comprises
 CC amplifying the locus of interest, dephosphorylation of the unused
 CC reagents, hybridising a primer to the locus of interest, incorporating a
 CC nucleotide, mixing the products with CleanResin, transferring products to
 CC SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer
 CC is adjacent to the locus of interest. The determination of the sequence
 CC of the alleles may also comprise amplifying the locus of interest,
 CC treating the products with exonuclease, single stranded DNA is annealed
 CC to an oligonucleotide, incorporating a nucleotide using the annealed
 CC template and primer, and detecting the incorporated nucleotide. The
 CC method is useful for detecting a chromosomal abnormality in a sample.
 CC Specifically, the method is useful for detecting chromosomal
 CC abnormalities in a fetus including translocations, transversions,
 CC monosomies, trisomies, and other aneuploidies, deletions, additions,
 CC amplifications, and arrangements. The method of the invention can also be
 CC used for prenatal diagnosis. This sequence represents a PCR primer used
 CC to amplify human SNP's from chromosome 21.
 XX
 SQ Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 29.0%; Score 8.4; DB 1; Length 12;
 Best Local Similarity 90.0%; Pred. No. 2e+02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 10 TGCTGTGTGA 19
 |||||
 Db 12 TTCTGTGTGA 3
 RESULT 441
 ADR98062/c
 ID ADR98062 standard; DNA; 12 BP.
 XX
 AC ADR98062;
 XX 02-DEC-2004 (first entry)
 DT
 DE Human SNP TSC0470003 multiplex PCR primer #2.
 XX
 KW ss; chromosomal abnormality; detection; foetus; translocation;
 KW transversion; monosomy; trisomy; aneuploidy; deletion; addition;
 KW amplification; prenatal diagnosis; PCR; primer; SNP;
 KW single nucleotide polymorphism; human; multiplex; TSC0470003.
 XX
 OS Homo sapiens.
 XX
 PN WO2004079011-A1.
 XX
 PD 16-SEP-2004.
 XX
 XX 29-AUG-2003; 2003WO-US027308.
 XX
 PR 28-FEB-2003; 2003WO-US006198.
 XX
 XX (RAVG-) RAVGEN INC.
 XX
 XX Dhallan R;
 XX
 DR WPI; 2004-677127/66.
 XX
 XX Detecting a chromosomal abnormality, e.g. translocations, transversions,
 PT monosomies, trisomies, aneuploidies, deletions, or arrangements, comprises
 PT determining the sequence of alleles of a locus of interest in the sample
 PT from template DNA.
 XX
 XX Example 12; Page 200; 429pp; English.
 PS
 XX This invention describes a novel method for detecting a chromosomal
 CC abnormality in a sample which comprises determining the sequence of
 CC alleles of a locus of interest in a sample from template DNA where

determining the sequence of the alleles comprises amplifying the locus of interest, hybridising the amplified loci to GeneChip array, washing GeneChip array, staining the GeneChip array with detectable reagents, and scanning GeneChip array. The amplification method is self-sustained sequence reaction, ligase chain reaction, rapid amplification of cDNA ends, PCR and ligase chain reaction, Q-beta phage amplification, strand displacement amplification, or splice overlap extension PCR, preferably PCR. The determination of the sequence of the alleles comprises amplifying the locus of interest, fragmenting the amplicon, hybridising fragmented amplicons to CodeLink Arrays, extension reaction to incorporate a nucleotide and detecting incorporated nucleotides. The amplicon fragmentation is by exonuclease digestion. Detecting a chromosomal abnormality in a sample comprises determining the sequence of alleles of a locus of interest from template DNA, where determining the sequence of the alleles comprises using BeadArray Technology. The determination of the sequence of the alleles may also be done by amplifying the locus of interest, dephosphorylation of the unused reagents, in vitro transcription reaction of the products, RNase A cleavage of the products, mixing the products with CleanResin, transferring products to SpectroCHIP, and analysing the SpectroCHIP. The dephosphorylation reaction is with shrimp alkaline phosphatase. Alternatively, the determination of the sequence of the alleles comprises amplifying the locus of interest, dephosphorylation of the unused reagents, hybridising a primer to the locus of interest, incorporating a nucleotide, mixing the products with CleanResin, transferring products to SpectroCHIP, and analysing the SpectroCHIP. The hybridisation of primer is adjacent to the locus of interest. The determination of the sequence of the alleles may also comprise amplifying the locus of interest, treating the products with exonuclease, single stranded DNA is annealed to an oligonucleotide, incorporating a nucleotide using the annealed template and primer, and detecting the incorporated nucleotide. The method is useful for detecting a chromosomal abnormality in a sample. Specifically, the method is useful for detecting chromosomal abnormalities in a fetus including translocations, deletions, additions, monosomies, trisomies, and other aneuploidies. The method can also be used for prenatal diagnosis. This sequence represents a multiplex PCR primer used to amplify the human SNP TSC0470003.

XX Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ACCTGCTGTG 16
||| |||||
Db 10 ACCCGCTGTG 1

RESULT 442
ADS08925/c
ID ADS08925 standard; DNA; 12 BP.

XX ADS08925;

XX 02-DEC-2004 (first entry)

XX Human DNA PCR primer #262.

XX Human; PCR; primer; ss; nucleic acid detection; cell lysis;
KW chromosomal abnormality; cancer; carcinoma; bladder; breast; bronchus;
KW colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas;
KW stomach; cervix; thyroid; prostate; skin; small cell lung cancer;
KW squamous cell carcinoma; leukaemia; lymphoma; myelodysplastic syndrome;
KW fibrosarcoma; rhabdomyosarcoma; astrocytoma; neuroblastoma; glioma;
KW schwannoma; melanoma; seminoma; teratocarcinoma; osteosarcoma.

XX Homo sapiens.

XX WO2004078994-A2.

XX 16-SEP-2004.

XX 01-MAR-2004; 2004WO-US006337.

XX 28-FEB-2003; 2003WO-US006198.

XX (RAVG-) RAVGEN INC.

XX Dhallan R;

XX WPI; 2004-662434/54.

XX Detecting presence or absence of nucleic acid, containing mutation,
PT involves isolating nucleic acid from sample containing cell lysis
PT inhibitor, and detecting presence or absence of nucleic acid.

XX Example 12; Page 232; 440pp; English.

XX The invention relates to a method for detecting a nucleic acid, involving
CC isolating a nucleic acid from a sample, where an agent that impedes cell
CC lysis was added to the sample, and detecting the presence or absence of
CC the nucleic acid. The invention also relates to a method for detecting
CC chromosomal abnormalities in a DNA sample and determining the sequence of
CC foetal DNA from a sample of a pregnant female. The nucleic acid contains
CC at least one mutation chosen from a single point mutation, multiple point
CC mutations, an insertion, a frameshift, a truncation, a deletion, a
CC duplication and a transversion. The method is useful for detecting
CC nucleic acid in a sample obtained from a source chosen from bacteria,
CC viruses, fungi, mycobacteria, protozoa, molds, yeasts, plants, humans,
CC non-humans, multi-cellular parasites, animals and archaeobacteria. The
CC method is useful for detecting, diagnosing or monitoring a disease such
CC as cancer chosen from carcinoma of the bladder, breast, bronchus, colon,
CC kidney, liver, lung, oesophagus, gall bladder, ovary, pancreas, stomach,
CC cervix, thyroid, prostate and skin, small cell lung cancer, squamous cell
CC carcinoma, haematopoietic tumours of lymphoid lineage, leukaemia, acute
CC lymphocytic leukaemia, acute lymphoblastic leukaemia, B-cell lymphoma, T-
CC cell-lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma, hairy cell
CC lymphoma, Burkett's lymphoma, haematopoietic tumours of myeloid lineage,
CC acute and chronic myelogenous leukaemias, myelodysplastic syndrome and
CC promyelocytic leukaemia, tumours of mesenchymal origin, fibrosarcoma and
CC rhabdomyosarcoma, tumours of the central and peripheral nervous system,
CC astrocytoma, neuroblastoma, glioma and schwannomas, melanoma, seminoma,
CC teratocarcinoma and osteosarcoma. The method is also useful for
CC monitoring response to treatment chosen from surgery, radiation,
CC lifestyle change, dietary protocol and supplementation and administration
CC of a drug. The drug is chosen from chemotherapeutic agents, anti-
CC bacterial agents, anti-viral agents, anti-fungal agents, targeted-cancer
CC drugs, cytotoxic agents, cytostatic agents and anti-proliferative agents.
XX This sequence represents a PCR primer used in the scope of the invention.

XX Sequence 12 BP; 5 A; 5 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGCTGTGTGA 19
||| |||||
Db 12 TTCTGTGTGA 3

RESULT 443
ADS08749/c
ID ADS08749 standard; DNA; 12 BP.

XX ADS08749;

XX 02-DEC-2004 (first entry)

XX Human DNA PCR primer #86.

XX Human; PCR; primer; ss; nucleic acid detection; cell lysis;
KW chromosomal abnormality; cancer; carcinoma; bladder; breast; bronchus;
KW colon; kidney; liver; lung; oesophagus; gall bladder; ovary; pancreas;


```

PD 07-APR-2005.
XX
XX PF
XX 30-SEP-2004; 2004WO-JP014784.
XX
XX PR
XX 30-SEP-2003; 2003JP-00342519.
XX
XX PR
XX 28-MAY-2004; 2004JP-00158717.
XX
XX
XX (RIKE ) RIKEN KK.
XX (STAG-) STAGEN CO LTD.
XX (SEKI/) SEKINE A.
XX (IIDA/) IIDA A.
XX (SAIT/) SAITO S.
XX
XX Sekine A, Iida A, Saito S, Nakamura Y, Kamatani N;
XX WPI; 2005-305936/31.
XX
XX Analyzing haplotype, by detecting polymorphism in drug-related genes,
XX electing common polymorphism (CP), building haplotype block using CP,
XX specifying CP within block, specifying tag polymorphism from CP within
XX block.
XX
XX Disclosure; SEQ ID NO 1339; 1290pp; Japanese.
XX
XX The invention relates to a method of analyzing haplotype, by detecting
XX gene polymorphism in drug-related genes such as aryl acetylarnide
XX deacetylase, arylalkylamine N-acetyl transferase or ATP-binding cassette,
XX sub-family A (ABC1), member 1. The method is useful for analyzing
XX haplotype. The method is useful for estimating the sensitivity or disease
XX of a medicine or a foreign material, for selecting medicine for
XX preventing or treating diseases, for determining appropriate dosage of
XX medicine for treating or treating a disease, for analyzing a drug
XX interaction, and for determining the related polymorphism relative to the
XX sensitivity of the medicine, foreign material or disease. The diseases
XX include malignant tumor, immune disorder circulatory disease, metabolic
XX disease, kidney disease, respiratory disease and muscle associated
XX disease. The method enables analysis of the individual differences
XX related to the sensitivity of a medicine, using a haplotype, without
XX using each single nucleotide polymorphism. The present sequence
XX represents a human SNP detection related oligonucleotide.
XX
XX Sequence 12 BP; 1 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 14 GTGTGACCTG 23
XX ||||| ||||
XX 2 GTGTGGCCTG 11
XX
XX RESULT 446
XX AEA50022
XX ID AEA50022 standard; DNA; 12 BP.
XX
XX AC AEA50022;
XX
XX 25-AUG-2005 (first entry)
XX
XX Construct Fc-pcDNA3 DNA fragment #2.
XX
XX ds; immunoglobulin Fc receptor; autoimmune disease; multiple sclerosis;
XX systemic lupus erythematosus; rheumatoid arthritis; scleroderma;
XX Sjogrens syndrome; Bencets disease; inflammation;
XX inflammatory bowel disease; ulcerative colitis; Crohns disease; uveitis;
XX cancer; neoplasm; tumor; lung tumor; brain tumor; liver tumor; allergy;
XX immune disorder; asthma; respiratory disease; atopic dermatitis;
XX dermatological disease; drug delivery;
XX endothelial immunoglobulin receptor; elgR; anti allergy;
XX immunosuppressive; antiasthmatic; dermatological; antiinflammatory;
XX vasotropic; gastrointestinal-Gen.; neuroprotective; antiarthritic;
XX antirheumatic; antiulcer; ophthalmological.

```

```

XX OS Synthetic.
XX PN WO2005056597-A1.
XX PD 23-JUN-2005.
XX
XX 05-NOV-2004; 2004WO-JP016804.
XX
XX 09-DEC-2003; 2003JP-00410136.
XX
XX (RIKE ) RIKEN KK.
XX
XX Ohno H, Takatsu H;
XX WPI; 2005-445145/45.
XX
XX Novel immunoglobulin Fc receptor protein having activity of binding to Fc
XX of IGM and IGA, useful as medical agent for treatment of autoimmune
XX disease e.g. multiple sclerosis, inflammatory disease, lung cancer and
XX allergic disease.
XX
XX Example 3; Fig 5; 87pp; Japanese.
XX
XX This invention describes a novel immunoglobulin Fc receptor which can be
XX used to screen for an agonist or antagonist for the treatment of
XX autoimmune disease. the invention also describes 1) a protein consisting
XX of partial amino acid sequence of the receptor; 2) a fusion protein
XX comprising the receptor and another peptide; 3) a gene encoding the
XX receptor; 4) a recombinant vector containing the gene; 5) transformed
XX host transformed by the gene; 6) a method of preparing the receptor; 7)
XX an antibody which specifically recognizes the Fc receptor; 8) a reagent
XX for detecting the Fc receptor, comprising the antibody; 9) a method for
XX screening an agonist or antagonist of the receptor, which involves
XX reacting the Fc receptor with IGM or IGA in the presence of test sample
XX and selecting the substance which promotes or inhibits binding of the
XX receptor with IGM or IGA and 10) a pharmaceutical for controlling immune
XX response, comprising the Fc receptor or its gene, or the agonist or
XX antagonist obtained by the method in 9), as an active ingredient. The
XX receptor is useful as a medical agent for treatment of autoimmune disease
XX (e.g. multiple sclerosis, systemic lupus erythematosus, rheumatoid
XX arthritis, scleroderma, multiple myositis, Sjogren's syndrome, Bencet's
XX disease), inflammatory disease (e.g. inflammatory bowel disease,
XX ulcerative colitis, Crohn's disease, uveitis), tumor (e.g. lung cancer,
XX brain tumor, hepatic carcinoma), allergic disease (e.g. bronchial asthma,
XX atopic dermatitis), etc. The receptor is useful for elucidating the
XX immunological mechanism and for the development of drug delivery system.
XX The isolated Fc receptor gene capable of binding with IGA/IGM was
XX screened by BLAST program of National Center for Biotechnology
XX Information (NCBI). As a result, an Fc receptor gene having 36% homology
XX to a known Fc receptor of human and mouse was identified. The identified
XX gene was specific for endothelial cell and hence, the protein encoded by
XX the gene was named as endothelial immunoglobulin receptor (elgR). This
XX sequence represents a fragment of construct Fc-pcDNA3 which is used in
XX the method of the invention.
XX
XX Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 29.0%; Score 8.4; DB 1; Length 12;
XX Best Local Similarity 90.0%; Pred. No. 2e+02;
XX Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 20 CCTGTGTAAT 29
XX ||||| |||||
XX 1 CCGGGTAAT 10
XX
XX RESULT 447
XX ABK09921
XX ID ABK09921 standard; DNA; 10 BP.
XX
XX AC ABK09921;
XX

```

DT 14-MAR-2002 (first entry)

DE P2RY1 gene allele-specific oligonucleotide #72.

XX Purinergic receptor P2Y, G-protein coupled 1; P2RY1; anticoagulant;

XX coagulant; platelet aggregation; haplotyping; drug screening;

KW transgenic animal; human; allele-specific oligonucleotide; ss.

KW

XX Homo sapiens.

OS

XX WO200190117-A2.

XX

XX 29-NOV-2001.

XX

XX 21-MAY-2001; 2001WO-US016432.

XX

XX 19-MAY-2000; 2000US-0205996P.

XX

XX (GENA-) GENAISSANCE PHARM INC.

XX

XX Kazemi A, Koshy B, Tanguay DA;

XX

XX WPI; 2002-083074/11.

XX

XX New purinergic receptor P2Y G-protein coupled 1 (P2RY1) gene polymorphic

XX variants, useful e.g. in studying the expression and function of P2RY1

XX and screening candidate drugs for treating diseases related to P2RY1

XX activity.

XX

XX Claim 18; Page 14; 79pp; English.

XX

XX The invention relates to a novel isolated polypeptide comprising a

XX sequence which is a polymorphic variant of a reference sequence for the

XX purinergic receptor P2Y, G-protein coupled, 1 (P2RY1) protein or its

XX fragment. The polymorphic variant comprises one or more variant amino

XX acids selected from valine at a position 34 and glycine at a position

XX 262. The polymorphic variants are useful in studying the expression and

XX function of P2RY1, in expressing P2RY1 protein for use in screening for

XX candidate drugs to treat diseases related to P2RY1 activity. In studying

XX the effect of the variation on the biological activity of P2RY1, and the

XX binding affinity of candidate drugs targeting P2RY1 for the treatment of

XX disorders related to platelet aggregation. The haplotyping methods are

XX useful in validating P2RY1 as a candidate target for treating a specific

XX condition or disease predicted to be associated with P2RY1 activity, or

XX in the design of clinical trials of candidate drugs for treating a

XX specific condition or disease associated with P2RY1 activity. The

XX transgenic animals are useful for studying expression of the P2RY1

XX isogenes in vivo, for in vivo screening and testing of drugs targeted

XX against P2RY1 protein, and for testing the efficacy of therapeutic agents

XX and compounds for disorders related to platelet aggregation in a

XX biological system. ABK0950-ABK09924 represent human purinergic receptor

XX P2Y, G-coupled protein 1 (P2RY1) gene allele-specific oligonucleotides of

XX the invention

XX

SQ Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 25.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TGACCTGGT 25

1 |||||

Db 2 TTACCTGGT 10

RESULT 448

ADU19159/C

ID ADU19159 standard; DNA; 10 BP.

XX

XX AC ADU19159;

XX

DT 13-JAN-2005 (first entry)

XX

DE Hypoxia-related tumorigenesis-related SAGE tag #950.

XX

XX screening; hypoxia-related tumorigenesis;

KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.

KW

XX Unidentified.

OS

XX WO2004092198-A2.

XX

XX 28-OCT-2004.

XX

XX 09-APR-2004; 2004WO-US011087.

XX

XX 09-APR-2003; 2003US-0461712P.

XX

XX (GENZ) GENZYME CORP.

XX

XX Nacht M;

XX

XX WPI; 2004-758333/74.

XX

XX Identifying agents that alter biological activity of a polypeptide

XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis

XX comprises contacting an agent with a target cell and monitoring activity

XX of expressed product.

XX

XX Disclosure; Page 74; 100pp; English.

XX

XX The invention comprises a method of screening for candidate agents

XX capable of altering the biological activity of a protein encoded by a

XX nucleotide involved in hypoxia-related tumorigenesis. The method of the

XX invention involves: contacting a test agent with a target cell expressing

XX the nucleotide, and monitoring the activity of the expressed protein

XX product; if the test agent modifies the activity of the expressed protein

XX then this is a candidate agent. The method of the invention is useful for

XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing

XX or treating tumours. The present DNA sequence represents a SAGE tag that

XX was used in the exemplification of the invention.

XX

XX SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 25.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 2.5e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACTGGTAA 27

|||||

Db 10 ACCTGGTCA 2

Search completed: May 15, 2006, 15:03:40

Job time : 2 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 14:28:05 ; Search time 0.001 Seconds
(without alignments)
1.392 Million cell updates/sec

Title: US-09-904-968A-3-COPY

Perfect score: 29

Sequence: 1 ccatccacctgtgtgtgacctggtgataat 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 2 segs, 24 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 2 summaries

Database : estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9.4	32.4	13	1	CW020522
2	9	31.0	11	1	CZ171464

ALIGNMENTS

RESULT 1
CW020522
LOCUS
DEFINITION GC0792 TIGEM gene trap library Mus musculus cDNA clone m4.E4.D08, mRNA sequence.

ACCESSION CW020522

VERSION CW020522.1 GI:52789782

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 13)

Barbarisi, M., Nicolau, G., Iovino, M., Romito, A., Marra, E.,

Ballabio, A., and Cortese, R.

Tagging genes with cassette-exchange sites

Nucleic Acids Res. 33 (4), e44 (2005)

15741177

CONTACT: TIGEM

107

TIGEM

Via P. Castellino, 111, 80131 NAPOLI, ITALY

Tel: +390816132205

Fax: +390815790919

Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from TIGEM. Annotation information available from TIGEM
Class: Gene trap.

FEATURES

source

Location/Qualifiers
1..13
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/clone="m4.E4.D08"
/sex="male"
/cell_type="Embryonic stem cell"
/cell_line="E14"
/clone_lib="TIGEM gene trap library"
/notes="Vector: pFLIP1"

Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACTGGT 25

Db 2 TGGGACCTGGT 12

RESULT 2

CZ171464

LOCUS

DEFINITION

CZ171464 11 bp DNA linear GSS 31-JAN-2005
MTAA-107116b.b1 Meloidogyne incognita BAC end sequence library
(MIAAGSS 001) Meloidogyne incognita genomic, genomic survey
sequence.

ACCESSION CZ171464

VERSION CZ171464.1 GI:58339757

KEYWORDS GSS.

SOURCE

ORGANISM

Meloidogyne incognita (southern root-knot nematode)
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Meloidogynidae; Meloidogyninae; Meloidogyne.

REFERENCE 1 (bases 1 to 11)

AUTHORS

Mitreva, M., McCarter, J.P., Pape, D., Martin, J., Wylie, T.,

Clifton, S., Budiman, A., Lakey, N., Opperman, C. and Bird, D. McK.

Genome Survey sequences from the parasitic nematode Meloidogyne

incognita

Unpublished (2005)

CONTACT: Mitreva M

Washington University in St. Louis

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: nematode@watson.wustl.edu

BAC ends sequenced by Washington University Genome Sequencing

Center

Class: BAC ends.

Location/Qualifiers

1..11

/organism="Meloidogyne incognita"

/mol_type="genomic DNA"

/strain="Race 1"

/db_xref="taxon:6306"

/dev_stage="L2"

/clone_lib="Meloidogyne incognita BAC end sequence library

(MIAAGSS 001)"

/note="Vector: pCUG1; Site 1: HindIII; Site 2: HindIII;

BAC library constructed by Arief Budiman and Nathan Lakey

at Orion Genomics, and David Bird and Charles Opperman at

Center for the Biology of Nematode Parasitism at NCSU."

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;

est.res

Mon May 15 15:24:53 2006

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCATCCACC 9
| | | | | | |
Db 3 CCATCCACC 11

Search completed: May 15, 2006, 14:28:05
Job time : 0.001 secs

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 15, 2006, 14:55:23 ; Search time 0.001 Seconds
(without alignments)
288.028 Million cell updates/sec

Title: US-09-904-968A-3-COPY

Perfect score: 29

Sequence: 1 ccattccactgctgtgtgacctgtaaat 29

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 411 seqs, 4966 residues

Total number of hits satisfying chosen parameters: 822

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 412 summaries

Database : gedb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	29	100.0	29	1	AX404099	1	ACCESSION:AX404099
2	15.6	53.8	22	1	AX684211	2	ACCESSION:AX684211
3	15.2	52.4	21	1	AX299686	3	ACCESSION:AX299686
4	14.8	51.0	20	1	AX297605	4	ACCESSION:AX297605
5	14.4	49.7	19	1	CS050343	5	ACCESSION:CS050343
6	14.2	49.0	20	1	AR099203	6	ACCESSION:AR099203
7	14.2	49.0	20	1	AR154297	7	ACCESSION:AR154297
8	14.2	49.0	20	1	BD136591	8	ACCESSION:BD136591
9	14.2	49.0	20	1	AR361853	9	ACCESSION:AR361853
10	14.2	49.0	20	1	AR432409	10	ACCESSION:AR432409
11	14.2	49.0	20	1	AR475830	11	ACCESSION:AR475830
12	14.2	49.0	20	1	AR679662	12	ACCESSION:AR679662
13	14.2	49.0	20	1	AX591358	13	ACCESSION:AX591358
14	14.2	49.0	20	1	AX591503	14	ACCESSION:AX591503
15	13.4	46.2	19	1	AR294747	15	ACCESSION:AR294747
16	12.8	44.1	17	1	E13312	16	ACCESSION:E13312
17	12.8	44.1	17	1	AX532129	17	ACCESSION:AX532129
18	12.8	44.1	17	1	AX532130	18	ACCESSION:AX532130
19	12.8	44.1	18	1	AR038733	19	ACCESSION:AR038733
20	12.8	44.1	18	1	AR059619	20	ACCESSION:AR059619
21	12.8	44.1	18	1	BD243945	21	ACCESSION:BD243945
22	12.8	44.1	18	1	AR196740	22	ACCESSION:AR196740
23	12.8	44.1	18	1	AR594350	23	ACCESSION:AR594350
24	12.4	42.8	17	1	CO617431	24	ACCESSION:CO617431
25	12.4	42.8	17	1	CO617432	25	ACCESSION:CO617432
26	12.4	42.8	17	1	CO617433	26	ACCESSION:CO617433
27	12.4	42.8	17	1	CO617434	27	ACCESSION:CO617434
28	12.4	42.8	17	1	AR458494	28	ACCESSION:AR458494
29	12.4	42.8	17	1	AR458495	29	ACCESSION:AR458495
30	12.4	42.8	17	1	AR458496	30	ACCESSION:AR458496
31	12.4	42.8	17	1	AR458497	31	ACCESSION:AR458497
32	12.4	42.8	17	1	AX733424	32	ACCESSION:AX733424
33	12.4	42.8	17	1	AX733431	33	ACCESSION:AX733431

34	12.4	42.8	17	1	AX738031	1	ACCESSION:AX738031
35	12.2	42.1	17	1	AX532131	17	ACCESSION:AX532131
36	12.2	42.1	17	1	AX532132	17	ACCESSION:AX532132
37	12.2	42.1	17	1	AX532133	17	ACCESSION:AX532133
38	12.2	42.1	17	1	AX615973	17	ACCESSION:AX615973
39	12	41.4	17	1	CO617429	17	ACCESSION:CO617429
40	12	41.4	17	1	CO617430	17	ACCESSION:CO617430
41	12	41.4	17	1	AR458492	17	ACCESSION:AR458492
42	12	41.4	17	1	AR458493	17	ACCESSION:AR458493
43	12	41.4	17	1	AX671858	17	ACCESSION:AX671858
44	12	41.4	17	1	AX758887	17	ACCESSION:AX758887
45	11.2	38.6	16	1	AR134350	16	ACCESSION:AR134350
46	11.2	38.6	16	1	BD078236	16	ACCESSION:BD078236
47	11.2	38.6	16	1	CO858631	16	ACCESSION:CO858631
48	11.2	38.6	16	1	AR328258	16	ACCESSION:AR328258
49	11	37.9	15	1	I07726	15	ACCESSION:I07726
50	11	37.9	15	1	CO828994	15	ACCESSION:CO828994
51	10.8	37.2	15	1	A88223	15	ACCESSION:A88223
52	10.8	37.2	15	1	A90190	15	ACCESSION:A90190
53	10.8	37.2	15	1	AR033319	15	ACCESSION:AR033319
54	10.8	37.2	15	1	AR113141	15	ACCESSION:AR113141
55	10.8	37.2	15	1	BD065736	15	ACCESSION:BD065736
56	10.8	37.2	15	1	BD207052	15	ACCESSION:BD207052
57	10.8	37.2	15	1	I57548	15	ACCESSION:I57548
58	10.4	35.9	13	1	CQ794305	13	ACCESSION:CQ794305
59	10.4	35.9	14	1	A40464	14	ACCESSION:A40464
60	10.4	35.9	14	1	A88991	14	ACCESSION:A88991
61	10.4	35.9	14	1	BD066504	14	ACCESSION:BD066504
62	10.4	35.9	14	1	BD176783	14	ACCESSION:BD176783
63	10.4	35.9	14	1	AR232744	14	ACCESSION:AR232744
64	10.4	35.9	14	1	AR300215	14	ACCESSION:AR300215
65	10.4	35.9	14	1	AX316360	14	ACCESSION:AX316360
66	10	34.5	11	1	CO828943	11	ACCESSION:CO828943
67	10	34.5	11	1	AX394511	11	ACCESSION:AX394511
68	10	34.5	11	1	AX394518	11	ACCESSION:AX394518
69	10	34.5	11	1	AX471278	11	ACCESSION:AX471278
70	10	34.5	11	1	AX624482	11	ACCESSION:AX624482
71	10	34.5	11	1	AX625948	11	ACCESSION:AX625948
72	10	34.5	11	1	AX627058	11	ACCESSION:AX627058
73	10	34.5	11	1	AX631903	11	ACCESSION:AX631903
74	10	34.5	12	1	CO828958	12	ACCESSION:CO828958
75	10	34.5	12	1	CO828995	12	ACCESSION:CO828995
76	10	34.5	12	1	AX770861	12	ACCESSION:AX770861
77	10	34.5	14	1	A89161	14	ACCESSION:A89161
78	10	34.5	14	1	BD066674	14	ACCESSION:BD066674
79	10	34.5	14	1	BD209352	14	ACCESSION:BD209352
80	10	34.5	14	1	BD235127	14	ACCESSION:BD235127
81	9.8	33.8	13	1	AR175360	13	ACCESSION:AR175360
82	9.8	33.8	13	1	AX572357	13	ACCESSION:AX572357
83	9.8	33.8	13	1	AX572382	13	ACCESSION:AX572382
84	9.8	33.8	14	1	A40478	14	ACCESSION:A40478
85	9.8	33.8	14	1	A88219	14	ACCESSION:A88219
86	9.8	33.8	14	1	A89005	14	ACCESSION:A89005
87	9.8	33.8	14	1	A89321	14	ACCESSION:A89321
88	9.8	33.8	14	1	A90186	14	ACCESSION:A90186
89	9.8	33.8	14	1	BD065732	14	ACCESSION:BD065732
90	9.8	33.8	14	1	BD066518	14	ACCESSION:BD066518
91	9.8	33.8	14	1	BD066834	14	ACCESSION:BD066834
92	9.8	33.8	14	1	AR232758	14	ACCESSION:AR232758
93	9.8	33.8	14	1	AX316374	14	ACCESSION:AX316374
94	9.8	33.8	14	1	AX572354	14	ACCESSION:AX572354
95	9.8	33.8	14	1	AX572358	14	ACCESSION:AX572358
96	9.8	33.8	14	1	AX572372	14	ACCESSION:AX572372
97	9.8	33.8	14	1	AX572374	14	ACCESSION:AX572374
98	9.8	33.8	14	1	AX572377	14	ACCESSION:AX572377
99	9.8	33.8	14	1	AX572381	14	ACCESSION:AX572381
100	9.4	32.4	11	1	BD124223	11	ACCESSION:BD124223
101	9.4	32.4	11	1	BD124438	11	ACCESSION:BD124438
102	9.4	32.4	11	1	CO836739	11	ACCESSION:CO836739
103	9.4	32.4	11	1	CO837792	11	ACCESSION:CO837792
104	9.4	32.4	11	1	CS058325	11	ACCESSION:CS058325
105	9.4	32.4	11	1	AR301473	11	ACCESSION:AR301473
106	9.4	32.4	11	1	AR301688	11	ACCESSION:AR301688

Genbank/EMBL

C 107	9.4	32.4	11	1	AX036264	ACCESSION:AX036264	C 180	8.4	29.0	10	1	AR490725	ACCESSION:AR490725
C 108	9.4	32.4	11	1	AX470508	ACCESSION:AX470508	C 181	8.4	29.0	10	1	AR532498	ACCESSION:AR532498
C 109	9.4	32.4	11	1	AX623763	ACCESSION:AX623763	C 182	8.4	29.0	10	1	AX018751	ACCESSION:AX018751
C 110	9.4	32.4	11	1	AX625616	ACCESSION:AX625616	C 183	8.4	29.0	10	1	AX112967	ACCESSION:AX112967
C 111	9.4	32.4	11	1	AX625941	ACCESSION:AX625941	C 184	8.4	29.0	10	1	AX152117	ACCESSION:AX152117
C 112	9.4	32.4	11	1	AX627200	ACCESSION:AX627200	C 185	8.4	29.0	10	1	AX152126	ACCESSION:AX152126
C 113	9.4	32.4	11	1	AX627837	ACCESSION:AX627837	C 186	8.4	29.0	10	1	AX152191	ACCESSION:AX152191
C 114	9.4	32.4	11	1	AX628604	ACCESSION:AX628604	C 187	8.4	29.0	10	1	AX152676	ACCESSION:AX152676
C 115	9.4	32.4	11	1	AX631184	ACCESSION:AX631184	C 188	8.4	29.0	10	1	BD007884	ACCESSION:BD007884
C 116	9.4	32.4	12	1	A91475	ACCESSION:A91475	C 189	8.4	29.0	11	1	AR051278	ACCESSION:AR051278
C 117	9.4	32.4	12	1	BD248272	ACCESSION:BD248272	C 190	8.4	29.0	11	1	AR074507	ACCESSION:AR074507
C 118	9.4	32.4	12	1	BD248273	ACCESSION:BD248273	C 191	8.4	29.0	11	1	AR077230	ACCESSION:AR077230
C 119	9.4	32.4	12	1	I07725	ACCESSION:I07725	C 192	8.4	29.0	11	1	AR081187	ACCESSION:AR081187
C 120	9.4	32.4	12	1	BD023257	ACCESSION:BD023257	C 193	8.4	29.0	11	1	AR085384	ACCESSION:AR085384
C 121	9.4	32.4	13	1	I43005	ACCESSION:I43005	C 194	8.4	29.0	11	1	AR088132	ACCESSION:AR088132
C 122	9.4	32.4	13	1	AR363773	ACCESSION:AR363773	C 195	8.4	29.0	11	1	AR104291	ACCESSION:AR104291
C 123	9	31.0	10	1	BD239019	ACCESSION:BD239019	C 196	8.4	29.0	11	1	AR143553	ACCESSION:AR143553
C 124	9	31.0	10	1	BD239139	ACCESSION:BD239139	C 197	8.4	29.0	11	1	AR171459	ACCESSION:AR171459
C 125	9	31.0	10	1	BD240212	ACCESSION:BD240212	C 198	8.4	29.0	11	1	AR171630	ACCESSION:AR171630
C 126	9	31.0	10	1	C0766709	ACCESSION:C0766709	C 199	8.4	29.0	11	1	BD057177	ACCESSION:BD057177
C 127	9	31.0	10	1	C0766752	ACCESSION:C0766752	C 200	8.4	29.0	11	1	BD061634	ACCESSION:BD061634
C 128	9	31.0	10	1	C0828944	ACCESSION:C0828944	C 201	8.4	29.0	11	1	BD124454	ACCESSION:BD124454
C 129	9	31.0	10	1	AX152110	ACCESSION:AX152110	C 202	8.4	29.0	11	1	BD243220	ACCESSION:BD243220
C 130	9	31.0	10	1	BD007825	ACCESSION:BD007825	C 203	8.4	29.0	11	1	CO766284	ACCESSION:CO766284
C 131	9	31.0	11	1	AR074494	ACCESSION:AR074494	C 204	8.4	29.0	11	1	CO833247	ACCESSION:CO833247
C 132	9	31.0	11	1	AR081174	ACCESSION:AR081174	C 205	8.4	29.0	11	1	CO833289	ACCESSION:CO833289
C 133	9	31.0	11	1	AR085371	ACCESSION:AR085371	C 206	8.4	29.0	11	1	CO833356	ACCESSION:CO833356
C 134	9	31.0	11	1	AR088119	ACCESSION:AR088119	C 207	8.4	29.0	11	1	CO835321	ACCESSION:CO835321
C 135	9	31.0	11	1	AR104278	ACCESSION:AR104278	C 208	8.4	29.0	11	1	CO835588	ACCESSION:CO835588
C 136	9	31.0	11	1	AR143540	ACCESSION:AR143540	C 209	8.4	29.0	11	1	CO835701	ACCESSION:CO835701
C 137	9	31.0	11	1	AR171446	ACCESSION:AR171446	C 210	8.4	29.0	11	1	CO836236	ACCESSION:CO836236
C 138	9	31.0	11	1	AR171617	ACCESSION:AR171617	C 211	8.4	29.0	11	1	CO836553	ACCESSION:CO836553
C 139	9	31.0	11	1	BD080109	ACCESSION:BD080109	C 212	8.4	29.0	11	1	CO836684	ACCESSION:CO836684
C 140	9	31.0	11	1	BD243207	ACCESSION:BD243207	C 213	8.4	29.0	11	1	CO836692	ACCESSION:CO836692
C 141	9	31.0	11	1	CS058646	ACCESSION:CS058646	C 214	8.4	29.0	11	1	CO836910	ACCESSION:CO836910
C 142	9	31.0	11	1	AR214824	ACCESSION:AR214824	C 215	8.4	29.0	11	1	CO837506	ACCESSION:CO837506
C 143	9	31.0	11	1	AR569645	ACCESSION:AR569645	C 216	8.4	29.0	11	1	CO837969	ACCESSION:CO837969
C 144	9	31.0	11	1	AX393112	ACCESSION:AX393112	C 217	8.4	29.0	11	1	CS058181	ACCESSION:CS058181
C 145	9	31.0	11	1	AX470507	ACCESSION:AX470507	C 218	8.4	29.0	11	1	CS058234	ACCESSION:CS058234
C 146	9	31.0	11	1	AX623057	ACCESSION:AX623057	C 219	8.4	29.0	11	1	CS058596	ACCESSION:CS058596
C 147	9	31.0	11	1	AX630236	ACCESSION:AX630236	C 220	8.4	29.0	11	1	AR301532	ACCESSION:AR301532
C 148	9	31.0	11	1	AX630478	ACCESSION:AX630478	C 221	8.4	29.0	11	1	AR301704	ACCESSION:AR301704
C 149	9	31.0	12	1	AX395393	ACCESSION:AX395393	C 222	8.4	29.0	11	1	AR569658	ACCESSION:AR569658
C 150	8.8	30.3	12	1	AR014245	ACCESSION:AR014245	C 223	8.4	29.0	11	1	AX085766	ACCESSION:AX085766
C 151	8.8	30.3	12	1	AR038696	ACCESSION:AR038696	C 224	8.4	29.0	11	1	AX470852	ACCESSION:AX470852
C 152	8.8	30.3	12	1	AR058492	ACCESSION:AR058492	C 225	8.4	29.0	11	1	AX470941	ACCESSION:AX470941
C 153	8.8	30.3	12	1	BD064895	ACCESSION:BD064895	C 226	8.4	29.0	11	1	AX471016	ACCESSION:AX471016
C 154	8.8	30.3	12	1	BD271980	ACCESSION:BD271980	C 227	8.4	29.0	11	1	AX471168	ACCESSION:AX471168
C 155	8.8	30.3	12	1	C0766158	ACCESSION:C0766158	C 228	8.4	29.0	11	1	AX471345	ACCESSION:AX471345
C 156	8.8	30.3	12	1	I23750	ACCESSION:I23750	C 229	8.4	29.0	11	1	AX471608	ACCESSION:AX471608
C 157	8.8	30.3	12	1	I73177	ACCESSION:I73177	C 230	8.4	29.0	11	1	AX623509	ACCESSION:AX623509
C 158	8.8	30.3	12	1	AR302271	ACCESSION:AR302271	C 231	8.4	29.0	11	1	AX623560	ACCESSION:AX623560
C 159	8.8	30.3	12	1	AR308098	ACCESSION:AR308098	C 232	8.4	29.0	11	1	AX624060	ACCESSION:AX624060
C 160	8.8	30.3	12	1	S55766	ACCESSION:S55766	C 233	8.4	29.0	11	1	AX624161	ACCESSION:AX624161
C 161	8.8	30.3	12	1	S7311852	ACCESSION:S7311852	C 234	8.4	29.0	11	1	AX624988	ACCESSION:AX624988
C 162	8.4	29.0	10	1	AR164924	ACCESSION:AR164924	C 235	8.4	29.0	11	1	AX626149	ACCESSION:AX626149
C 163	8.4	29.0	10	1	AR167603	ACCESSION:AR167603	C 236	8.4	29.0	11	1	AX626748	ACCESSION:AX626748
C 164	8.4	29.0	10	1	BD083179	ACCESSION:BD083179	C 237	8.4	29.0	11	1	AX626997	ACCESSION:AX626997
C 165	8.4	29.0	10	1	BD083230	ACCESSION:BD083230	C 238	8.4	29.0	11	1	AX627183	ACCESSION:AX627183
C 166	8.4	29.0	10	1	BD083332	ACCESSION:BD083332	C 239	8.4	29.0	11	1	AX627753	ACCESSION:AX627753
C 167	8.4	29.0	10	1	BD083352	ACCESSION:BD083352	C 240	8.4	29.0	11	1	AX627875	ACCESSION:AX627875
C 168	8.4	29.0	10	1	BD167115	ACCESSION:BD167115	C 241	8.4	29.0	11	1	AX627970	ACCESSION:AX627970
C 169	8.4	29.0	10	1	BD195102	ACCESSION:BD195102	C 242	8.4	29.0	11	1	AX628145	ACCESSION:AX628145
C 170	8.4	29.0	10	1	BD238856	ACCESSION:BD238856	C 243	8.4	29.0	11	1	AX628168	ACCESSION:AX628168
C 171	8.4	29.0	10	1	BD239707	ACCESSION:BD239707	C 244	8.4	29.0	11	1	AX628220	ACCESSION:AX628220
C 172	8.4	29.0	10	1	BD240160	ACCESSION:BD240160	C 245	8.4	29.0	11	1	AX628311	ACCESSION:AX628311
C 173	8.4	29.0	10	1	E06867	ACCESSION:E06867	C 246	8.4	29.0	11	1	AX628518	ACCESSION:AX628518
C 174	8.4	29.0	10	1	E39535	ACCESSION:E39535	C 247	8.4	29.0	11	1	AX629299	ACCESSION:AX629299
C 175	8.4	29.0	10	1	E39641	ACCESSION:E39641	C 248	8.4	29.0	11	1	AX629728	ACCESSION:AX629728
C 176	8.4	29.0	10	1	E54734	ACCESSION:E54734	C 249	8.4	29.0	11	1	AX629959	ACCESSION:AX629959
C 177	8.4	29.0	10	1	I43001	ACCESSION:I43001	C 250	8.4	29.0	11	1	AX630263	ACCESSION:AX630263
C 178	8.4	29.0	10	1	AR303393	ACCESSION:AR303393	C 251	8.4	29.0	11	1	AX630930	ACCESSION:AX630930
C 179	8.4	29.0	10	1	AR306856	ACCESSION:AR306856	C 252	8.4	29.0	11	1		

C 253	8.4	29.0	11	1	AX630981	ACCESSION:AX630981	326	8	27.6	11	1	CQ837896	ACCESSION:CQ837896
C 254	8.4	29.0	11	1	AX631481	ACCESSION:AX631481	327	8	27.6	11	1	CQ837956	ACCESSION:CQ837956
C 255	8.4	29.0	11	1	AX631582	ACCESSION:AX631582	328	8	27.6	11	1	AR301525	ACCESSION:AR301525
C 256	8.4	29.0	11	1	AX632409	ACCESSION:AX632409	C 329	8	27.6	11	1	AR632418	ACCESSION:AR632418
C 257	8.4	29.0	11	1	HSPMLEX43	ACCESSION:AX632409	C 330	8	27.6	11	1	AX470713	ACCESSION:AX470713
C 258	8.4	29.0	12	1	A71560	ACCESSION:AX63632	C 331	8	27.6	11	1	AX470904	ACCESSION:AX470904
C 259	8.4	29.0	12	1	AR167777	ACCESSION:A71560	C 332	8	27.6	11	1	AX470954	ACCESSION:AX470954
C 260	8.4	29.0	12	1	AR167827	ACCESSION:AR167777	C 333	8	27.6	11	1	AX471035	ACCESSION:AX471035
C 261	8.4	29.0	12	1	BD143765	ACCESSION:AR167827	C 334	8	27.6	11	1	AX471109	ACCESSION:AX471109
C 262	8.4	29.0	12	1	BD168627	ACCESSION:BD143765	C 335	8	27.6	11	1	AX471236	ACCESSION:AX471236
C 263	8.4	29.0	12	1	CQ766277	ACCESSION:BD168627	C 336	8	27.6	11	1	AX471465	ACCESSION:AX471465
C 264	8.4	29.0	12	1	CQ828759	ACCESSION:CQ766277	C 337	8	27.6	11	1	AX471492	ACCESSION:AX471492
C 265	8.4	29.0	12	1	CQ828760	ACCESSION:CQ828759	C 338	8	27.6	11	1	AX482032	ACCESSION:AX482032
C 266	8.4	29.0	12	1	CQ828918	ACCESSION:CQ828760	C 339	8	27.6	11	1	AX511271	ACCESSION:AX511271
C 267	8.4	29.0	12	1	E29661	ACCESSION:CQ828918	C 340	8	27.6	11	1	AX522962	ACCESSION:AX522962
C 268	8.4	29.0	12	1	E29711	ACCESSION:E29661	C 341	8	27.6	11	1	AX623083	ACCESSION:AX623083
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C 274	8.4	29.0	12	1	AR408074	ACCESSION:I34990	C 347	8	27.6	11	1	AX626143	ACCESSION:AX626143
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C 277	8.4	29.0	12	1	AX138534	ACCESSION:AX097958	C 350	8	27.6	11	1	AX627828	ACCESSION:AX627828
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C 285	8	27.6	10	1	BD239153	ACCESSION:BD239055	C 358	8	27.6	11	1	AX629352	ACCESSION:AX629352
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C 287	8	27.6	10	1	BD239212	ACCESSION:BD239196	C 360	8	27.6	11	1	AX629813	ACCESSION:AX629813
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C 306	8	27.6	10	1	AX153356	ACCESSION:AX152911	C 379	7.8	26.9	11	1	CQ837342	ACCESSION:CQ835054
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C 316	8	27.6	11	1	CQ832885	ACCESSION:CQ832685	C 389	7.8	26.9	11	1	AX471815	ACCESSION:AX471463
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C 321	8	27.6	11	1	CQ836490	ACCESSION:CQ835656	C 394	7.8	26.9	11	1	AX624312	ACCESSION:AX623975
C 322	8	27.6	11	1	CQ836499	ACCESSION:CQ836490	C 395	7.8	26.9	11	1	AX625384	ACCESSION:AX624312
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C	410	7.8	26.9	11	1	AX630793	ACCESSION:AX630793
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	412	7.8	26.9	11	1	AX631733	ACCESSION:AX631733

ALIGNMENTS

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RESULT 1
AX440499
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ACCESSION
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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Qy	1	CCATCCACCTGCTGTGTGACCTGGTAAAT	29	
Db	1	CCATCCACCTGCTGTGTGACCTGGTAAAT	29	

RESULT 2
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 DEFINITION
 Sequence 62 from Patent WO0246386.
 ACCESSION
 AX684211
 VERSION
 AX684211.1 GI:29371104
 KEYWORDS
 Homo sapiens (human)
 SOURCE
 Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 REFERENCE
 1
 AUTHORS
 Bolton,S., Clayton,R., Easton,A., Engel,L. and Messing,D.
 TITLE
 Aspergillus ochraceus 11 alpha hydroxylase and oxidoreductase
 JOURNAL
 Patent: WO 0246386-A 62 13-JUN-2002;
 Pharmacia Corporation (US) ; Bolton, Suzanne (US) ; Clayton, Robert
 (US) ; Easton, Alan (US) ; Engel, Leslie (US) ; Messing, Dean (US)
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RESULT 5
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LOCUS              Sequence 127 from Patent WO2005021757.
DEFINITION
ACCESSION          CS050343
VERSION            CS050343.1  GI:61889567
KEYWORDS
SOURCE             Homo sapiens (human)
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS            Tomme,P.H. and van Rompaey,L.
TITLE              Polypeptides and polynucleotides for use as a medicament
JOURNAL            Patent: WO 2005021757-A 127 10-MAR-2005;
Galapagos Genomics N.V. (BE)
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Db 3 ACTTGCTGTGTGACCT 18

RESULT 6
AR099203          AR099203          20 bp      DNA      linear      PAT 14-FEB-2001
LOCUS              Sequence 97 from patent US 6077692.
DEFINITION
ACCESSION          AR099203
VERSION            AR099203.1  GI:12808969
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unclassified.
1 (bases 1 to 20)
REFERENCE
AUTHORS            Ruben,S.M., Jimenez,P., Duan,D.Roxanne., Rampy,M.A., Mendrick,D.,
Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.
and Gentz,R.L.
TITLE              Keratinocyte growth factor-2
JOURNAL            Patent: US 6077692-A 97-20-JUN-2000;
FEATURES
source             Location/Qualifiers
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Oy 2 CATCCACCTGCTGTGTGAC 20
Db 1 CAACACCTGCAGGGTGAC 19

RESULT 7
AR154297          AR154297          20 bp      DNA      linear      PAT 08-AUG-2001
LOCUS              Sequence 18 from patent US 6238888.
DEFINITION
ACCESSION          AR154297
VERSION            AR154297.1  GI:15122350
KEYWORDS
SOURCE             Unknown.
ORGANISM            Unknown.
Unclassified.
1 (bases 1 to 20)
REFERENCE

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AUTHORS            Gentz,R.L., Chopra,A., Kaushal,P., Spitznagel,T., Unsworth,E. and
Khan,F.
TITLE              Keratinocyte growth factor-2 formulations
JOURNAL            Patent: US 6238888-A 18 29-MAY-2001;
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Db 1 CAACACCTGCAGGGTGAC 19

RESULT 8
BD136591          BD136591          20 bp      DNA      linear      PAT 18-SEP-2002
LOCUS              Therapeutic utilization of horny cell growth factor-2.
DEFINITION
ACCESSION          BD136591
VERSION            BD136591.1  GI:23231536
KEYWORDS            JP 2002507546-A/67.
SOURCE             Homo sapiens (human)
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 20)
REFERENCE
AUTHORS            Jimenez,P., Rampy,M.A., Mendrick,D., Russell,D. and Louie,A.
TITLE              Therapeutic utilization of horny cell growth factor-2
JOURNAL            Patent: JP 2002507546-A 67 12-MAR-2002;
HUMAN GENOME SCIENCES INC
COMMENT            OS Homo sapiens (human)
PN JP 2002507546-A/67
PD 12-MAR-2002
PF 12-FEB-1999 JP 2000531473
PR 13-FEB-1998 US 60/074585, 30-DEC-1998 US 60/114387 PI
PABLO JIMENEZ, MARK A RAMPY, DONNA MENDRICK, DEBORAH RUSSELL, PI
ARTHUR LOUIE
PC
AG1K38/00,AG1P1/00,AG1P7/00,AG1P7/04,AG1P7/06,AG1P11/00,AG1P11/ PC
02,
PC AG1P13/08,AG1P13/10,AG1P27/02,AG1P27/16,AG1P35/02,C07K14/475,
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PC AG1K48/00,C12N15/09,AG1K37/02,C12N15/00
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Location/Qualifiers
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Best Local Similarity 84.2%; Pred. No. 31;
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Db 1 CAACACCTGCAGGGTGAC 19

RESULT 9
AR361853          AR361853          20 bp      DNA      linear      PAT 17-AUG-2003
LOCUS              Sequence 97 from patent US 659879.
DEFINITION
ACCESSION          AR361853
VERSION            AR361853.1  GI:33769823

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KEYWORDS      .
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      Unclassified.
AUTHORS       1 (bases 1 to 20)
TITLE         Jimenez,P., Rampy,M.A., Mendrick,D., Russell,D. and Louie,A.
JOURNAL       Therapeutic uses of keratinocyte growth factor-2
              Patent: US 6599879-A 97 29-JUL-2003;
              Human Genome Sciences, Inc.; Rockville, MD
FEATURES      Location/Qualifiers
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Db      1 CAACACCCTGCAGGGTGAC 19

RESULT 10
LOCUS      AR432409                20 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6653284.
ACCESSION  AR432409
VERSION     AR432409.1 GI:40194731
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Gentz,R.L., Chopra,A., Kaushal,P., Spitznagel,T., Unsworth,E. and
          Khan,F.
TITLE     Keratinocyte growth factor-2 formulations
JOURNAL   Patent: US 6653284-A 18 25-NOV-2003;
          Human Genome Sciences, Inc.; Rockville, MD
FEATURES  Location/Qualifiers
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RESULT 11
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DEFINITION Sequence 97 from patent US 6693077.
ACCESSION  AR475830
VERSION     AR475830.1 GI:42715388
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ruben,S.M., Jimenez,P., Duan,D.R., Rampy,M.A., Mendrick,D.,
          Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.
          and Gentz,R.L.
TITLE     Keratinocyte growth factor-2
JOURNAL   Patent: US 6693077-A 97 17-FEB-2004;
          Human Genome Sciences, Inc.; Rockville, MD
FEATURES  Location/Qualifiers
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Db      1 CAACACCCTGCAGGGTGAC 19

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LOCUS      AR679662                20 bp      mRNA      linear      PAT 13-JUN-2005
DEFINITION Sequence 97 from patent US 6903072.
ACCESSION  AR679662
VERSION     AR679662.1 GI:67621396
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Ruben,S.M., Jimenez,P., Duan,D.R., Rampy,M.A., Mendrick,D.,
          Zhang,J., Ni,J., Moore,P.A., Coleman,T.A., Gruber,J.R., Dillon,P.J.
          and Gentz,R.L.
TITLE     Keratinocyte growth factor-2
JOURNAL   Patent: US 6903072-A 97 07-JUN-2005;
          Human Genome Sciences, Inc.; Rockville, MD
FEATURES  Location/Qualifiers
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Db      1 CAACACCCTGCAGGGTGAC 19

RESULT 13
LOCUS      AX591358                20 bp      DNA      linear      PAT 27-JAN-2003
DEFINITION Sequence 96 from Patent EP1247530.
ACCESSION  AX591358
VERSION     AX591358.1 GI:27949814
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS   Duan,R.D., Ruben,S.M., Jimenez,P., Rampy,M.A., Mendrick,D.,
          Zhang,J., Ni,J., Moore,P.A., Coleman,T.A. and Gentz,R.L.
TITLE     Keratinocyte growth factor-2 (kgf-2 or fibroblast growth factor-12,
          fgf-12)
JOURNAL   Patent: EP 1247530-A 96 09-OCT-2002;
          HUMAN GENOME SCIENCES, INC. (US)
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           /db_xref="taxon:9606"
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           Best Local Similarity 84.2%; Pred. No. 31;
           Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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ACCESSION AX591503
VERSION    AX591503.1 GI:27949936
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Duan,R.D., Ruben,S.M., Jimenez,P., Ramoy,M.A., Mendrick,D.,
            Zhang,J., Ni,J., Moore,P.A., Coleman,T.A. and Gentz,R.L.
TITLE      Keratinocyte growth factor-2 (kGF-2 or fibroblast growth factor-12,
            fGF-12)
JOURNAL    Patent: EP 1247862-A 96 09-OCT-2002;
            HUMAN GENOME SCIENCES, INC. (US)
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Query Match 49.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      1 CAACACCTGCAGGTGAC 19

RESULT 15
AR294747/c
LOCUS      19 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 6482 from patent US 6537751.
ACCESSION AR294747
VERSION    AR294747.1 GI:31682031
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE      Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
JOURNAL    Patent: US 6537751-A 6482 25-MAR-2003;
            Genset S.A.;
            FRX;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 46.2%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 CCACCTGCTGTGTGA 19
        |||||||||
Db      19 CCGCCTGCTGTGTGA 5

RESULT 16
E13312/c
LOCUS      17 bp      DNA      linear      PAT 27-APR-1998
DEFINITION PCR primer for gaining 4-coumaric acid coenzyme A-ligase gene.
ACCESSION E13312

```

```

VERSION    E13312.1 GI:3252117
KEYWORDS   JP 1997173069-A/1.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 17)
AUTHORS    Kajita,S. and Omori,S.
TITLE      4-COUMARIC ACID : COENZYME A LIGASE GENE AND REDUCTION OF LIGNIN IN
            PLANT USING THE SAME GENE
JOURNAL    Patent: JP 1997173069-A 1 08-JUL-1997;
            MITSUBISHI PAPER MILLS LTD
COMMENT    OS None
            OC Artificial sequences.
            PN JP 1997173069-A/1
            PD 08-JUL-1997
            PF 22-DEC-1995 JP 1995334834
            PI KAJITA SHINYA, OMORI SHUNJI
            PC C12N15/09,A01H5/00,C07H21/04,C12N5/10,C12N9/00, PC
            D21C9/00//A01H1/00,C12N1/21,
            PC C12S3/08,(C12N1/21,C12R1:19);
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: No;
            FH Key
            FH Location/Qualifiers
            FT source
            1..17
            /organism="Artificial sequences".
FEATURES   source
            1..17
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
Query Match 44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 45;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCATCCACCTGCTGTG 16
        |||||
Db      17 CCTCNACYGTGTG 2
        |||||

RESULT 17
AX532129
LOCUS      17 bp      DNA      linear      PAT 22-NOV-2002
DEFINITION Sequence 1638 from Patent EP1239051.
ACCESSION AX532129
VERSION    AX532129.1 GI:25256043
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Shannon,M.
TITLE      Human poesh-like protein 1
JOURNAL    Patent: EP 1239051-A 1638 11-SEP-2002;
            Aeomica, Inc. (US)
FEATURES   Location/Qualifiers
            source
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match 44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 ATCCACCTGCTGTG 18
        |||||||
Db      2 ATCCACCTCTCTGTG 17
        |||||||

```

```
RESULT 18
AX532130
LOCUS AX532130 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1639 from Patent EP1239051.
ACCESSION AX532130
VERSION AX532130.1 GI:25256045
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1639 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
Query Match 44.1%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ATCCACCTGCTGTGTG 18
DB 1 ATCCACCTCCTCTGTG 16
RESULT 19
AR038733/c
LOCUS AR038733 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 39 from patent US 5807681.
ACCESSION AR038733
VERSION AR038733.1 GI:5958096
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 18)
TITLE Giordano,A. and Baldi,A.
JOURNAL Human retinoblastoma-related (pRb2/p130) genomic DNA and methods
for detecting mutations therein
FEATURES
source
Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 TGTGTGACCTGGTAAA 28
DB 17 TTTGTGACCTGGCAAA 2
RESULT 20
AR059619/c
LOCUS AR059619 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 39 from patent US 5840506.
ACCESSION AR059619
VERSION AR059619.1 GI:5986069
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 18)
TITLE Giordano,A. and Baldi,A.
JOURNAL Human retinoblastoma-related (pRb2/p130) genomic DNA and methods
for detecting mutations therein
FEATURES
source
Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 TGTGTGACCTGGTAAA 28
DB 17 TTTGTGACCTGGCAAA 2
RESULT 21
BD243945/c
LOCUS BD243945 18 bp DNA linear PAT 17-JUL-2003
DEFINITION TREX, a novel gene of TRAF-interacting EXT gene family and
diagnostic and therapeutic uses thereof.
ACCESSION BD243945
VERSION BD243945.1 GI:33053715
KEYWORDS JP 2002525126-A/21.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 18)
TITLE Sato,T.
JOURNAL TREX, a novel gene of TRAF-interacting EXT gene family and
diagnostic and therapeutic uses thereof
Patent: JP 2002525126-A 21 13-AUG-2002;
THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
COMMENT
OS Linear
PN JP 2002525126-A/21
PD 13-AUG-2002
PF 17-SEP-1999 JP 2000572406
PR 17-SEP-1998 US 09/156191
PI TAKAAKI SATO
PC
C12N15/09,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
A61P35/00,
PC A61P35/04,A61P37/02,C07K14/47,C07K16/18,C12P21/02,C12Q1/68, PC
G01N33/15,
PC
G01N33/50,G01N33/566,G01N33/574//C12P21/08,(C12P21/02,C12R1:91) PC
,C12N15/00
CC TREX, a novel gene of TRAF-interacting EXT gene family and CC
diagnostic and
therapeutic uses thereof
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Linear'.
FEATURES
source
Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CCACCTGCTGTGTGAC 20
DB 18 CCACATGCTGTGTAC 3
RESULT 22
AR196740
LOCUS AR196740 18 bp DNA linear PAT 20-APR-2002
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```
DEFINITION Sequence 1205 from patent US 6350934.
ACCESSION AR196740
VERSION AR196740.1 GI:20246177
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P.Ann.Owens.,
Guo,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1205 26-FEB-2002;
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTGAC 20
    ||||| |||||
Db 2 CCACCTGATGTTGAC 17

RESULT 23
AR594350/c
LOCUS AR594350 18 bp DNA linear PAT 15-DEC-2004
DEFINITION Sequence 34 from patent US 6812326.
ACCESSION AR594350
VERSION AR594350.1 GI:56643986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sato,T.-A.
TITLE TREX, a novel gene of TRAF-interacting EXT gene family and
diagnostic and therapeutic uses thereof
JOURNAL Patent: US 6812326-A 34 02-NOV-2004;
The Trustees of Columbia University in the City of New York; New
York, NY
FEATURES
    source
        Location/Qualifiers
            1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 44.1%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 48;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTGAC 20
    ||||| ||||| |||||
Db 18 CCACATGCTGTGTTC 3

RESULT 24
CQ617431
LOCUS CQ617431 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2171 from Patent WO0192524.
ACCESSION CQ617431
VERSION CQ617431.1 GI:41667649
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2173 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

JOURNAL Patent: WO 0192524-A 2171 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
    ||||| ||||| |||||
Db 4 CCACCTGCTGTGAG 17

RESULT 25
CQ617432
LOCUS CQ617432 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2172 from Patent WO0192524.
ACCESSION CQ617432
VERSION CQ617432.1 GI:41667650
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2172 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
    ||||| ||||| |||||
Db 3 CCACCTGCTGTGAG 16

RESULT 26
CQ617433
LOCUS CQ617433 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2173 from Patent WO0192524.
ACCESSION CQ617433
VERSION CQ617433.1 GI:41667651
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2173 06-DEC-2001;
Aecomica, Inc. (US)
FEATURES
    source
        Location/Qualifiers
            1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
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Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
|||||
Db 2 CCACCTGCTGTGAG 15

RESULT 27
AR458494 LOCUS CQ617434 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 2174 from Patent WO0192524.
ACCESSION CQ617434
VERSION CQ617434.1 GI:41667652

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 2174 06-DEC-2001;
Aeomica, Inc. (US)

FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
|||||
Db 1 CCACCTGCTGTGAG 14

RESULT 28
AR458494 LOCUS AR458494 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2171 from patent US 6686188.
ACCESSION AR458494
VERSION AR458494.1 GI:42693551

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2171 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;

FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
|||||
Db 4 CCACCTGCTGTGAG 17

RESULT 29
AR458495 LOCUS AR458495 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2172 from patent US 6686188.
ACCESSION AR458495
VERSION AR458495.1 GI:42693552

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2172 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;

FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
|||||
Db 3 CCACCTGCTGTGAG 16

RESULT 30
AR458496 LOCUS AR458496 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2173 from patent US 6686188.
ACCESSION AR458496
VERSION AR458496.1 GI:42693553

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2173 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;

FEATURES
source Location/Qualifiers
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
|||||
Db 2 CCACCTGCTGTGAG 15

RESULT 31
AR458497 LOCUS AR458497 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 2174 from patent US 6686188.
ACCESSION AR458497
VERSION AR458497.1 GI:42693554

KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 2174 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTGTGTG 18
|||||
Db 1 CCACCTGCTGTGAG 14

RESULT 32
AX733424
LOCUS AX733424 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5058 from Patent WO03025175.
ACCESSION AX733424
VERSION AX733424.1 GI:30512767
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 5058 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTGT 15
|||||
Db 4 CATCCTGCTGTGT 17

RESULT 33
AX733431
LOCUS AX733431 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5065 from Patent WO03025175.
ACCESSION AX733431
VERSION AX733431.1 GI:30512774
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.

TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 5065 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTG 16
|||||
Db 2 ATCCACCTGCTTTG 15

RESULT 34
AX738031
LOCUS AX738031 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 3621 from Patent WO03025177.
ACCESSION AX738031
VERSION AX738031.1 GI:30517319
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL Patent: WO 03025177-A 3621 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 42.8%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCTGTG 16
|||||
Db 2 ATCCACCTGCTGTG 15

RESULT 35
AX532131
LOCUS AX532131 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1640 from Patent EP1239051.
ACCESSION AX532131
VERSION AX532131.1 GI:25256047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1640 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source 1..17

CQ617430
 LOCUS
 DEFINITION
 CQ617430
 Sequence 2170 from Patent WO0192524.
 17 bp DNA
 linear PAT 02-FEB-2004

ACCESSION CQ617430
 VERSION CQ617430.1 GI:41667648
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 2170 06-DEC-2001;
 Aeomica, Inc. (US)
 FEATURES source
 1. .17
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 41.4%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 CCACCTGCTGTG 16
 |||||
 Db 5 CCACCTGCTGTG 16
 |||||
 RESULT 41
 LOCUS AR458492 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 2169 from patent US 6686188.
 ACCESSION AR458492
 VERSION AR458492.1 GI:42693549
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 2169 03-FEB-2004;
 Amersham PLC; Buckinghamshire;
 GBX;
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 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 CCACCTGCTGTG 16
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 Db 6 CCACCTGCTGTG 17
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 RESULT 42
 LOCUS AR458493 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 2170 from patent US 6686188.
 ACCESSION AR458493
 VERSION AR458493.1 GI:42693550
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and

Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 2170 03-FEB-2004;
 Amersham PLC; Buckinghamshire;
 GBX;
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 Db 5 CCACCTGCTGTG 16
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 RESULT 43
 LOCUS AX671858 17 bp DNA linear PAT 27-MAR-2003
 DEFINITION Sequence 303 from Patent WO03004526.
 ACCESSION AX671858
 VERSION AX671858.1 GI:29330206
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Tellerman, A., Anson, R. and Tuijnder, M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines
 JOURNAL Patent: WO 03004526-A 303 16-JAN-2003;
 Molecular Engines Laboratories (FR)
 FEATURES source
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 Db 6 CCATCCACCTGC 17
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 RESULT 44
 LOCUS AX758887 17 bp DNA linear PAT 25-JUN-2003
 DEFINITION Sequence 2208 from Patent WO03040369.
 ACCESSION AX758887
 VERSION AX758887.1 GI:32253503
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 REFERENCE 1
 AUTHORS Tellerman, A., Anson, R. and Tuijnder, M.
 TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
 JOURNAL Patent: WO 03040369-A 2208 15-MAY-2003;
 Molecular Engines Laboratories (FR)

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DEFINITION		
ACCESSION		
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
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Query Match		
Best Local Similarity		
Matches		
Qy		
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DEFINITION		
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VERSION		
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ORGANISM		
REFERENCE		
AUTHORS		
TITLE		
JOURNAL		
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FH		
FT		

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Qy 8 CCTGCTGTGTGACCTG 23
Db 1 CCTGCTGTGCGGCTG 16

RESULT 49
LOCUS I07726 12 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 31 from Patent EP 0364255.
ACCESSION I07726
VERSION I07726.1 GI:589733
KEYWORDS unknown.
SOURCE unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Caskey,C.T., Chamberlain,J.S., Gibbs,R.A., Rainer,J.E. and
Nguyen,P.N.
TITLE Multiplex genomic DNA amplification for deletion detection
JOURNAL Patent: EP 0364255-A2 31 18-APR-1990;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAAT 29
Db 1 ACCTGGTAAAT 11

RESULT 50
LOCUS CQ828994/c 15 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 712 from Patent WO2004053120.
ACCESSION CQ828994
VERSION CQ828994.1 GI:49732477
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
TITLE Weihe,E., Bieller,A. and Schaefer,M.K.
JOURNAL Regulatory elements in the 5' region of the vrl gene
Gruenenthal GmbH (DE)
FEATURES Location/Qualifiers
source 1..15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/ncbi="V$247_01"

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Qy 2 CATCCACCTGC 12
Db 14 CATCCACCTGC 4

RESULT 51
LOCUS A88223 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 371 from Patent WO9833904.
ACCESSION A88223
VERSION A88223.1 GI:6736793

KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 371 06-AUG-1998;
FEATURES Location/Qualifiers
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Db 1 CCATCCACTTGATG 14

RESULT 52
LOCUS A90190 15 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 371 from Patent EP0856579.
ACCESSION A90190
VERSION A90190.1 GI:6738704
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 371 05-AUG-1998;
FEATURES Location/Qualifiers
source 1..15
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/mol_type="unassigned DNA"
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Query Match 37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
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Qy 1 CCATCCACCTGCTG 14
Db 1 CCATCCACTTGATG 14

RESULT 53
LOCUS AR033319/c 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 85 from patent US 5869253.
ACCESSION AR033319
VERSION AR033319.1 GI:5948924
KEYWORDS unknown.
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 85 09-FEB-1999;
FEATURES Location/Qualifiers
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Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
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Qy 16 GTGACCTGGTAAAT 29
Db 15 GTGACCTGATACAT 2

RESULT 54
AR113141/c
LOCUS AR113141 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 85 from patent US 6132966.
ACCESSION AR113141
VERSION AR113141
KEYWORDS AR113141.1 GI:14093463
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 85 17-OCT-2000;
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Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
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Qy 16 GTGACCTGGTAAAT 29
Db 15 GTGACCTGATACAT 2

RESULT 55
BD065736
LOCUS BD065736 15 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065736
VERSION BD065736.1 GI:22611339
KEYWORDS JP 2001511000-A/371.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Schlengensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 371 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/371
PD JP 2001511000-A/371
PF 30-JAN-1998 JP 19980532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11.C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GTGACCTGGTAAAT 29
Db 15 GTGACCTGATACAT 2

RESULT 56
BD207052/c
LOCUS BD207052 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207052
VERSION BD207052.1 GI:33016822
KEYWORDS JP 2002512791-A/642.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., Mewiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 642 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/642
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO.
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
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Best Local Similarity 85.7%; Pred. No. 89;
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Db 15 GTGACCTGATACAT 2

RESULT 57
I57548/c
LOCUS I57548 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 85 from patent US 5610054.
ACCESSION I57548
VERSION I57548.1 GI:2482612
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 85 11-MAR-1997;
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Query Match      37.2%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29
Db 15 GTGACCTGATACAT 2

RESULT 58
LOCUS CQ794305
DEFINITION Sequence 46 from Patent WO2004024953.
ACCESSION CQ794305
VERSION CQ794305.1 GI:46406940
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini,
JOURNAL Hominidae; Homo.
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Query Match      35.9%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTGG 24
Db 2 TGTATGACCTGG 13

RESULT 59
LOCUS A40464/c
DEFINITION Sequence 1 from Patent WO9425578.
ACCESSION A40464
VERSION A40464.1 GI:2296499
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS unclassified sequences.
TITLE 1 (bases 1 to 14)
JOURNAL Antisense-oligonucleotides for the treatment of immunosuppressive
FEATURES
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/db_xref="taxon:32644"

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/mol_type="unassigned DNA"

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Best Local Similarity 85.7%; Pred. No. 89;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTAAAT 29
Db 15 GTGACCTGATACAT 2

RESULT 60
LOCUS A88991/c
DEFINITION Sequence 1139 from Patent WO9833904.
ACCESSION A88991
VERSION A88991.1 GI:6737561
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Brysch, W. and Schlingsensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1139 06-AUG-1998;
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Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCATCCACCTGC 12
Db 13 CTATCCACCTGC 2

RESULT 61
LOCUS BD066504/c
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066504
VERSION BD066504.1 GI:22612107
KEYWORDS JP 2001511000-A/1139.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingsensiepen, K.H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1139 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/1139
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGSIEPEN, WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
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QY 1 CCATCCACCTGC 12
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RESULT 62
BD176783
LOCUS AR232744/c 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176783
VERSION BD176783.1 GI:29122495
KEYWORDS WO 02074951-A/30.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 14)
Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
Patent: WO 02074951-A 30 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
OS Homo sapiens (human)
PN WO 02074951-A/30
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Method of constructing cDNA tag for identifying expressed gene
and method
CC of analyzing gene expression
FH Key Location/Qualifiers
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Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 13 TGTGTGACCTGG 24
Db 2 TGTATGACCTGG 13
RESULT 63
AR232744/c
LOCUS AR232744 14 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6455689.
ACCESSION AR232744
VERSION AR232744.1 GI:27275082
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for transforming growth factor- .beta.
(TGF- .beta.)
JOURNAL Patent: US 6455689-A 1 24-SEP-2002;
Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
Gottlingen;
EPX;
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Db 2 TGTATGACCTGG 13
RESULT 64
AR300215/c
LOCUS AR300215 14 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 17 from patent US 6537775.
ACCESSION AR300215
VERSION AR300215.1 GI:31687634
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Tournier-Iasserve,E., Joutel,A., Bousser,M.-G. and Bach,J.-F.
TITLE Gene involved in cadasil, method of diagnosis and therapeutic
application
JOURNAL Patent: US 6537775-A 17 25-MAR-2003;
Institut National de la Sante et de la Recherche (INSERM) and
Assistance Publique - Hopitaux de Paris; Paris;
FRX;
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/mol_type="genomic DNA"
Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 14 CCACCCACCTGC 3
RESULT 65
AX316360/c
LOCUS AX316360 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 1 from Patent EP1160319.
ACCESSION AX316360
VERSION AX316360.1 GI:17899533
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 1 05-DEC-2001;
BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DB)
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Best Local Similarity 91.7%; Pred. No. 97;
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Db 13 CTATCCACCTGC 2
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Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 13 CTATCCACCTGC 2
RESULT 64
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LOCUS AR300215 14 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 17 from patent US 6537775.
ACCESSION AR300215
VERSION AR300215.1 GI:31687634
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Tournier-Iasserve,E., Joutel,A., Bousser,M.-G. and Bach,J.-F.
TITLE Gene involved in cadasil, method of diagnosis and therapeutic
application
JOURNAL Patent: US 6537775-A 17 25-MAR-2003;
Institut National de la Sante et de la Recherche (INSERM) and
Assistance Publique - Hopitaux de Paris; Paris;
FRX;
1..14
Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 14 CCACCCACCTGC 3
RESULT 65
AX316360/c
LOCUS AX316360 14 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 1 from Patent EP1160319.
ACCESSION AX316360
VERSION AX316360.1 GI:17899533
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
Schlingensiepen,R. and Bogdahn,U.
TITLE Antisense-oligonucleotides for the treatment of immunosuppressive
effects of transforming growth factor-beta (tgf-beta)
JOURNAL Patent: EP 1160319-A 1 05-DEC-2001;
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Query Match 35.9%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 97;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 13 CTATCCACCTGC 2
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SOURCE	synthetic construct	synthetic construct	other sequences; artificial sequences.
REFERENCE	1		
AUTHORS	Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.		
TITLE	Detection of cyp2d6 polymorphisms		
JOURNAL	Patent: WO 0218638-A 63 07-MAR-2002;		
GENOMICS	Gemini Genomics PLC (GB)		
FEATURES	Location/Qualifiers		
source	1..11		
	/organism="synthetic construct"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:32630"		
	/note="Synthetic oligonucleotide"		
Query Match	34.5%; Score 10; DB 1; Length 11;		
Best Local Similarity	100.0%; Pred. No. 87;		
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 CCATCCACCT 10		
Db	1 CCATCCACCT 10		
RESULT 69			
LOCUS	AX471278	11 bp	DNA linear PAT 09-AUG-2002
DEFINITION	Sequence 855 from Patent WO02053773.		
ACCESSION	AX471278		
VERSION	AX471278.1 GI:22206403		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Hofmann,K., Conradt,M. and Petersohn,D.		
TITLE	Method for determining skin stress or skin ageing in vitro		
JOURNAL	Patent: WO 02053773-A 855 11-JUL-2002;		
GENOMICS	HENKEL KGAA (DE)		
FEATURES	Location/Qualifiers		
source	1..11		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	34.5%; Score 10; DB 1; Length 11;		
Best Local Similarity	100.0%; Pred. No. 87;		
Matches	10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	3 ATCCACCTGC 12		
Db	1 ATCCACCTGC 10		
RESULT 70			
LOCUS	AX624482	11 bp	DNA linear PAT 24-FEB-2003
DEFINITION	Sequence 1523 from Patent WO02053774.		
ACCESSION	AX624482		
VERSION	AX624482.1 GI:28452423		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Petersohn,D., Conradt,M. and Hofmann,K.		
TITLE	Method for determining homeostasis of the skin		
JOURNAL	Patent: WO 02053774-A 1523 11-JUL-2002;		
GENOMICS	Henkel Kommanditgesellschaft auf Aktien (DE)		

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FEATURES
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        /db_xref="taxon:9606"

Query Match
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Best Local Similarity 100.0%; Pred. No. 87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  3 ATCCACCTGC 12
  |||||
Db
  1 ATCCACCTGC 10

RESULT 71
LOCUS
  AX625948
  Sequence 2989 from Patent WO02053774.
  11 bp DNA linear PAT 21-FEB-2003
ACCESSION
  AX625948
VERSION
  AX625948.1 GI:28453986
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 2989 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
JOURNAL
  Location/Qualifiers
FEATURES
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    1. .11
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  10 TGCTGTGTGA 19
  |||||
Db
  2 TGCTGTGTGA 11

RESULT 72
LOCUS
  AX627058
  Sequence 4099 from Patent WO02053774.
  11 bp DNA linear PAT 21-FEB-2003
ACCESSION
  AX627058
VERSION
  AX627058.1 GI:28455096
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 4099 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
JOURNAL
  Location/Qualifiers
FEATURES
  source
    1. .11
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  3 ATCCACCTGC 12
  |||||
Db
  12 ATCCACCTGC 3

RESULT 73
LOCUS
  AX631903
  Sequence 8945 from Patent WO02053774.
  11 bp DNA linear PAT 21-FEB-2003
ACCESSION
  AX631903
VERSION
  AX631903.1 GI:28460041
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 8945 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
JOURNAL
  Location/Qualifiers
FEATURES
  source
    1. .11
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

Query Match
  34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  3 ATCCACCTGC 12
  |||||
Db
  1 ATCCACCTGC 10

RESULT 74
LOCUS
  CQ828958
  Sequence 676 from Patent WO2004053120.
  12 bp DNA linear PAT 05-JUL-2004
ACCESSION
  CQ828958
VERSION
  CQ828958.1 GI:49732441
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
  1
  Weihe,E., Bieller,A. and Schaefer,M.K.
  Regulatory elements in the 5' region of the vrl gene
  Patent: WO 2004053120-A 676 24-JUN-2004;
  Gruenthal GmbH (DE)
JOURNAL
  Location/Qualifiers
FEATURES
  source
    1. .12
      /organism="Homo sapiens"
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      /db_xref="taxon:9606"
      /note="V$LMO2COM 01"

Query Match
  34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
  3 ATCCACCTGC 12
  |||||
Db
  12 ATCCACCTGC 3

RESULT 75
LOCUS
  CQ828995/c
  Sequence 4099 from Patent WO02053774.
  11 bp DNA linear PAT 21-FEB-2003
ACCESSION
  CQ828995/c
VERSION
  CQ828995/c.1 GI:28455096
KEYWORDS
  Homo sapiens (human)
SOURCE
  Homo sapiens
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 4099 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
JOURNAL
  Location/Qualifiers
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Query Match
  34.5%; Score 10; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS CQ828995 12 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 713 from Patent WO2004053120.
ACCESSION CQ828995
VERSION CQ828995.1 GI:49732478
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Weihe, E., Bieller, A. and Schaefer, M. K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 713 24-JUN-2004;
Gruenenthal GmbH (DE)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="V\$LMO2COM 01"
Query Match 34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATCCACCTGC 12
|||||
Db 12 ATCCACCTGC 3
RESULT 76
AX770861/c
LOCUS AX770861 12 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 50 from Patent WO03022875.
ACCESSION AX770861
VERSION AX770861.1 GI:32438026
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Alarcon-Riquelme, M. and Prokunina, L.
TITLE Polymorphisms of pd-1
JOURNAL Patent: WO 03022875-A 50 20-MAR-2003;
Everygene AB (SE)
FEATURES
source Location/Qualifiers
1..12
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 34.5%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCCACCT 10
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Db 12 CCATCCACCT 3
RESULT 77
A89161/c
LOCUS A89161 14 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1309 from Patent WO9833904.
ACCESSION A89161
VERSION A89161.1 GI:6737731
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.

REFERENCE 1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiefen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1309 06-AUG-1998;
BIOGOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATCCACCTGC 12
|||||
Db 10 ATCCACCTGC 1
RESULT 78
BD066674/c
LOCUS BD066674 14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066674
VERSION BD066674.1 GI:22612277
KEYWORDS JP 2001511000-A/1309.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiefen, K. H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1309 07-AUG-2001;
BIOGOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1309
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEFEN WOLFGANG BRYSCH
PC CL2N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH
Location/Qualifiers
1..14
FT source /organism="Unknown".
FEATURES
source Location/Qualifiers
1..14
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 ATCCACCTGC 12
|||||
Db 10 ATCCACCTGC 1
RESULT 79
BD209352
LOCUS BD209352 14 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD209352
VERSION BD209352.1 GI:33019122
KEYWORDS JP 2002512791-A/2942.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)

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AUTHORS      Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE        Enzymatic nucleic acid treatment of diseases or conditions related
              to hepatitis C virus infection
JOURNAL      Patent: JP 2002512791-A 2942 08-MAY-2002;
              RIBOZYME PHARMACEUTICALS INC
COMMENT      OS Hepatitis virus (hepatitis C virus)
              PN JP 2002512791-A/2942
              PD 08-MAY-2002
              PF 26-APR-1999 JP 2000545991
              PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
              25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
              LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
              PAVCO,
              PI DENNIS MACEJAK
              PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
              PC A61K37/66,
              PC C12N15/00
              CC Enzymatic nucleic acid treatment of diseases or conditions CC
                 related to
              CC hepatitis C virus infection.
              FH Key Location/Qualifiers
              FT source 1..14
              FT virus)'Hepatitis virus (hepatitis C FT
              FT Location/Qualifiers
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              source 1..14
                 /organism="unidentified"
                 /mol_type="genomic RNA"
                 /db_xref="taxon:32644"

Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 4 CTGCTGTGTG 13

RESULT 80
BD235127 14 bp DNA linear PAT 17-JUL-2003
LOCUS      Detection of non-viral organisms with SRP RNA.
DEFINITION BD235127
ACCESSION  BD235127.1 GI:33044897
VERSION     JP 2002518026-A/6.
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Boles,C.T., Weir,L. and Stone,B.B.
TITLE       Detection of non-viral organisms with SRP RNA
JOURNAL     Patent: JP 2002518026-A 6 25-JUN-2002;
            MOSAIC TECHNOLOGIES
COMMENT     OS Artificial Sequence
            PN JP 2002518026-A/6
            PD 25-JUN-2002
            PF 18-JUN-1999 JP 2000554886
            PR 19-JUN-1998 US 60/090063
            PI CHRISTIAN T BOLES,LAWRENCE WEIR,BENJAMIN B STONE PC
            C12N15/09,C07H21/04,C12Q1/68//C12Q1/68,C12R1/93,C12N15/00 CC
            Description of Artificial Sequence:complement of conserved B. CC
            coli 4.5S
            CC RNA region nucleotides preferred shorter probe for detection
            of bacteria
            FH Key Location/Qualifiers
            FT source 1..14
            FT /organism='Artificial Sequence'.
            FT Location/Qualifiers
            FEATURES
            source 1..14
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match 34.5%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGCCCT 13

RESULT 82
AX572357/c 13 bp DNA linear PAT 29-NOV-2002
LOCUS      Sequence 397 from Patent WO02055741.
DEFINITION AX572357
ACCESSION  AX572357
VERSION     AX572357.1 GI:26004447
KEYWORDS    Human immunodeficiency virus
SOURCE      Human immunodeficiency virus
ORGANISM    Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE       Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL     Patent: WO 02055741-A 397 18-JUL-2002;
            INNOGENETICS N.V. (BE)
COMMENT     FEATURES
            source 1..13
               /organism="Human immunodeficiency virus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:12721"

Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGCCCT 13

RESULT 81
AR175360 13 bp DNA linear PAT 17-DEC-2001
LOCUS      AR175360
DEFINITION Sequence 83 from patent US 6309823.
ACCESSION  AR175360
VERSION     AR175360.1 GI:17916659
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A.,
            Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and
            Sheldon,E.L.
TITLE       Arrays of nucleic acid probes for analyzing biotransformation genes
            and methods of using the same
JOURNAL     Patent: US 6309823-A 83 30-OCT-2001;
            Location/Qualifiers
            FEATURES
            source 1..13
               /organism="unknown"
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Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
Db 1 TGGTGTGTGCCCT 13

RESULT 82
AX572357/c 13 bp DNA linear PAT 29-NOV-2002
LOCUS      Sequence 397 from Patent WO02055741.
DEFINITION AX572357
ACCESSION  AX572357
VERSION     AX572357.1 GI:26004447
KEYWORDS    Human immunodeficiency virus
SOURCE      Human immunodeficiency virus
ORGANISM    Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE       Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL     Patent: WO 02055741-A 397 18-JUL-2002;
            INNOGENETICS N.V. (BE)
COMMENT     FEATURES
            source 1..13
               /organism="Human immunodeficiency virus"
               /mol_type="unassigned DNA"
               /db_xref="taxon:12721"

Query Match 33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CATCCACCTGCTG 14
Db 13 CATCCACGTACTG 1

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RESULT 83
LOCUS      AX572382/c      13 bp      DNA      linear      PAT 29-NOV-2002
DEFINITION Sequence 422 from Patent WO02055741.
ACCESSION  AX572382
VERSION     AX572382.1  GI:26004472
KEYWORDS    Human immunodeficiency virus
SOURCE      Human immunodeficiency virus
ORGANISM    Human immunodeficiency virus
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE       Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL     Patent: WO 02055741-A 422 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES    source
            1..13
            Location/Qualifiers
            /organism="Human immunodeficiency virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:12721"

Query Match      33.8%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  CATCCACTGCTG 14
        |||||
Db      13 CATCCAGTACTG 1

RESULT 84
LOCUS      A40478      14 bp      DNA      linear      PAT 05-MAR-1997
DEFINITION Sequence 15 from Patent WO9425578.
ACCESSION  A40478
VERSION     A40478.1  GI:2296513
KEYWORDS    unidentified
SOURCE      unclassified sequences.
ORGANISM    unclassified sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       ANTISENSE-OLIGONUCLEOTIDES FOR THE TREATMENT OF IMMUNOSUPPRESSIVE
            EFFECTS OF TRANSFORMING GROWTH FACTOR--g(b) (TGF--g(b))
JOURNAL     Patent: WO 9425578-A 15 10-NOV-1994;
            BIOGNOSTIK GES (DE)
FEATURES    source
            1..14
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      10 TGCTGTGTGACCT 22
        |||||
Db      1  TGCTGTGTGTACT 13

RESULT 85
LOCUS      A88219      14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 367 from Patent WO9833904.
ACCESSION  A88219
VERSION     A88219.1  GI:6736789
KEYWORDS    unidentified
SOURCE      unclassified sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1469 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    source
            1..14
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      11 GCTGTGTGACCTG 23
        |||||
Db      1  GCTGTGTGCACAG 13

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REFERENCE   1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 367 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    source
            1..14
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      11 GCTGTGTGACCTG 23
        |||||
Db      1  GCTGTGTGCACAG 13

RESULT 86
LOCUS      A89005      14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1153 from Patent WO9833904.
ACCESSION  A89005
VERSION     A89005.1  GI:6737575
KEYWORDS    unidentified
SOURCE      unclassified sequences.
ORGANISM    unclassified sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1153 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    source
            1..14
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      10 TGCTGTGTGACCT 22
        |||||
Db      1  TGCTGTGTGTACT 13

RESULT 87
LOCUS      A89321/c      14 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1469 from Patent WO9833904.
ACCESSION  A89321
VERSION     A89321.1  GI:6737891
KEYWORDS    unidentified
SOURCE      unclassified sequences.
ORGANISM    unclassified sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1469 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES    source
            1..14
            Location/Qualifiers
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      11 GCTGTGTGACCTG 23
        |||||
Db      1  GCTGTGTGTACT 13

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Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTG 24
|||||
Db 13 CTGTGTGACCTG 1

RESULT 88
A90186
LOCUS
DEFINITION Sequence 367 from Patent EP0856579. linear PAT 22-JAN-2000
ACCESSION A90186
VERSION A90186.1 GI:6738700
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 367 05-AUG-1998;
BIOGNOSTIK GES (DE)
FEATURES
source
1..14
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GCTGTGTGACCTG 23
|||||
Db 1 GCTGTGTGACCTG 13

RESULT 89
BD065732
LOCUS
DEFINITION An antisense oligonucleotide preparation method. linear PAT 27-AUG-2002
ACCESSION BD065732
VERSION BD065732.1 GI:22611335
KEYWORDS JP 2001511000-A/367.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 367 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/367
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..14
/organism="Unknown".
Location/Qualifiers

FEATURES
source
1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 11 GCTGTGTGACCTG 23
|||||
Db 1 GCTGTGTGACCTG 13

RESULT 90
BD066518
LOCUS
DEFINITION An antisense oligonucleotide preparation method. linear PAT 27-AUG-2002
ACCESSION BD066518
VERSION BD066518.1 GI:22612121
KEYWORDS JP 2001511000-A/1153.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1153 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/1153
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..14
/organism="Unknown".
Location/Qualifiers

FEATURES
source
1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 TGCTGTGTGACCT 22
|||||
Db 1 TGCTGTGTGTACT 13

RESULT 91
BD066834/c
LOCUS
DEFINITION An antisense oligonucleotide preparation method. linear PAT 27-AUG-2002
ACCESSION BD066834
VERSION BD066834.1 GI:22612437
KEYWORDS JP 2001511000-A/1469.
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 14)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1469 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/1469
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..14
/organism="Unknown".
Location/Qualifiers

FEATURES
source
1..14
/organism="Unknown".
Location/Qualifiers


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source      1..14
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CTGTGTGACCTGG 24
Db 13 CTGTGTGACATGG 1

RESULT 92
AR232758
LOCUS      AR232758
DEFINITION Sequence 15 from patent US 6455689.
ACCESSION AR232758
VERSION    AR232758.1 GI:27275096
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Schlingensiepen,G.-F., Brysch,W., Schlingensiepen,K.-H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE        Antisense-oligonucleotides for transforming growth factor--beta.
            (TGF-beta.)
JOURNAL      Patent: US 6455689-A 15 24-SEP-2002;
            Biognostik Gesellschaft fur Biomolekulare Diagnostik mbH;
            Göttingen;
            EPX;
FEATURES     Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22
Db 1 TGCTGTGTGTACT 13

RESULT 93
AX316374
LOCUS      AX316374
DEFINITION Sequence 15 from Patent EP1160319.
ACCESSION AX316374
VERSION    AX316374.1 GI:17899547
KEYWORDS   .
SOURCE      unidentified
ORGANISM    unclassified sequences.
REFERENCE   1
AUTHORS     Schlingensiepen,G.F., Brysch,W., Schlingensiepen,K.H.,
            Schlingensiepen,R. and Bogdahn,U.
TITLE        Antisense-oligonucleotides for the treatment of immunosuppressive
            effects of transforming growth factor-beta (tgf-beta)
JOURNAL      Patent: EP 1160319-A 15 05-DEC-2001;
            BIOGNOSTIK GESELLSCHAFT FUER BIOMOLEKULARE DIAGNOSTIK mbH (DE)
FEATURES     Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
            /note="Description of unknown: unknown"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;

source      1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TGCTGTGTGACCT 22
Db 1 TGCTGTGTGTACT 13

RESULT 94
AX572354/c
LOCUS      AX572354/c
DEFINITION Sequence 394 from Patent WO02055741.
ACCESSION AX572354
VERSION    AX572354.1 GI:26004444
KEYWORDS   .
SOURCE      Human immunodeficiency virus
ORGANISM    Human immunodeficiency virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE        Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL      Patent: WO 02055741-A 394 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES     Location/Qualifiers
            source
            1..14
            /organism="Human immunodeficiency virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:12721"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14
Db 14 CATCCACGTACTG 2

RESULT 95
AX572358/c
LOCUS      AX572358
DEFINITION Sequence 398 from Patent WO02055741.
ACCESSION AX572358
VERSION    AX572358.1 GI:26004448
KEYWORDS   .
SOURCE      Human immunodeficiency virus
ORGANISM    Human immunodeficiency virus
            Viruses; Retro-transcribing viruses; Retroviridae;
            Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE   1
AUTHORS     de Smet,K. and Stuyver,L.
TITLE        Method for detection of drug-induced mutations in the hiv reverse
            transcriptase gene
JOURNAL      Patent: WO 02055741-A 398 18-JUL-2002;
            INNOGENETICS N.V. (BE)
FEATURES     Location/Qualifiers
            source
            1..14
            /organism="Human immunodeficiency virus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:12721"

Query Match      33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGCTG 14
Db 14 CATCCACATACTG 2

RESULT 96
AX572372/c

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LOCUS AX572372 14 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 412 from Patent WO02055741.
ACCESSION AX572372
VERSION AX572372.1 GI:26004462
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE 1
AUTHORS de Smet,K. and Stuyver,L.
TITLE Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
JOURNAL Patent: WO 02055741-A 412 18-JUL-2002;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
1. .14
/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CATCCACCTGCTG 14
|||||
Db 14 CATCCACGTACTG 2
RESULT 97
AX572374/c
LOCUS AX572374 14 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 414 from Patent WO02055741.
ACCESSION AX572374
VERSION AX572374.1 GI:26004464
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE 1
AUTHORS de Smet,K. and Stuyver,L.
TITLE Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
JOURNAL Patent: WO 02055741-A 414 18-JUL-2002;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
1. .14
/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CATCCACCTGCTG 14
|||||
Db 14 CATCCACGTACTG 2
RESULT 98
AX572377/c
LOCUS AX572377 14 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 417 from Patent WO02055741.
ACCESSION AX572377
VERSION AX572377.1 GI:26004467
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.

REFERENCE 1
AUTHORS de Smet,K. and Stuyver,L.
TITLE Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
JOURNAL Patent: WO 02055741-A 417 18-JUL-2002;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
1. .14
/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CATCCACCTGCTG 14
|||||
Db 13 CATCCACATACTG 1
RESULT 99
AX572381/c
LOCUS AX572381 14 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 421 from Patent WO02055741.
ACCESSION AX572381
VERSION AX572381.1 GI:26004471
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE 1
AUTHORS de Smet,K. and Stuyver,L.
TITLE Method for detection of drug-induced mutations in the hiv reverse
transcriptase gene
JOURNAL Patent: WO 02055741-A 421 18-JUL-2002;
INNOGENETICS N.V. (BE)
FEATURES
source Location/Qualifiers
1. .14
/organism="Human immunodeficiency virus"
/mol_type="unassigned DNA"
/db_xref="taxon:12721"
Query Match 33.8%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CATCCACCTGCTG 14
|||||
Db 13 CATCCACGTACTG 1
RESULT 100
BD124223/c
LOCUS BD124223 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124223
VERSION BD124223.1 GI:23219168
KEYWORDS JP 2002503460-A/54.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Katz,E.H.
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 54 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/54
PD 05-FEB-2002

PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
FT /organism="Mus musculus (mouse)".

FEATURES
source
1..11 Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23
|||||
Db 11 TGTGTGCGCTG 1

RESULT 101
BD124438
LOCUS 11 bp DNA linear PAT 18-SEP-2002
DEFINITION Compositions and method for healing wound.
ACCESSION BD124438
VERSION BD124438.1 GI:23219383
KEYWORDS JP 2002503460-A/269.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 11)
Katz, E.H.
AUTHORS
TITLE Compositions and method for healing wound
JOURNAL Patent: JP 2002503460-A 269 05-FEB-2002;
THE WISTAR INSTITUTE
COMMENT OS Mus musculus (mouse)
PN JP 2002503460-A/269
PD 05-FEB-2002
PF 12-FEB-1998 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key Location/Qualifiers
FT source 1..11
FT /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

FEATURES
source
1..11 Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGT 15
|||||
Db 1 CCACCTCCTGT 11

RESULT 102
CQ836739
LOCUS 11 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 1797 from Patent WO2004059001.
ACCESSION CQ836739
VERSION CQ836739.1 GI:50836273
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1797 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGTCT 13
|||||
Db 1 ATCCGCGCTGT 11

RESULT 103
CQ837792
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2950 from Patent WO2004059001.
ACCESSION CQ837792
VERSION CQ837792.1 GI:50837326
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2850 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGTGTGT 15
|||||
Db 1 CCACCTGTCTTT 11

RESULT 104
CS058325
LOCUS 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 222 from Patent WO2005028671.
ACCESSION CS058325
VERSION CS058325.1 GI:62551508
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 222 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGCT 13
Db 1 ATCGCGCTGCT 11

RESULT 105
AR301473/c
LOCUS AR301473 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 54 from patent US 6538173.
ACCESSION AR301473
VERSION AR301473.1 GI:31689275
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 54 25-MAR-2003;
The Wistar Institute; Philadelphia, PA;
WOX;
FEATURES
source Location/Qualifiers
1. .11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23
Db 11 TGTGTGGCCTG 1

RESULT 106
AR301688
LOCUS AR301688 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 269 from patent US 6538173.
ACCESSION AR301688
VERSION AR301688.1 GI:31689490
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 269 25-MAR-2003;
The Wistar Institute; Philadelphia, PA;
WOX;
FEATURES
source Location/Qualifiers
1. .11
/organism="unknown"
/mol_type="genomic DNA"

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Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGT 15
Db 1 CCACCTCCTGT 11

RESULT 107
AX036264/c
LOCUS AX036264 11 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent EP1043407.
ACCESSION AX036264
VERSION AX036264.1 GI:11225880
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
REFERENCE 1
AUTHORS Prljic,J., Metlas,R., Veljkovic,N. and Veljkovic,V.
TITLE Nucleotide sequence for detection and characterization of the hiv-1
field isolates participating in the recombination processes
directed by the chi sequence
JOURNAL Patent: EP 1043407-A 2 11-OCT-2000;
DIAPHARM LIMITED (GB)
FEATURES
source Location/Qualifiers
1. .11
/organism="Human immunodeficiency virus 1"
/mol_type="unassigned DNA"
/db_xref="taxon:11676"

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Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCACCTGCTG 14
Db 11 TCCACCAGCTG 1

RESULT 108
AX470508
LOCUS AX470508 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 85 from Patent WO2053773.
ACCESSION AX470508
VERSION AX470508.1 GI:22205633
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hofmann,K., Conrad,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 85 11-JUL-2002;
HENKEL KGAA (DE)
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source Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGAGTGA 11

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RESULT 109
AX623763          AX623763          11 bp      DNA      linear      PAT 24-FEB-2003
LOCUS
DEFINITION       Sequence 804 from Patent WO02053774.
ACCESSION        AX623763
VERSION          AX623763.1 GI:28451704
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 804 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
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SOURCE           1. .11
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                  /db_xref="taxon:9606"
Query Match      32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACCTGCT 25
      ||| |||||
Db 1 TGTACCTGCT 11

RESULT 110
AX625616          AX625616          11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION       Sequence 2657 from Patent WO02053774.
ACCESSION        AX625616
VERSION          AX625616.1 GI:28453557
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 2657 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE           1. .11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 TGTGACCTGCT 25
      ||| |||||
Db 1 TGTACCTGCT 11

RESULT 111
AX625941          AX625941          11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION       Sequence 2982 from Patent WO02053774.
ACCESSION        AX625941
VERSION          AX625941.1 GI:28453979
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 2982 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
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SOURCE           1. .11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCT 22
      ||| |||||
Db 1 CTGTGAGACCT 11

RESULT 112
AX627200          AX627200          11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION       Sequence 4241 from Patent WO02053774.
ACCESSION        AX627200
VERSION          AX627200.1 GI:28455238
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 4241 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE           1. .11
                  /organism="Homo sapiens"
                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"
Query Match      32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTGT 17
      ||| |||||
Db 1 ACTTGCTGTGT 11

RESULT 113
AX627837          AX627837          11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION       Sequence 4878 from Patent WO02053774.
ACCESSION        AX627837
VERSION          AX627837.1 GI:28455875
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 4878 11-JUL-2002;
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SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 2982 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
SOURCE           1. .11
                  /organism="Homo sapiens"
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Query Match      32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGCT 13
      ||| |||||
Db 1 ATCCGCTGCT 11

RESULT 112
AX627200          AX627200          11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION       Sequence 4241 from Patent WO02053774.
ACCESSION        AX627200
VERSION          AX627200.1 GI:28455238
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 4241 11-JUL-2002;
                  Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      32.4%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ACCTGCTGTGT 17
      ||| |||||
Db 1 ACTTGCTGTGT 11

RESULT 113
AX627837          AX627837          11 bp      DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION       Sequence 4878 from Patent WO02053774.
ACCESSION        AX627837
VERSION          AX627837.1 GI:28455875
KEYWORDS
SOURCE           Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominiidae; Homo.
REFERENCE
AUTHORS          Petersohn,D., Conradt,M. and Hofmann,K.
TITLE            Method for determining homeostasis of the skin
JOURNAL          Patent: WO 02053774-A 4878 11-JUL-2002;
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Henkel Kommanditgesellschaft auf Aktien (DE)									
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32.4%; Score 9.4; DB 1; Length 11;									
Best Local Similarity 90.9%; Pred. No. 1.1e+02;									
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY 5 CCACCTGCTGT 15									
Db 1 CCACCTGCTTT 11									
RESULT 114									
AX628604									
LOCUS									
AX628604 11 bp DNA linear PAT 21-FEB-2003									
DEFINITION									
Sequence 5645 from Patent WO2053774.									
ACCESSION									
AX628604									
VERSION									
AX628604.1 GI:28456642									
KEYWORDS									
Homo sapiens (human)									
ORGANISM									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
1									
Petersohn,D., Conradt,M. and Hofmann,K.									
AUTHORS									
Method for determining homeostasis of the skin									
TITLE									
Patent: WO 02053774-A 5645 11-JUL-2002;									
JOURNAL									
Henkel Kommanditgesellschaft auf Aktien (DE)									
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QY 9 CTGCTGTGTGA 19									
Db 1 CTGCTGAGTGA 11									
RESULT 115									
AX631184									
LOCUS									
AX631184 11 bp DNA linear PAT 21-FEB-2003									
DEFINITION									
Sequence 8226 from Patent WO2053774.									
ACCESSION									
AX631184									
VERSION									
AX631184.1 GI:28459228									
KEYWORDS									
Homo sapiens (human)									
ORGANISM									
Homo sapiens									
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;									
Hominidae; Homo.									
REFERENCE									
1									
Petersohn,D., Conradt,M. and Hofmann,K.									
AUTHORS									
Method for determining homeostasis of the skin									
TITLE									
Patent: WO 02053774-A 8226 11-JUL-2002;									
JOURNAL									
Henkel Kommanditgesellschaft auf Aktien (DE)									
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Best Local Similarity 90.9%; Pred. No. 1.1e+02;									
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY 15 TGTGACCTGGT 25									
Db 1 TGTTACCTGGT 11									
RESULT 116									
A91475									
LOCUS									
A91475 12 bp DNA linear PAT 22-JAN-2000									
DEFINITION									
Sequence 2 from Patent WO9824928.									
ACCESSION									
A91475									
VERSION									
A91475.1 GI:6740430									
KEYWORDS									
unidentified									
SOURCE									
unidentified									
ORGANISM									
unclassified sequences.									
1 (bases 1 to 12)									
Pallisgaard,N. and Hokland,P.									
AUTHORS									
DETECTION OF CHROMOSOMAL ABNORMALITIES									
TITLE									
Patent: WO 9824928-A 2 11-JUN-1998;									
JOURNAL									
PALLISGAARD NIELS (DK); HOKLAND PETER (DK)									
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Location/Qualifiers									
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32.4%; Score 9.4; DB 1; Length 12;									
Best Local Similarity 90.9%; Pred. No. 1.2e+02;									
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY 9 CTGCTGTGTGA 19									
Db 1 CTGCTGGGTGA 11									
RESULT 117									
BD248272									
LOCUS									
BD248272 12 bp DNA linear PAT 17-JUL-2003									
DEFINITION									
Short-chain oligonucleotide for inhibiting VEGF expression.									
ACCESSION									
BD248272									
VERSION									
BD248272.1 GI:33058042									
KEYWORDS									
JP 2002524038-A/91.									
SOURCE									
synthetic construct									
ORGANISM									
other sequences; artificial sequences.									
1 (bases 1 to 12)									
Uhlmann,E., Peyman,A., Bitonti,A. and Woessner,R.									
AUTHORS									
Short-chain oligonucleotide for inhibiting VEGF expression									
TITLE									
Patent: JP 2002524038-A 91 06-AUG-2002;									
JOURNAL									
AVENTIS PHARMA DEUTSCHLAND GMBH									
COMMENT									
OS Artificial Sequence									
JP 2002524038-A/91									
PD 06-AUG-2002									
PF 29-JUL-1999 JP 2000563768									
PP 07-AUG-1998 EP 98114853.9									
PR EUGEN UHLMANN,ANUSCHIRWAN PEYMAN,ALAN BITONTI,RICHARD WOESSNER									
PC C12N15/09,A61K31/711,A61K31/712,A61K31/715,A61K31/712 PC									
,A61K48/00,A61P9/00,									
PC A61P13/12,A61P17/16,A61P27/02,A61P29/00,A61P35/00,A61P43/00,									
PC C12N15/00									
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Location/Qualifiers									
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Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24
Db 1 GTGTGACCTGG 11

RESULT 118
BD248273
LOCUS BD248273 12 bp DNA linear PAT 17-JUL-2003
DEFINITION Short-chain oligonucleotide for inhibiting VEGF expression.
ACCESSION BD248273
VERSION BD248273.1 GI:33058043
KEYWORDS JP 2002524038-A/92.
SOURCE synthetic construct
ORGANISM
REFERENCE 1 (bases 1 to 12)
AUTHORS Uhlmann,E., Peyman,A., Bitonti,A. and Woessner,R.
TITLE Short-chain oligonucleotide for inhibiting VEGF expression
JOURNAL Patent: JP 2002524038-A 92 06-AUG-2002;
COMMENT AVENTIS PHARMA DEUTSCHLAND GMBH
OS Artificial Sequence
PN JP 2002524038-A/92
PD 06-AUG-2002
PF 29-JUL-1999 JP 2000563768
PR 07-AUG-1998 EP 98114853.9
PI EUGEN UHLMANN,ANUSCHIRWAN PEYMAN,ALAN BITONTI,RICHARD WOESSNER
PC C12N15/09,A61K31/711,A61K31/7115,A61K31/712,A61K31/7125 PC
,A61K48/00,A61P9/00,
PC A61P13/12,A61P17/16,A61P27/02,A61P29/00,A61P35/00,A61P43/00,
PC C12N15/00
CC Description of Artificial Sequence: Antisense FH Key
FT Location/Qualifiers
source 1..12
FT Location/Qualifiers
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Query Match 32.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTGG 24
Db 1 GTGTGACCTGG 11

RESULT 119
I07725
LOCUS I07725 12 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 30 from Patent EP 0364255.
ACCESSION I07725
VERSION I07725.1 GI:589732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Caskey,C.T., Chamberlain,J.S., Gibbs,R.A., Rainer,J.E. and
Nguyen,P.N.
TITLE Multiplex genomic DNA amplification for deletion detection
JOURNAL Patent: EP 0364255-A2 30 18-APR-1990;
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Query Match 32.4%; Score 9.4; DB 1; Length 12;

Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGTGTGA 11

Query Match 32.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGTGTGA 11

Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGTGTGA 11

Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 ACCTGGTAAT 29
Db 1 ACCTGGAAAT 11

RESULT 120
BD023257
LOCUS BD023257 12 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023257
VERSION BD023257.1 GI:22564480
KEYWORDS JP 2001505428-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 12)
AUTHORS Parisgard,N. and Hukurando,P.
TITLE Method for detecting abnormality in chromosome
JOURNAL Patent: JP 2001505428-A 2 24-APR-2001;
COMMENT NEILLS PARISGARD
PN JP 2001505428-A/2
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILLS PARISGARD,PATER HOKURANDO
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'DNA (synthetic)';
PH Key Location/Qualifiers.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 32.4%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 1.2e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGTGTGA 11

RESULT 121
I43005
LOCUS I43005 13 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 27 from patent US 5631115.
ACCESSION I43005
VERSION I43005.1 GI:2468249
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Ohtsuka,E. and Koizumi,M.
TITLE Looped, hairpin ribozyme
JOURNAL Patent: US 5631115-A 27 20-MAY-1997;
FEATURES
source 1..13
/organism="unknown"
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Query Match 32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
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QY 9 CTGCTGTGTGA 19
Db 1 CTGCTGTGTGA 19

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Db          ||| |||||
3 CTGTTGTGA 13

RESULT 122
AR363773    AR363773      13 bp  DNA      linear  PAT 03-SEP-2003
LOCUS       AR363773
DEFINITION  Sequence 13 from patent US 5225537.
ACCESSION   AR363773
VERSION     AR363773.1  GI:34425778
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 13)
AUTHORS    Foster,D.C.
TITLE      Methods for producing hybrid phospholipid-binding proteins
JOURNAL    Patent: US 5225537-A 13 06-JUL-1993;
ZymoGenetics, Inc.; Seattle, WA
FEATURES   source
            1..13
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      32.4%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TGACCTGTGTA 27
Db 3 TGACTTGTGA 13

RESULT 123
BD239019
LOCUS       BD239019      10 bp  DNA      linear  PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239019
VERSION     BD239019.1  GI:33048789
KEYWORDS    JP 2002534056-A/437.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 437 15-OCT-2002;
GENZYME CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/437
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090073 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090043 PR
            19-JUN-1998 US 60/090044,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
            G01N37/00,
            PC C12N15/00,C12N5/00,C12N15/00
            CC Preparation and use of superior vaccines
            FH Key Location/Qualifiers
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FEATURES   source
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            /db_xref="taxon:9606"

Query Match      31.0%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGTCT 13
Db 1 CCACCTGTCT 9

RESULT 124
BD239139
LOCUS       BD239139      10 bp  DNA      linear  PAT 17-JUL-2003
DEFINITION  Preparation and use of superior vaccines.
ACCESSION   BD239139
VERSION     BD239139.1  GI:33048909
KEYWORDS    JP 2002534056-A/557.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 557 15-OCT-2002;
GENZYME CORP
COMMENT     OS Homo sapiens (human)
            PN JP 2002534056-A/557
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
            19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
            19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090073 PR
            19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
            19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
            19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
            19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
            19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090036 PR
            19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090043 PR
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            19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089844 PR
            19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
            19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
            19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            08-DEC-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
            G01N37/00,
            PC C12N15/00,C12N5/00,C12N15/00
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            FH Key Location/Qualifiers
            FT source 1..10 /organism='Homo sapiens (human)'.

FEATURES   source
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Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 133
AR085371/c
LOCUS AR085371 11 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 73 from patent US 5981711.
ACCESSION AR085371
VERSION AR085371.1 GI:10012140
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 73 09-NOV-1999;
FEATURES
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Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 136
AR143540/c
LOCUS AR143540 11 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 73 from patent US 6204370.
ACCESSION AR143540
VERSION AR143540.1 GI:15104826
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 73 20-MAR-2001;
FEATURES
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            /mol_type="unassigned DNA"

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 137
AR171446/c
LOCUS AR171446 11 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 73 from patent US 6297041.
ACCESSION AR171446
VERSION AR171446.1 GI:17910396
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 73 02-OCT-2001;
FEATURES
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            /mol_type="unassigned DNA"

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 135
AR104278/c
LOCUS AR104278 11 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 73 from patent US 6093548.
ACCESSION AR104278
VERSION AR104278.1 GI:12816986
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
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RESULT 138
AR171617/C
LOCUS AR171617 11 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 73 from patent US 6297051.
ACCESSION AR171617
VERSION AR171617.1 GI:17910567
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297051-A 73 02-OCT-2001;
FEATURES
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Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 139
BD080109
LOCUS BD080109 11 bp DNA linear PAT 27-AUG-2002
DEFINITION Method of identifying cell- or tissue-specific artificial
transcriptional regulatory region.
ACCESSION BD080109
VERSION BD080109.1 GI:22625712
KEYWORDS JP 2001509395-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 11)
AUTHORS Schwartz,R.J., Eastman,E.M., Li,X. and Nordstrom,J.
TITLE Method of identifying cell- or tissue-specific artificial
transcriptional regulatory region
JOURNAL Patent: Jp 2001509395-A 3 24-JUL-2001;
COMMENT VALENTIS INC.
OS Artificial Sequence
PN JP 2001509395-A/3
PD 24-JUL-2001
PF 14-JUL-1998 JP 2000502228
PR 14-JUL-1997 US 60/052403
PI ROBERT J SCHWARTZ,ERIC M EASTMAN,XUYANG LI,JEFF NORDSTROM PC
C12Q1/68,C12N15/09,C12N15/00
CC Method of identifying cell- or tissue-specific artificial CC
transcriptional
CC regulatory region
FH Key Location/Qualifiers
FT source 1..11
/organism='Artificial Sequence'.
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        /organism="synthetic construct"
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        /db_xref="taxon:32630"
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 CACCTGCTG 14
Db 3 CACCTGCTG 11

RESULT 140
BD243207/C
LOCUS BD243207 11 bp DNA linear PAT 17-JUL-2003
DEFINITION MN gene and protein.
ACCESSION BD243207
VERSION BD243207.1 GI:33052977
KEYWORDS JP 2002528085-A/56.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: JP 2002528085-A 56 03-SEP-2002;
COMMENT INSTITUTE OF VIROLOGY
OS Homo sapiens (human)
PN JP 2002528085-A/56
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578465
PR 23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P35/00, PC
C07K14/47,
PC C12Q1/02,G01N33/566/(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
CC MN gene and protein
FH Key Location/Qualifiers
FT source 1..11
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        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CCACCTGCT 13
Db 9 CCACCTGCT 1

RESULT 141
CS058646
LOCUS CS058646 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 543 from Patent WO2005028671.
ACCESSION CS058646
VERSION CS058646.1 GI:62551829
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 543 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 10 TGCTGTGTG 18
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Db 1 TGCTGTGTG 9

RESULT 142
AR214824
LOCUS AR214824 11 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 3 from patent US 6410228.
ACCESSION AR214824
VERSION AR214824.1 GI:23312758
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Schwartz,R.J., Eastman,E.M., Li,X. and Nordstrom,J.
TITLE Method for the identification of synthetic cell- or tissue-specific transcriptional regulatory regions
JOURNAL Patent: US 6410228-A 3 25-JUN-2002;
Baylor College of Medicine and Valentis, Inc.; Houston, TX
FEATURES
source Location/Qualifiers
1..11
/organism="unknown"
/mol_type="genomic DNA"

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCTGCTG 14
|||||
Db 3 CACCTGCTG 11

RESULT 143
AR569645/c
LOCUS AR569645 11 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 73 from patent US 6770438.
ACCESSION AR569645
VERSION AR569645.1 GI:56570274
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6770438-A 73 03-AUG-2004;
Institute of Virology, Slovak Academy of Sciences; Bratislava; CZX;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCTGCT 13
|||||
Db 9 CCACCTGCT 1

RESULT 144
AX393112/c
LOCUS AX393112 11 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 42 from Patent WO0210217.
ACCESSION AX393112
VERSION AX393112.1 GI:19701162
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.
TITLE Endothelial cell expression patterns
JOURNAL Patent: WO 0210217-A 42 07-FEB-2002;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
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Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
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Db 10 GCTGTGTGA 2

RESULT 145
AX470507/c
LOCUS AX470507 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 84 from Patent WO02053773.
ACCESSION AX470507
VERSION AX470507.1 GI:22205632
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 84 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 31.0%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCTGTGTGA 19
|||||
Db 10 GCTGTGTGA 2

RESULT 146
AX623057/c
LOCUS AX623057 11 bp DNA linear PAT 24-FEB-2003
DEFINITION Sequence 98 from Patent WO02053774.
ACCESSION AX623057
VERSION AX623057.1 GI:28450998
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 98 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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FEATURES
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Query Match
Best Local Similarity 31.0%; Score 9; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2

RESULT 147
LOCUS AX630236 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7277 from Patent WO02053774.
ACCESSION AX630236
VERSION AX630236.1 GI:28458274
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL Patent: WO 02053774-A 7277 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TGCTGTGTG 18
Db 1 TGCTGTGTG 9

RESULT 148
AX630478/c
LOCUS AX630478 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7519 from Patent WO02053774.
ACCESSION AX630478
VERSION AX630478.1 GI:28458516
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1 Petersohn,D., Conradt,M. and Hofmann,K.
  TITLE Method for determining homeostasis of the skin
  JOURNAL Patent: WO 02053774-A 7519 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
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Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCTGTGTGA 19
Db 10 GCTGTGTGA 2

RESULT 149
LOCUS AX395393 12 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 30 from Patent WO0206495.
ACCESSION AX395393
VERSION AX395393.1 GI:21066368
KEYWORDS synthetic construct
SOURCE synthetic construct
  ORGANISM other sequences; artificial sequences.
REFERENCE
  1 Chamberlain,J.S. and Hauschka,S.D.
  TITLE Mutant muscle-specific enhancers
  JOURNAL Patent: WO 0206495-A 30 24-JAN-2002;
  THE REGENTS OF THE UNIVERSITY OF MICHIGAN (US)
FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic"

Query Match
Best Local Similarity 100.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTGCTG 14
Db 3 CACCTGCTG 11

RESULT 150
AR014245
LOCUS AR014245 12 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 9 from patent US 5773278.
ACCESSION AR014245
VERSION AR014245.1 GI:3971699
KEYWORDS
SOURCE Unknown.
  ORGANISM Unclassified.
REFERENCE
  1 (bases 1 to 12)
  AUTHORS Schuchman,E.H. and Desnick,R.J.
  TITLE Acid sphingomyelinase gene
  JOURNAL Patent: US 5773278-A 9 30-JUN-1998;
  Location/Qualifiers
FEATURES
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    Location/Qualifiers
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        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 30.3%; Score 8.8; DB 1; Length 12;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12

RESULT 151
AR038696/c
LOCUS AR038696 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 30 from patent US 5807678.
ACCESSION AR038696
VERSION AR038696.1 GI:5958059
KEYWORDS
SOURCE Unknown.

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MIMAKI,REI FUKUSHIMA, PI KAZURO NISHIKAWA PC C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC Synthetic DNA FH Key Location/Qualifiers FT source 1..12 /organism='Artificial Sequence'. FT Location/Qualifiers 1..12 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 CTGCTGTGTGAC 20
DB 1 CTGCTGAGTCAC 12
RESULT 154
BD271980 12 bp DNA linear PAT 17-JUL-2003
LOCUS Methods and for mutations for the separation of biological macromolecules.
DEFINITION
ACCESSION BD271980
VERSION BD271980.1 GI:33081748
KEYWORDS JP 2002529734-A/3.
SOURCE Bacteriophage M13mp18
ORGANISM Bacteriophage M13mp18 Viruses.
REFERENCE 1 (bases 1 to 12)
AUTHORS Martinez,M.C.R.
TITLE Methods and for mutations for the separation of biological macromolecules
JOURNAL Patent: JP 2002529734-A 3 10-SEP-2002; CURAGEN CORP
COMMENT OS Bacteriophage M13mp18 PN JP 2002529734-A/3 PD 10-SEP-2002 PF 10-NOV-1999 JP 2000581443 PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI MARIE C RUIZ MARTINEZ PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415 PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26, PC C12N15/00 CC Methods and for mutations for the separation of biological macromolecules
FH Key Location/Qualifiers FT source 1..12 /organism='Bacteriophage M13mp18'. FT Location/Qualifiers 1..12 /organism='Bacteriophage M13mp18' /mol_type='genomic DNA' /db_xref='taxon:28360'
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 TCCACCTGCTGT 15
DB 1 TCCACCTGGTTT 12
RESULT 155
CQ766158 12 bp DNA linear PAT 03-MAR-2004
LOCUS Sequence 119 from Patent WO2004005547
DEFINITION

Unknown. Unclassified. REFERENCE 1 (bases 1 to 12) AUTHORS Miller,W.L., Lin,D. and Strauss,J.F. III. TITLE Identification of gene mutations associated with congenital lipoid adrenal hyperplasia JOURNAL Patent: US 5807678-A 30 15-SEP-1998; FEATURES Location/Qualifiers source 1..12 /organism='unknown' /mol_type='unassigned DNA'
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GACCTGGTAAT 29
DB 12 GACCTGGTGAT 1
RESULT 152
AR058492 12 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 69 from patent US 5837832.
DEFINITION
ACCESSION AR058492
VERSION AR058492.1 GI:5984069
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 69 17-NOV-1998; FEATURES Location/Qualifiers source 1..12 /organism='unknown' /mol_type='unassigned DNA'
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 TGTGTGCACCTGG 24
DB 1 TGTGTGTGCTGG 12
RESULT 153
BD064895 12 bp DNA linear PAT 27-AUG-2002
LOCUS Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA.
DEFINITION
ACCESSION BD064895
VERSION BD064895.1 GI:22610498
KEYWORDS JP 2001275678-A/107.
SOURCE synthetic construct synthetic construct other sequences; artificial sequences.
ORGANISM 1 (bases 1 to 12)
REFERENCE Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and Nishikawa,K.
AUTHORS Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA
TITLE
JOURNAL Patent: JP 2001275678-A 107 09-OCT-2001; SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT OS Artificial Sequence PN JP 2001275678-A/107 PD 09-OCT-2001 PF 31-MAR-2000 JP 2000096306 PI TOSHIOKI KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI

MIMAKI,REI FUKUSHIMA, PI KAZURO NISHIKAWA PC C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC Synthetic DNA FH Key Location/Qualifiers FT source 1..12 /organism='Artificial Sequence'. FT Location/Qualifiers 1..12 /organism='synthetic construct' /mol_type='genomic DNA' /db_xref='taxon:32630'
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 9 CTGCTGTGTGAC 20
DB 1 CTGCTGAGTCAC 12
RESULT 154
BD271980 LOCUS 12 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and for mutations for the separation of biological macromolecules.
ACCESSION BD271980
VERSION BD271980.1 GI:33081748
KEYWORDS JP 2002529734-A/3.
SOURCE Bacteriophage M13mp18
ORGANISM Bacteriophage M13mp18 Viruses.
REFERENCE 1 (bases 1 to 12)
AUTHORS Martinez,M.C.R.
TITLE Methods and for mutations for the separation of biological macromolecules
JOURNAL Patent: JP 2002529734-A 3 10-SEP-2002; CURAGEN CORP
COMMENT OS Bacteriophage M13mp18 PN JP 2002529734-A/3 PD 10-SEP-2002 PF 10-NOV-1999 JP 2000581443 PR 10-NOV-1998 US 60/107798,13-AUG-1999 US 09/374174 PI MARIE C RUIZ MARTINEZ PC G01N27/447,G01N27/447,B01D57/02,B03C5/00,C08K5/20,C08K5/21, PC C08K5/3415 PC C08L33/26,C12N15/09//C12Q1/68,G01N33/483,G01N27/26,G01N27/26, CC C12N15/00 CC Methods and for mutations for the separation of biological macromolecules
FH Key Location/Qualifiers FT source 1..12 /organism='Bacteriophage M13mp18'. FT Location/Qualifiers 1..12 /organism='Bacteriophage M13mp18' /mol_type='genomic DNA' /db_xref='taxon:28360'
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QY 4 TCCACCTGCTGT 15
DB 1 TCCACCTGGTTT 12
RESULT 155
CQ766158 LOCUS 12 bp DNA linear PAT 03-MAR-2004
DEFINITION Sequence 119 from Patent WO2004005547

Unknown. Unclassified. 1 (bases 1 to 12) Miller,W.L., Lin,D. and Strauss,J.F. III. Identification of gene mutations associated with congenital lipoid adrenal hyperplasia Patent: US 5807678-A 30 15-SEP-1998; Location/Qualifiers OS Artificial Sequence PN JP 2001275678-A/107 PD 09-OCT-2001 PF 31-MAR-2000 JP 2000096306 PI TOSHIOKI KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GACCTGGTAAT 29
DB 12 GACCTGGTGAT 1
RESULT 152
AR058492 LOCUS 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 69 from patent US 5837832.
ACCESSION AR058492
VERSION AR058492.1 GI:5984069
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 69 17-NOV-1998; Location/Qualifiers 1..12 /organism='unknown' /mol_type='unassigned DNA'
Query Match 30.3%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 1.5e+02; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 13 TGTGTGCACCTGG 24
DB 1 TGTGTGTGCTGG 12
RESULT 153
BD064895 LOCUS 12 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA.
ACCESSION BD064895
VERSION BD064895.1 GI:22610498
KEYWORDS JP 2001275678-A/107.
SOURCE synthetic construct synthetic construct other sequences; artificial sequences.
ORGANISM 1 (bases 1 to 12)
REFERENCE Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and Nishikawa,K.
AUTHORS Method for detecting the extent of binding of transcriptional regulatory protein to oligoDNA
TITLE Patent: JP 2001275678-A 107 09-OCT-2001; SUMITOMO ELECTRIC INDUSTRIES LTD
JOURNAL OS Artificial Sequence PN JP 2001275678-A/107 PD 09-OCT-2001 PF 31-MAR-2000 JP 2000096306 PI TOSHIOKI KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI

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ACCESSION CQ766158
VERSION CQ766158.1 GI:44908418
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Weinzierl,R.
TITLE Patent: WO 2004005547-A 119 15-JAN-2004;
JOURNAL IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
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Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCATCCACCTGC 12
Db 1 CCACCATCTGC 12
RESULT 156
123750/c
LOCUS I23750 12 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 15 from patent US 5538844.
ACCESSION I23750
VERSION I23750.1 GI:1603620
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Duyao,M.P., Macdonald,M.E. and Gusella,J.F.
TITLE Transport protein gene from the Huntington's disease region
JOURNAL Patent: US 5538844-A 15 23-JUL-1996;
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Query Match 30.3%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
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Qy 3 ATCCACCTGCTG 14
Db 12 ACCCACCTACTG 1
RESULT 157
I73177
LOCUS I73177 12 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 29 from patent US 5686240.
ACCESSION I73177
VERSION I73177.1 GI:3009316
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Schuchman,E.H. and Desnick,R.J.
TITLE Acid sphingomyelinase gene and diagnosis of Niemann-Pick disease
JOURNAL Patent: US 5686240-A 29 11-NOV-1997;
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Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12
RESULT 158
AR302271
LOCUS AR302271 12 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 9 from patent US 6541218.
ACCESSION AR302271
VERSION AR302271.1 GI:31690510
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Schuchman,E.H. and Desnick,R.J.
TITLE Acid sphingomyelinase protein and methods of treating type B
Niemann-Pick disease
JOURNAL Patent: US 6541218-A 9 01-APR-2003;
The Mount Sinai School of Medicine of the city University of New
York; New York, NY
FEATURES
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Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 12 CTGTGTGACCTG 23
Db 1 CTGTGCCACCTG 12
RESULT 159
AR308098
LOCUS AR308098 12 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6554985.
ACCESSION AR308098
VERSION AR308098.1 GI:31699106
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Ruiz-Martinez,M.C., Berka,J. and Simpson,J.W.
TITLE Methods and formulations for the separation of biological
macromolecules
JOURNAL Patent: US 6554985-A 3 29-APR-2003;
CuraGen Corporation; New Haven, CT
FEATURES
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Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCCACCTGCTGT 15
Db 1 TCCACCTGGTTT 12
RESULT 160
S55766
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LOCUS	S55766	12 bp	DNA	linear	PRI 04-MAY-2000			
DEFINITION	Homo sapiens acid sphingomyelinase gene, partial cds.							
ACCESSION	S55766							
VERSION	S55766.1	GI:234719						
KEYWORDS								
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	1 (bases 1 to 12) Levan, O., Desnick, R.J. and Schuchman, E.H.							
TITLE	Niemann-pick type B disease. Identification of a single codon deletion in the acid sphingomyelinase gene and genotype/phenotype correlations in type A and B patients							
JOURNAL	J. Clin. Invest. 88 (3), 806-810 (1991)							
PUBMED	1985770							
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 55766] from the original journal article.							
COMMENT	3 bp deletion.							
FEATURES	Location/Qualifiers							
source	1..12							
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	<1..>12							
	/note="lysosomal hydrolase"							
	/codon_start=1							
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	/db_xref="GI:234720"							
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Best Local Similarity	83.3%; Pred. No. 1.5e+02;							
Matches 10; Conservative	0; Mismatches 2; Indels 0; Gaps 0;							
QY	12 CTGTGTCACCTG 23							
Db	1 CTGTGCCACCTG 12							
RESULT 161								
S73118S2								
LOCUS	S73118S2	12 bp	DNA	linear	PRI 07-MAY-1993			
DEFINITION	dystrophin [intragenic deletion] (human, Genomic Mutant, 12 nt, segment 2 of 2).							
ACCESSION	S73119							
VERSION	S73119.1	GI:241101						
KEYWORDS								
SEGMENT	2 of 2							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE	1 (bases 1 to 12) Love,D.R., Flint,T.J., Genet,S.A., Middleton-Price,H.R. and Davies,K.E.							
AUTHORS	Becker muscular dystrophy patient with a large intragenic dystrophin deletion: implications for functional minigenes and gene therapy							
TITLE	J. Med. Genet. 28 (12), 860-864 (1991)							
JOURNAL	1757963							
PUBMED	GenBank							
REMARK	entry [NCBI gibbsq 73119] from the original journal article.							
FEATURES	Location/Qualifiers							
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	/db_xref="taxon:9606"							


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PD 27-NOV-2001
PF 22-MAY-2000 JP 2000150562
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI,SHIGENORI PI
NAGAI
PC C12N15/09,C07K14/47,C07K16/18//C12P21/02,C12P21/08,C12N15/00
CC
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FEATURES
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Best Local Similarity 29.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 13 TGTGTGACCT 22
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Db 1 TGTGTGAGCT 10

RESULT 168
BD167115/c
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD167115
VERSION BD167115.1 GI:27872927
KEYWORDS JP 2002209591-A/660.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 660 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/660
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
PC C12P21/08,
PC C12N15/00,
PC Human liver disease-expressing genes
CC Human liver Location/Qualifiers
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Db 10 CTTGCTGTGT 1

RESULT 169
BD195102
LOCUS
DEFINITION Screening methods for compounds useful in the regulation of body
weight.
ACCESSION BD195102
VERSION BD195102.1 GI:33004861
KEYWORDS JP 2002514041-A/5.

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
1 (bases 1 to 10)
AUTHORS Lee,F., Huszar,D. and Gu,W.
TITLE Screening methods for compounds useful in the regulation of body
JOURNAL Patent: JP 2002514041-A 5 14-MAY-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2002514041-A/5
PD 14-MAY-2002
PF 09-JUN-1997 JP 1998501745
PR 10-JUN-1996 US 08/662560,08-JAN-1997 US 08/780749 PR
O6-JUN-1997 US 08/870511
PI FRANK LEE, DENNIS HUSZAR, WEI GU
PC A61K38/16, A61K39/395, A61K48/00, C07H21/04, C12N15/11, C12Q1/68,
PC G01N33/53,
PC C12Q1/25, C12Q1/66, C12Q1/68
CC Description of artificial sequence: primer
FH Key Location/Qualifiers
FT source 1..10
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Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 10;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACTGTC 12
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Db 1 ATCCACTGTC 10

RESULT 170
BD238856/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238856
VERSION BD238856.1 GI:33048626
KEYWORDS JP 2002534056-A/274.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 274 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/274
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
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08-DEC-1998 US 60/111715

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PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
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FEATURES
source
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Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGCTGTGT 17
Db 10 CTTGCTGTGT 1

RESULT 171
LOCUS BD239707 10 bp DNA linear PAT 17-JUL-2003
DEFINITION BD239707 Preparation and use of superior vaccines.
ACCESSION BD239707
VERSION BD239707.1 GI:33049477
KEYWORDS JP 2002534056-A/1125.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
PATENT: JP 2002534056-A 1125 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1125
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Db 1 CTGCTATGTG 10
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Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGTC 12
Db 1 ATCCGCTGTC 10

RESULT 172
LOCUS BD240160 10 bp DNA linear PAT 17-JUL-2003
DEFINITION BD240160 Preparation and use of superior vaccines.
ACCESSION BD240160
VERSION BD240160.1 GI:33049930
KEYWORDS JP 2002534056-A/1578.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
PATENT: JP 2002534056-A 1578 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/1578
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
/organism='Homo sapiens (human)'.

FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 1 CTGCTATGTG 10
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RESULT 173
E06867
LOCUS       E06867               10 bp    RNA        linear    PAT 29-SEP-1997
DEFINITION   Substrate of ribozyme.
ACCESSION   E06867
VERSION     E06867.1  GI:5708532
KEYWORDS    JP 1994070774-A/15.
SOURCE      synthetic construct
ORGANISM    other sequences: artificial sequences.
            1 (bases 1 to 10)
REFERENCE    Otsuka,E. and Koizumi,M.
AUTHORS     RIBOZYME HAVING THERMODYNAMICALLY STABLE LOOP STRUCTURE
TITLE       Patent: JP 1994070774-A 15 15-MAR-1994;
JOURNAL     SANKYO CO LTD
COMMENT     OS Artificial gene
            OC Artificial sequence; Genes.
            PN JP 1994070774-A/15
            PD 15-MAR-1994
            PF 01-JUL-1993 JP 1993163530
            PR 02-JUL-1992 JP 92P 175706
            PI OTSUKA EIKO, KOIZUMI MAKOTO
            PC C12N15/11,C12N1/21,C12N9/00,C12N15/10,(C12N1/21,C12R1:19); CC
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: No;
            FH Key
            FH Key
            FT misc_feature 1..10
            FT Location/Qualifiers
            FT 1..10
            FT /note="Substrate of ribozyme".
            FT /organism="synthetic construct"
            FT /mol_type="genomic RNA"
            FT /db_xref="taxon:32630"

Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGTGTGTGTA 19
Db 1 TGTGTGTGTA 10

RESULT 174
E39535/c
LOCUS       E39535               10 bp    DNA        linear    PAT 31-JAN-2002
DEFINITION   Genes with human dendritic cell expression.
ACCESSION   E39535
VERSION     E39535.1  GI:18621626
KEYWORDS    JP 2000279181-A/68.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 10)
REFERENCE    Hashimoto,S., Matsushima,K. and Suzuki,T.
AUTHORS     Genes with human dendritic cell expression
TITLE       Patent: JP 2000279181-A 68 10-OCT-2000;
JOURNAL     SCIENCE & TECH AGENCY
COMMENT     OS Homo sapiens (human)
            PN JP 2000279181-A/68
            PD 10-OCT-2000
            PF 01-APR-1999 JP 1999095481
            PR SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
            C12N15/09,C07K14/475,C07K16/18,C12N15/00
            CC

Query Match          29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGTGTGTGTA 19
Db 1 TGTGTGTGTA 10

RESULT 176
E54734/c
LOCUS       E54734               10 bp    DNA        linear    PAT 27-AUG-2002
DEFINITION   Human normal liver cell expression genes.
ACCESSION   E54734
VERSION     E54734.1  GI:22556217
KEYWORDS    JP 2001211883-A/86.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
            1 (bases 1 to 10)
REFERENCE    1 (bases 1 to 10)

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AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 86 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/86
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CCTGCTGTGT 17
Db 10 CTTGCTGTGT 1
RESULT 177
I43001
LOCUS I43001 10 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 23 from patent US 5631115.
ACCESSION I43001
VERSION I43001.1 GI:2468245
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ohtsuka,E. and Koizumi,M.
TITLE Looped, hairpin ribozyme
JOURNAL Patent: US 5631115-A 23 20-MAY-1997;
FEATURES
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 10 TGCTGTGTGA 19
Db 1 TGTGTGTGA 10
RESULT 178
AR303393/c
LOCUS AR303393 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 118 from patent US 6544736.
ACCESSION AR303393
VERSION AR303393.1 GI:31692169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 118 08-APR-2003;
Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo;
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 86 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/86
PD 07-AUG-2001
PF 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09,C07K16/18,C12P21/02,C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 8 CCTGCTGTGT 17
Db 10 CTTGCTGTGT 1
RESULT 179
AR306856
LOCUS AR306856 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 8 from patent US 6551476.
ACCESSION AR306856
VERSION AR306856.1 GI:31697256
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Scherba,E.S.
TITLE Noble-metal coated inert anode for aluminum production
JOURNAL Patent: US 6551476-A 8 22-APR-2003;
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CATCCACCTG 11
Db 1 CATCCCCCTG 10
RESULT 180
AR490725/c
LOCUS AR490725 10 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 130 from patent US 6713277.
ACCESSION AR490725
VERSION AR490725.1 GI:47258124
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Moore,K. and Nagle,D.L.
TITLE Methods and composition for the diagnosis and treatment of body weight disorders, including obesity
JOURNAL Patent: US 6713277-A 130 30-MAR-2004;
Millennium Pharmaceuticals, Inc.; Cambridge, MA
FEATURES
source 1..10
/organism="unknown"
/mol_type="genomic DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 12 CTGTGTGACC 21
Db 10 CTGTGTGTCC 1

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RESULT 181
AR532498/c
LOCUS AR532498 10 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 129 from patent US 6727348.
ACCESSION AR532498
VERSION AR532498.1 GI:53921716
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS Moore,K. and Nagle,D.L.
TITLE Compositions and methods for the diagnosis and treatment of body
weight disorders, including obesity
JOURNAL Patent: US 6727348-A 129 27-APR-2004;
Millennium Pharmaceuticals, Inc.; Cambridge, MA
FEATURES
source 1..10
Location/Qualifiers
/mol_type="genomic DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CTGTGTGACC 21
Db 10 CTGTGTGTCC 1
RESULT 182
AX018751/c
LOCUS AX018751 10 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 9 from Patent WO9943848.
ACCESSION AX018751
VERSION AX018751.1 GI:10042874
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Ong,C.J. and Jirik,F.R.
TITLE Protein interaction and transcription factor trap
JOURNAL Patent: WO 9943848-A 9 02-SEP-1999;
ONG CHRISTOPHER J (CA); UNIV BRITISH COLUMBIA (CA); JIRIK FRANK R
(CA)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligomer containing a splice acceptor sequence"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 15 TGTGACCTGG 24
Db 10 TGCACCTGG 1
RESULT 183
AX112967
LOCUS AX112967 10 bp DNA linear PAT 01-MAY-2001
DEFINITION Sequence 14 from Patent WO0127267.
ACCESSION AX112967
VERSION AX112967.1 GI:13939402
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

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Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Adams,E., Waldmann,H., Cobbold,S. and Zelenika,D.
TITLE Genes differentially expressed in tr1 cells and their use in the
manufacture of immunoregulatory compositions
JOURNAL Patent: WO 0127267-A 14 19-APR-2001;
ISIS INNOVATION LIMITED (GB)
FEATURES
source Location/Qualifiers
1..10
/organism="Mus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10095"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 9 CTGCTGTGTG 18
Db 1 CTGCTTTGTG 10
RESULT 184
AX152117
LOCUS AX152117 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 32 from Patent WO0138577.
ACCESSION AX152117
VERSION AX152117.1 GI:14533768
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 32 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CTGTGTGACC 21
Db 1 CTGTGTGCCC 10
RESULT 185
AX152126
LOCUS AX152126 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 41 from Patent WO0138577.
ACCESSION AX152126
VERSION AX152126.1 GI:14533777
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 41 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source Location/Qualifiers
1..10

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACC 21
|||||
Db 1 CTGTGTGCC 10

RESULT 186
AX152191
LOCUS AX152191 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 106 from Patent WO0138577.
ACCESSION AX152191
VERSION AX152191.1 GI:14533842
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 106 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CTGTGTGACC 21
|||||
Db 1 CTGTGTGCC 10

RESULT 187
AX152676
LOCUS AX152676 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 591 from Patent WO0138577.
ACCESSION AX152676
VERSION AX152676.1 GI:14534327
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 591 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
|||||
Db 1 CTGCTGTGTG 10

RESULT 189
AR051278
LOCUS AR051278 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5830661.
ACCESSION AR051278
VERSION AR051278.1 GI:5974642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sarfarazi,M.
TITLE Diagnosis and treatment of glaucoma
JOURNAL Patent: US 5830661-A 15 03-NOV-1998;
FEATURES
source
1..11
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGTGATAA 28
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Db 1 ACCTGTGATAA 28
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1 CTGCTGAGTG 10

RESULT 188
BD007884
LOCUS BD007884 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007884
VERSION BD007884.1 GI:18636257
KEYWORDS JP 2001069993-A/160.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 160 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/160
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source
1..10
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
|||||
Db 1 CTGCTGTGTG 10

RESULT 189
AR051278
LOCUS AR051278 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5830661.
ACCESSION AR051278
VERSION AR051278.1 GI:5974642
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sarfarazi,M.
TITLE Diagnosis and treatment of glaucoma
JOURNAL Patent: US 5830661-A 15 03-NOV-1998;
FEATURES
source
1..11
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGTGATAA 28
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Db          ||| ||| ||| |||
1 ACCAGGTAAA 10

RESULT 190
AR074507/c
LOCUS      AR074507          11 bp      DNA      linear      PAT 28-AUG-2000
DEFINITION Sequence 86 from patent US 5955075.
ACCESSION  AR074507
VERSION     AR074507.1 GI:10001262
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL     Patent: US 5955075-A 86 21-SEP-1999;
FEATURES
source
Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
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Db      10 CCTTCTGTGT 1

RESULT 191
AR077230
LOCUS      AR077230          11 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 15 from patent US 5962230.
ACCESSION  AR077230
VERSION     AR077230.1 GI:10003976
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Sarfarazi,M.
TITLE       Diagnosis and treatment of glaucoma
JOURNAL     Patent: US 5962230-A 15 05-OCT-1999;
FEATURES
source
Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| ||| ||| |||
Db      10 CCTTCTGTGT 1

RESULT 192
AR081187/c
LOCUS      AR081187          11 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 86 from patent US 5972353.
ACCESSION  AR081187
VERSION     AR081187.1 GI:10007915
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN proteins, polypeptides, fusion proteins and fusion polypeptides

JOURNAL     Patent: US 5972353-A 86 26-OCT-1999;
FEATURES
source
Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      19 ACCTGGTAAA 28
      ||| ||| ||| |||
Db      1 ACCAGGTAAA 10

RESULT 193
AR085384/c
LOCUS      AR085384          11 bp      DNA      linear      PAT 01-SEP-2000
DEFINITION Sequence 86 from patent US 5981711.
ACCESSION  AR085384
VERSION     AR085384.1 GI:10012153
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN-specific antibodies and hybridomas
JOURNAL     Patent: US 5981711-A 86 09-NOV-1999;
FEATURES
source
Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| ||| ||| |||
Db      10 CCTTCTGTGT 1

RESULT 194
AR088132/c
LOCUS      AR088132          11 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 86 from patent US 5989838.
ACCESSION  AR088132
VERSION     AR088132.1 GI:10014895
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL     Patent: US 5989838-A 86 23-NOV-1999;
FEATURES
source
Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 CCTGCTGTGT 17
      ||| ||| ||| |||
Db      10 CCTTCTGTGT 1

RESULT 195
AR104291/c
LOCUS      AR104291          11 bp      DNA      linear      PAT 07-SEP-2000
DEFINITION Sequence 86 from patent US 5989838.
ACCESSION  AR104291
VERSION     AR104291.1 GI:10014895
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN proteins, polypeptides, fusion proteins and fusion polypeptides
```

LOCUS AR104291 11 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6093548.
ACCESSION AR104291
VERSION AR104291.1 GI:12816999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 86 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
| | | | |
Db 10 CCTTCTGTGT 1

RESULT 196
LOCUS AR143553/c
DEFINITION Sequence 86 from patent US 6204370.
ACCESSION AR143553
VERSION AR143553.1 GI:15104839
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 86 20-MAR-2001;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
| | | | |
Db 10 CCTTCTGTGT 1

RESULT 197
LOCUS AR171459/c
DEFINITION Sequence 86 from patent US 6297041.
ACCESSION AR171459
VERSION AR171459.1 GI:17910409
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 86 02-OCT-2001;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
| | | | |
Db 10 CCTTCTGTGT 1

RESULT 198
LOCUS AR171630
DEFINITION Sequence 86 from patent US 6297051.
ACCESSION AR171630
VERSION AR171630.1 GI:17910580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297051-A 86 02-OCT-2001;
FEATURES Location/Qualifiers
source 1..11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CCTGCTGTGT 17
| | | | |
Db 10 CCTTCTGTGT 1

RESULT 199
LOCUS BD057177
DEFINITION Diagnosis and treatment of glaucoma.
ACCESSION BD057177
VERSION BD057177.1 GI:22602783
KEYWORDS JP 2001512969-A/15.
SOURCE Synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 11)
AUTHORS Sarfarazi,M.
TITLE Diagnosis and treatment of glaucoma
JOURNAL Patent: JP 2001512969-A 15 28-AUG-2001;
COMMENT THE UNIVERSITY OF CONNECTICUT
PN JP 2001512969-A/15
PD 28-AUG-2001
PF 12-FEB-1998 JP 1998535963
PR 13-FEB-1997 US 08/800036,10-SEP-1997 US 08/926492 PI
MANSOOR SARFARAZI
PC C12Q1/68,G01N33/50
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES Location/Qualifiers
source 1..11
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 19 ACCTGGTAAA 28
| | | | |


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JOURNAL Patent: WO 2004059002-A 727 15-JUL-2004;
FEATURES Henkel Kommanditgesellschaft auf Aktien (DE)
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
Db 1 ACCCAGCTGC 10

RESULT 208
CQ835321
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 379 from Patent WO2004059001.
ACCESSION CQ835321
VERSION CQ835321.1 GI:50834955
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 379 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GTGTGACCTG 23
Db 2 GTGAGACCTG 11

RESULT 209
CQ835588/c
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 646 from Patent WO2004059001.
ACCESSION CQ835588
VERSION CQ835588.1 GI:50835122
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 646 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db 11 CCTCCTGTGT 2

RESULT 210
CQ835701
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 759 from Patent WO2004059001.
ACCESSION CQ835701
VERSION CQ835701.1 GI:50835235
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 759 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATCCACCTG 11
Db 1 CATCCATCTG 10

RESULT 211
CQ836236
LOCUS 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1294 from Patent WO2004059001.
ACCESSION CQ836236
VERSION CQ836236.1 GI:50835770
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1294 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
Db 3 ATCCACCTGC 12

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Db      1 ATCACCCGC 10

RESULT 212
LOCUS   CQ836553/c
DEFINITION
Sequence 1611 from Patent WO2004059001.
ACCESSION
CQ836553
VERSION  CQ836553.1 GI:50836087
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
  Conradt,M. and Hofmann,K.
  Method for determining markers of human facial skin
  Patent: WO 2004059001-A 1611 15-JUL-2004;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTGCTGTGTG 18
Db      10 CTGCTTTGTG 1

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9 CTGCTGTGTG 18
Db      10 CTGCTTTGTG 1

RESULT 213
LOCUS   CQ836684
DEFINITION
Sequence 1742 from Patent WO2004059001.
ACCESSION
CQ836684
VERSION  CQ836684.1 GI:50836218
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
  Conradt,M. and Hofmann,K.
  Method for determining markers of human facial skin
  Patent: WO 2004059001-A 1742 15-JUL-2004;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 CACCTGTGCT 15
Db      2 CACTTGTGCT 11

RESULT 214
LOCUS   CQ836692/c
DEFINITION
Sequence 1750 from Patent WO2004059001.

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ACCESSION CQ836692
VERSION   CQ836692.1 GI:50836226
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
  Conradt,M. and Hofmann,K.
  Method for determining markers of human facial skin
  Patent: WO 2004059001-A 1750 15-JUL-2004;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 TCCACCTGCT 13
Db      11 TCCACCTTCT 2

RESULT 215
LOCUS   CQ836910
DEFINITION
Sequence 1968 from Patent WO2004059001.
ACCESSION
CQ836910
VERSION  CQ836910.1 GI:50836444
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
  Conradt,M. and Hofmann,K.
  Method for determining markers of human facial skin
  Patent: WO 2004059001-A 1968 15-JUL-2004;
  Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 TCCACCTGCT 13
Db      2 TCCACCTGCT 11

RESULT 216
LOCUS   CQ837506/c
DEFINITION
Sequence 2564 from Patent WO2004059001.
ACCESSION
CQ837506
VERSION  CQ837506.1 GI:50837040
KEYWORDS
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2564 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 TCCACCTGCT 13
           |||||
Db          11 TCCACCTGCT 2

RESULT 217
CQ837969/c
LOCUS       CQ837969
DEFINITION Sequence 3027 from Patent WO2004059001.
ACCESSION  CQ837969
VERSION     CQ837969.1 GI:50837503
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3027 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 TCCACCTGCT 13
           |||||
Db          11 TCCACCTGCT 2

RESULT 218
CQ837969/c
LOCUS       CQ837969
DEFINITION Sequence 3027 from Patent WO2004059001.
ACCESSION  CQ837969
VERSION     CQ837969.1 GI:50837503
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3027 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 TCCACCTGCT 13
           |||||
Db          11 TCCACCTGCT 2

RESULT 219
CQ837969/c
LOCUS       CQ837969
DEFINITION Sequence 3027 from Patent WO2004059001.
ACCESSION  CQ837969
VERSION     CQ837969.1 GI:50837503
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 3027 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 TCCACCTGCT 13
           |||||
Db          11 TCCACCTGCT 2

RESULT 220
CS058596
LOCUS       CS058596
DEFINITION Sequence 493 from Patent WO2005028671.
ACCESSION  CS058596
VERSION     CS058596.1 GI:62551779
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS      Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
              Kessler-Becker,D.
TITLE        Method for determining hair cycle markers
JOURNAL      Patent: WO 2005028671-A 493 31-MAR-2005;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;

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FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Location/Qualifiers
              29.0%; Score 8.4; DB 1; Length 11;
              Best Local Similarity 90.0%; Pred. No. 1.7e+02;
              Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          3 ATCCACCTGC 12
           |||||
Db          1 ATCCACCTGC 10

RESULT 219
CS058234/c
LOCUS       CS058234
DEFINITION Sequence 131 from Patent WO2005028671.
ACCESSION  CS058234
VERSION     CS058234.1 GI:62551417
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS      Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
              Kessler-Becker,D.
TITLE        Method for determining hair cycle markers
JOURNAL      Patent: WO 2005028671-A 131 31-MAR-2005;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          4 TCCACCTGCT 13
           |||||
Db          11 TCCACCTGCT 2

RESULT 220
CS058596
LOCUS       CS058596
DEFINITION Sequence 493 from Patent WO2005028671.
ACCESSION  CS058596
VERSION     CS058596.1 GI:62551779
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE
AUTHORS      Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
              Kessler-Becker,D.
TITLE        Method for determining hair cycle markers
JOURNAL      Patent: WO 2005028671-A 493 31-MAR-2005;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;

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Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 2 CACTTGCTGT 11

RESULT 221
AR301532
LOCUS AR301532 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 113 from patent US 6538173.
ACCESSION AR301532
VERSION AR301532.1 GI:316899334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 113 25-MAR-2003;
The Wistar Institute; Philadelphia, PA;
WOX;
FEATURES
source
Location/Qualifiers
1..11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 1 CTGCTTTGTG 10

RESULT 222
AR301704
LOCUS AR301704 11 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 285 from patent US 6538173.
ACCESSION AR301704
VERSION AR301704.1 GI:31689506
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Heber-Katz,E.
TITLE Compositions and methods for wound healing
JOURNAL Patent: US 6538173-A 285 25-MAR-2003;
The Wistar Institute; Philadelphia, PA;
WOX;
FEATURES
source
Location/Qualifiers
1..11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CTGCTGTGTG 18
Db 1 CTGCTTTGTG 10

RESULT 223
AR569658
LOCUS AR569658 11 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 86 from patent US 6770438.
ACCESSION AR569658
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VERSION AR569658.1 GI:56570287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6770438-A 86 03-AUG-2004;
Institute of Virology, Slovak Academy of Sciences; Bratislava;
CZX;
FEATURES
source
Location/Qualifiers
1..11
/organism="unknown"
/mol_type="genomic DNA"
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 CTGCTGTGTG 17
Db 10 CCTTCTGTGT 1

RESULT 224
AX085766
LOCUS AX085766 11 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 28 from Patent WO0112858.
ACCESSION AX085766
VERSION AX085766.1 GI:13275716
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS He,T.C., Kinzler,K.W. and Vogelstein,B.
TITLE ppar_g(d) links apc to chemopreventive drugs
JOURNAL Patent: WO 0112858-A 28 22-FEB-2001;
The Johns Hopkins University (US)
FEATURES
source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAAT 29
Db 1 CCTGGTCAAT 10

RESULT 225
AX470852
LOCUS AX470852 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 429 from Patent WO02053773.
ACCESSION AX470852
VERSION AX470852.1 GI:22205977
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conrad,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 429 11-JUL-2002;
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LOCUS AX471608 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1185 from Patent WO02053773.
ACCESSION AX471608
VERSION AX471608.1 GI:22206733
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1185 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCACCTGCT 13
Db 2 TCACGCTGCT 11

RESULT 231
AX623509/c
LOCUS AX623509 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 550 from Patent WO02053774.
ACCESSION AX623509
VERSION AX623509.1 GI:28451450
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 550 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCACCTGCT 13
Db 11 TCACCTCCT 2

RESULT 232
AX623560/c
LOCUS AX623560 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 601 from Patent WO02053774.
ACCESSION AX623560
VERSION AX623560.1 GI:28451501
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 601 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCACCTGCT 13
Db 11 TCACCTCCT 2

RESULT 233
AX624060
LOCUS AX624060 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1101 from Patent WO02053774.
ACCESSION AX624060
VERSION AX624060.1 GI:28452001
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1101 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db 11 CCTCTGTGT 2

RESULT 234
AX624161/c
LOCUS AX624161 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1202 from Patent WO02053774.
ACCESSION AX624161
VERSION AX624161.1 GI:28452102
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1202 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 601 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CCTGCTGTGT 17
Db 11 CCTCTGTGT 2

RESULT 233
AX624060
LOCUS AX624060 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1101 from Patent WO02053774.
ACCESSION AX624060
VERSION AX624060.1 GI:28452001
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1101 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

Query Match
Best Local Similarity 29.0%; Score 8.4; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATCCACCTGC 12
Db 1 ATCCGCTGC 10

RESULT 234
AX624161/c
LOCUS AX624161 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1202 from Patent WO02053774.
ACCESSION AX624161
VERSION AX624161.1 GI:28452102
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1202 11-JUL-2002;
HENKEL Kommanditgesellschaft auf Aktien (DE)
FEATURES             Location/Qualifiers
     source          1..11
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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KEYWORDS      Homo sapiens (human)
SOURCE
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 4224 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source        1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy           9 CTCTGTGTG 18
              |||||||
Db           1 CTTCTGTGTG 10

RESULT 240
AX627753
LOCUS         AX627753      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION   Sequence 4794 from Patent WO02053774.
ACCESSION    AX627753
VERSION      AX627753.1 GI:28455791
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 4794 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source        1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy           3 ATCCACCTGC 12
              |||||||
Db           1 ATCCACCCGC 10

RESULT 241
AX627875/c
LOCUS         AX627875      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION   Sequence 4916 from Patent WO02053774.
ACCESSION    AX627875
VERSION      AX627875.1 GI:28455913
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 4916 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source        1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy           3 ATCCACCTGC 12
              |||||||
Db           1 ATCCACCCGC 10

RESULT 242
AX627970
LOCUS         AX627970      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION   Sequence 5011 from Patent WO02053774.
ACCESSION    AX627970
VERSION      AX627970.1 GI:28456008
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 5011 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source        1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy           4 TCCACCTGCT 13
              |||||||
Db           11 TCCACCTGCT 2

RESULT 243
AX628145/c
LOCUS         AX628145      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION   Sequence 5186 from Patent WO02053774.
ACCESSION    AX628145
VERSION      AX628145.1 GI:28456183
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 5186 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source        1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match   29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy           3 ATCCACCTGC 12
              |||||||
Db           1 ACCCACCTGC 10

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6340 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4  TCCACCTGCT 13
    |||||
Db   11 TCCAGCTGCT 2

RESULT 249
AX629728
LOCUS      AX629728 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6769 from Patent WO02053774.
ACCESSION  AX629728
VERSION     AX629728.1 GI:28457766
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6769 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  13 TGTGTGACCT 22
    |||||
Db   1  TCTGTGACCT 10

RESULT 250
AX629959
LOCUS      AX629959 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7000 from Patent WO02053774.
ACCESSION  AX629959
VERSION     AX629959.1 GI:28457997
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7000 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6340 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  10 TGCTGTGTGA 19
    |||||
Db   2  TGCTGCGTGA 11

RESULT 251
AX630263/c
LOCUS      AX630263 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7304 from Patent WO02053774.
ACCESSION  AX630263
VERSION     AX630263.1 GI:28458301
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7304 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  ATCCACCTGC 12
    |||||
Db   10 AACCACTGC 1

RESULT 252
AX630930/c
LOCUS      AX630930 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7971 from Patent WO02053774.
ACCESSION  AX630930
VERSION     AX630930.1 GI:28458972
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7971 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4  TCCACCTGCT 13
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Db   4  TCCACCTGCT 13
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6340 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  10 TGCTGTGTGA 19
    |||||
Db   2  TGCTGCGTGA 11

RESULT 251
AX630263/c
LOCUS      AX630263 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7304 from Patent WO02053774.
ACCESSION  AX630263
VERSION     AX630263.1 GI:28458301
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7304 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
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Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  3  ATCCACCTGC 12
    |||||
Db   10 AACCACTGC 1

RESULT 252
AX630930/c
LOCUS      AX630930 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7971 from Patent WO02053774.
ACCESSION  AX630930
VERSION     AX630930.1 GI:28458972
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 7971 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source       1. .11
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches      9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  4  TCCACCTGCT 13
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Db   4  TCCACCTGCT 13
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Db      11  TCCACCTCT 2
|||||
RESULT 253
AX630981/c      11 bp  DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION      Sequence 8022 from Patent WO02053774.
ACCESSION      AX630981
VERSION        AX630981.1  GI:28459023
KEYWORDS
SOURCE
ORGANISM        Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 8022 11-JUL-2002;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  CCTGCTGTGT 17
        |||||
Db      11  CCTCCTGTGT 2

RESULT 254
AX631481
LOCUS
DEFINITION      Sequence 8523 from Patent WO02053774.
ACCESSION      AX631481
VERSION        AX631481.1  GI:28459547
KEYWORDS
SOURCE
ORGANISM        Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 8523 11-JUL-2002;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ATCCACTGTC 12
        |||||
Db      1  ATCCGCCTGC 10

RESULT 255
AX631582/c      11 bp  DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION      Sequence 8624 from Patent WO02053774.
ACCESSION      AX631582
VERSION
KEYWORDS
SOURCE
ORGANISM
                Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE
AUTHORS        Pandolfi,P., Alcalay,M., Fagioli,M., Zangrilli,D., Mencarelli,A.,
                HSPMLEX43
                H.sapiens pml gene, exon 4.
                LOCUS
                DEFINITION
                ACCESSION      X63632
                VERSION      X63632.1  GI:35538
                KEYWORDS      PML gene; PML protein.
                SOURCE        Homo sapiens (human)
                ORGANISM
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
                REFERENCE
                1 (bases 1 to 11)
                AUTHORS
                Pandolfi,P., Alcalay,M., Fagioli,M., Zangrilli,D., Mencarelli,A.,

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VERSION
KEYWORDS
SOURCE
ORGANISM        Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 8624 11-JUL-2002;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  CCTGCTGTGT 17
        |||||
Db      10  CTTGCTGTGT 1

RESULT 256
AX632409/c      11 bp  DNA      linear      PAT 21-FEB-2003
LOCUS
DEFINITION      Sequence 9451 from Patent WO02053774.
ACCESSION      AX632409
VERSION        AX632409.1  GI:28468024
KEYWORDS
SOURCE
ORGANISM        Homo sapiens (human)
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
REFERENCE
AUTHORS        Petersohn,D., Conradt,M. and Hofmann,K.
TITLE          Method for determining homeostasis of the skin
JOURNAL        Patent: WO 02053774-A 9451 11-JUL-2002;
                Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      29.0%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches          9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ATCCACTGTC 12
        |||||
Db      10  ATCCCACTGC 1

RESULT 257
HSPMLEX43
LOCUS
DEFINITION      H.sapiens pml gene, exon 4.
ACCESSION      X63632
VERSION      X63632.1  GI:35538
KEYWORDS      PML gene; PML protein.
SOURCE        Homo sapiens (human)
ORGANISM
                Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homnidae; Homo.
                REFERENCE
                1 (bases 1 to 11)
                AUTHORS
                Pandolfi,P., Alcalay,M., Fagioli,M., Zangrilli,D., Mencarelli,A.,

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/db xref="taxon:10090"
/note="V$MYOD 01"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  3 ATCCACCTGC 12
    |||||
Db  12 AGCCACCTGC 3

RESULT 265
LOCUS      CQ828760/c
DEFINITION Sequence 478 from Patent WO2004053120.
ACCESSION  CQ828760
VERSION     CQ828760.1 GI:49732243
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus
REFERENCE  1
AUTHORS    Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE      Regulatory elements in the 5' region of the vrl gene
JOURNAL    Gruenthal GmbH (DE)
FEATURES   Location/Qualifiers
            source
              1..12
                /organism="Mus musculus"
                /mol_type="unassigned DNA"
                /db_xref="taxon:10090"
                /note="V$LMO2COM 01"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  3 ATCCACCTGC 12
    |||||
Db  12 AGCCACCTGC 3

RESULT 266
LOCUS      CQ828918/c
DEFINITION Sequence 636 from Patent WO2004053120.
ACCESSION  CQ828918
VERSION     CQ828918.1 GI:49732401
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE      Regulatory elements in the 5' region of the vrl gene
JOURNAL    Gruenthal GmbH (DE)
FEATURES   Location/Qualifiers
            source
              1..12
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
                /note="V$LMO2COM 01"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  3 ATCCACCTGC 12
    |||||
Db  12 AGCCACCTGC 3

RESULT 267
LOCUS      E29661
DEFINITION Method for amplifying DNA fragment, method for estimating state of
ACCESSION  E29661
VERSION     E29661.1 GI:13021164
KEYWORDS   JP 1999276176-A/141.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Koichi,I.
TITLE      Method for amplifying DNA fragment, method for estimating state of
JOURNAL    microorganism existing and method for estimating state of waste
COMMENT    Patent: JP 1999276176-A 141 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
            OS Unidentified
            PN JP 1999276176-A/141
            PD 12-OCT-1999
            PP 31-MAR-1998 JP 1998087652
            PR
            PI KOICHI INOUE

FEATURES   Location/Qualifiers
            source
              1..12
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  6 CACCTGCTGT 15
    |||||
Db  1 CTCCTGCTGT 10

RESULT 268
LOCUS      E29711/c
DEFINITION Method for amplifying DNA fragment, method for estimating state of
ACCESSION  E29711
VERSION     E29711.1 GI:13021214
KEYWORDS   JP 1999276176-A/191.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 12)
AUTHORS    Koichi,I.
TITLE      Method for amplifying DNA fragment, method for estimating state of
JOURNAL    microorganism existing and method for estimating state of waste
COMMENT    Patent: JP 1999276176-A 191 12-OCT-1999;
            SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
            FORESTRY AND FISHERIES
            OS Unidentified
            PN JP 1999276176-A/191
            PD 12-OCT-1999
            PP 31-MAR-1998 JP 1998087652
            PR
            PI KOICHI INOUE

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PC C12N15/09,B09B3/00,C12Q1/00,C12Q1/68,C12N15/00,B09B3/00 CC
Strandedness: Single;
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
/organism='Unidentified'.

FEATURES
source
1..12 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2

RESULT 269
E38767
LOCUS E38767 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION E38767
VERSION E38767.1 GI:18621429
KEYWORDS JP 200270867-A/141.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Inoue,K.
TITLE Method and device for amplifying DNA fragment
JOURNAL Patent: JP 200270867-A 141 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 200270867-A/141
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
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CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
/organism='Unidentified'.

FEATURES
source
1..12 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2

RESULT 270
E38817
LOCUS E38817 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION E38817
VERSION E38817.1 GI:18621479
KEYWORDS JP 200270867-A/191.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Inoue,K.
TITLE Method and device for amplifying DNA fragment
JOURNAL Patent: JP 200270867-A 141 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 200270867-A/141
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
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CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
/organism='Unidentified'.

FEATURES
source
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/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 270
E38817/c
LOCUS E38817 12 bp DNA linear PAT 31-JAN-2002
DEFINITION Method and device for amplifying DNA fragment.
ACCESSION E38817
VERSION E38817.1 GI:18621479
KEYWORDS JP 200270867-A/191.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Inoue,K.
TITLE Method and device for amplifying DNA fragment
JOURNAL Patent: JP 200270867-A 141 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 200270867-A/141
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
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FEATURES
source
1..12 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10
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REFERENCE 1 (bases 1 to 12)
AUTHORS Inoue,K.
TITLE Method and device for amplifying DNA fragment
JOURNAL Patent: JP 200270867-A 191 03-OCT-2000;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Unidentified
PN JP 200270867-A/191
PD 03-OCT-2000
PF 19-MAR-1999 JP 1999076844
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
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CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
/organism='Unidentified'.

FEATURES
source
1..12 Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
Db 11 CCACCTCCTG 2

RESULT 271
E64193
LOCUS E64193 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method
for analyzing a group of microorganisms, and method for assaying
contaminating substance.
ACCESSION E64193
VERSION E64193.1 GI:13019597
KEYWORDS JP 1999341989-A/141.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences: artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi,I.
TITLE Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method for
analyzing a group of microorganisms, and method for assaying
contaminating substance
JOURNAL Patent: JP 1999341989-A 141 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Artificial Sequence
PN JP 1999341989-A/141
PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC C12N15/09,C12M1/00,C12Q1/68,C12N15/00
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
/organism='Artificial Sequence'.

FEATURES
source
1..12 Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 29.0%; Score 8.4; DB 1; Length 12;
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Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 272
E64243/c
LOCUS 12 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method
for analyzing a group of microorganisms, and method for assaying
contaminating substance.
E64243
ACCESSION E64243.1 GI:13019647
VERSION JP 1999341989-A/191.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 12)
AUTHORS Koichi, I.
TITLE Method for amplifying DNA fragment, amplification apparatus of DNA
fragment, method for assaying a group of microorganisms, method for
analyzing a group of microorganisms, and method for assaying
contaminating substance
JOURNAL Patent: JP 1999341989-A 191 14-DEC-1999;
SANYO ELECTRIC CO LTD, SOCIETY FOR TECHNO-INNOVATION OF AGRICULTURE
FORESTRY AND FISHERIES
COMMENT OS Artificial Sequence
PN JP 1999341989-A/191
PD 14-DEC-1999
PF 16-MAR-1999 JP 1999069694
PR KOICHI INOUE
PI C12N15/09,C12M1/00,C12Q1/68,C12N15/00
PC
CC
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
1..12
/organism="Artificial Sequence".

FEATURES
source
1..12
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CCACCTGCTG 14
Db 11 CCACCTGCTG 2

RESULT 273
I34990/c
LOCUS 12 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 76 from patent US 5599704.
ACCESSION I34990
VERSION I34990.1 GI:2087958
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE ErbB2/neu targeted ribozymes
JOURNAL Patent: US 5599704-A 76 04-FEB-1997;
Location/Qualifiers
1..12
/organism="unknown"

Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CACCTGCTGT 15
Db 1 CTCCTGCTGT 10

RESULT 274
E64243/c
LOCUS 12 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 167 from patent US 6632057.
ACCESSION AR408074
VERSION AR408074.1 GI:40158061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 167 14-OCT-2003;
GFI Aerospace; Paris;
FRX;

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/organism="unknown"
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Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13
Db 1 TCCACCTGCT 10

RESULT 275
AR630023
LOCUS 12 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 77 from patent US 6838556.
ACCESSION AR630023
VERSION AR630023.1 GI:59762226
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 77 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAT 29
Db 3 CCTGATAAT 12

RESULT 276

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/mol_type="unassigned DNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCATCCACT 10
Db 10 CCATCCACTT 1

RESULT 274
AR408074
LOCUS 12 bp RNA linear PAT 18-DEC-2003
DEFINITION Sequence 167 from patent US 6632057.
ACCESSION AR408074
VERSION AR408074.1 GI:40158061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 167 14-OCT-2003;
GFI Aerospace; Paris;
FRX;

FEATURES
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/organism="unknown"
/mol_type="unassigned RNA"

Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCCACCTGCT 13
Db 1 TCCACCTGCT 10

RESULT 275
AR630023
LOCUS 12 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 77 from patent US 6838556.
ACCESSION AR630023
VERSION AR630023.1 GI:59762226
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 77 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA
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Query Match 29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAT 29
Db 3 CCTGATAAT 12

RESULT 276

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AX097958/c
LOCUS       AX097958               12 bp    DNA          linear          PAT 30-MAR-2001
DEFINITION   Sequence 26 from Patent WO0118048.
ACCESSION   AX097958
VERSION     AX097958.1   GI:13514713
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     van Bijs,G.J., Hateboer,G. and Havenga,M.J.
TITLE       Smooth muscle cell promoter and uses thereof
JOURNAL     Patent: WO 0118048-A 26 15-MAR-2001;
            Introgene B.V. (NL)
FEATURES    Location/Qualifiers
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             /mol_type="unassigned DNA"
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             /note="variant intron-exon splice recognition sequences"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
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Db 12 ATCCAGTGC 3

RESULT 277
AX138534/c
LOCUS       AX138534               12 bp    DNA          linear          PAT 30-MAY-2001
DEFINITION   Sequence 26 from Patent EP1083231.
ACCESSION   AX138534
VERSION     AX138534.1   GI:14274429
KEYWORDS    .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Smooth muscle cell promoter and uses thereof
TITLE       Patent: EP 1083231-A 26 14-MAR-2001;
            Introgene B.V. (NL)
FEATURES    Location/Qualifiers
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Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ATCCACCTGC 12
    |||||
Db 12 ATCCAGTGC 3

RESULT 278
AX351125
LOCUS       AX351125               12 bp    DNA          linear          PAT 06-FEB-2002
DEFINITION   Sequence 77 from Patent WO0194600.
ACCESSION   AX351125
VERSION     AX351125.1   GI:18616479
KEYWORDS    .
SOURCE      Escherichia coli
            Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
ORGANISM    1
REFERENCE   1

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AUTHORS     Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
            Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
            Sheppard,L.T., Lim,M.Y. and Brulce,T.W.
TITLE       Promoters for regulated gene expression
JOURNAL     Patent: WO 0194600-A 77 13-DEC-2001;
            GENELABS TECHNOLOGIES, INC. (US)
FEATURES    Location/Qualifiers
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             /db_xref="taxon:562"

Query Match      29.0%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 20 CCTGGTAAT 29
    |||||
Db 3 CCTGATAAT 12

RESULT 279
AR071511
LOCUS       AR071511               10 bp    DNA          linear          PAT 18-FEB-2000
DEFINITION   Sequence 11 from patent US 5911982.
ACCESSION   AR071511
VERSION     AR071511.1   GI:7222399
KEYWORDS    .
SOURCE      Unknown.
            Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Chao,Y.-C.
TITLE       Hx-1 virus persistence-associated-gene 1 (PAG1) promoter uses
            therefor, and compositions containing same or products therefrom
JOURNAL     Patent: US 5911982-A 11 15-JUN-1999;
            Location/Qualifiers
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTGGTAAA 28
    |||||
Db 3 CTGGTAAA 10

RESULT 280
BD161300/c
LOCUS       BD161300               10 bp    DNA          linear          PAT 17-JAN-2003
DEFINITION   Human activated Th1 and Th2 cell expression genes.
ACCESSION   BD161300
VERSION     BD161300.1   GI:27867058
KEYWORDS    JP 2002186482-A/122.
SOURCE      Homo sapiens (human)
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
            1 (bases 1 to 10)
            Nagai,S., Matsushima,K. and Hashimoto,S.
            Human activated Th1 and Th2 cell expression genes
            Patent: JP 2002186482-A 122 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
            OS Homo sapiens (human)
            PN JP 2002186482-A/122
            PD 02-JUL-2002
            PF 19-DEC-2000 JP 2000385916
            PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human

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activated Th1 and Th2 cell expression genes FH	Key	
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Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 CCATCCAC 8	
Db	8 CCATCCAC 1	
RESULT 281		
BD166593/c	10 bp DNA linear	PAT 17-JAN-2003
LOCUS		
DEFINITION	Human liver disease-expressing genes.	
ACCESSION	BD166593	
VERSION	BD166593.1 GI:27872405	
KEYWORDS	JP 2002209591-A/138.	
SOURCE	unidentified	
ORGANISM	unclassified.	
REFERENCE		
AUTHORS	1 (bases 1 to 10)	
TITLE	Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.	
JOURNAL	Human liver disease-expressing Genes	
	Patent: JP 2002209591-A 138 30-JUL-2002;	
	JAPAN SCIENCE AND TECHNOLOGY CORP	
COMMENT	OS Homo sapiens (human)	
	PN JP 2002209591-A/138	
	PD 30-JUL-2002	
	PF 19-JAN-2001 JP 2001012328	
	PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI	
	YAMASHITA	
	PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,	
	PC C12P21/08,	
	PC C12N15/00	
	CC Human liver disease-expressing genes	
	FH Key Location/Qualifiers	
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	/db_xref='taxon:32644'	
Query Match	27.6%; Score 8; DB 1; Length 10;	
Best Local Similarity	100.0%; Pred. No. 1.7e+02;	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	11 GCTGTGTG 18	
Db	10 GCTGTGTG 3	
RESULT 282		
BD238629	10 bp DNA linear	PAT 17-JUL-2003
LOCUS		
DEFINITION	Preparation and use of superior vaccines.	
ACCESSION	BD238629	
VERSION	BD238629.1 GI:33048399	
KEYWORDS	JP 2002534056-A/47.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens (human)	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
	1 (bases 1 to 10)	
	Robert,B.L. and Shankara,S.	
	Preparation and use of superior vaccines	
	Patent: JP 2002534056-A 178 15-OCT-2002;	
	GENZYME CORP	
	OS Homo sapiens (human)	
	PN JP 2002534056-A/178	
	PD 15-OCT-2002	
	PF 18-JUN-1999 JP 2000554749	
	PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR	
	19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR	
	19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR	
	19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR	
	19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR	
	19-JUN-1998 US 60/089987,19-JUN-1998 US 60/089991 PR	
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	19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR	
	19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR	
	19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR	
	19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR	
	19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR	
	19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR	
	19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR	
	08-DEC-1998 US 60/111715	
	PI BRUCE L ROBERTS,SRINIVAS SHANKARA	
	PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC	
	C12N1/19,	
	PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC	
	G01N37/00,	
	PC C12N15/00,C12N5/00,C12N15/00	
	CC Preparation and use of superior vaccines	
	FH Key Location/Qualifiers	
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	FT /organism='Homo sapiens (human)'	
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	/mol_type='genomic DNA'	
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Query Match	27.6%; Score 8; DB 1; Length 10;	
Best Local Similarity	100.0%; Pred. No. 1.7e+02;	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	11 GCTGTGTG 18	
Db	3 GCTGTGTG 10	
RESULT 283		
BD238760/c	10 bp DNA linear	PAT 17-JUL-2003
LOCUS		
DEFINITION	Preparation and use of superior vaccines.	
ACCESSION	BD238760	
VERSION	BD238760.1 GI:33048530	
KEYWORDS	JP 2002534056-A/178.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens (human)	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontogli	


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source          1..10
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTGTGATAA 28
Db 2 CTGTGATAA 9

RESULT 286
BD239153/c
LOCUS          10 bp DNA linear PAT 17-JUL-2003
DEFINITION    Preparation and use of superior vaccines.
ACCESSION     BD239153
VERSION       BD239153.1 GI:33048923
KEYWORDS      JP 2002534056-A/571.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homiidae; Homo.
REFERENCE
AUTHORS       Roberts,B.L. and Shankara,S.
TITLE         Preparation and use of superior vaccines
JOURNAL       GENZYME CORP
COMMENT       OS Homo sapiens (human)
               PN JP 2002534056-A/571
               PD 15-OCT-2002
               PF 18-JUN-1999 JP 2000554749
               PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
               19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
               19-JUN-1998 US 60/08997,19-JUN-1998 US 60/090079 PR
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               PI BRUCE L ROBERTS,SRINIVAS SHANKARA
               PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
               C12N1/19,
               PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 CTGTGATAA 28
Db 9 CTGTGATAA 2

RESULT 288
BD239212/c
LOCUS          10 bp DNA linear PAT 17-JUL-2003
DEFINITION    Preparation and use of superior vaccines.
ACCESSION     BD239212
VERSION       BD239212.1 GI:33048982
KEYWORDS      JP 2002534056-A/614.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homiidae; Homo.
REFERENCE
AUTHORS       Roberts,B.L. and Shankara,S.
TITLE         Preparation and use of superior vaccines
JOURNAL       GENZYME CORP
COMMENT       OS Homo sapiens (human)
               PN JP 2002534056-A/614
               PD 15-OCT-2002
               PF 18-JUN-1999 JP 2000554749
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               PI BRUCE L ROBERTS,SRINIVAS SHANKARA
               PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 GTGTGACC 21
Db 8 GTGTGACC 1

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08-DEC-1998 US      60/111171S
PI  BRUCE L ROBERTS,SRINIVAS SHANKARA
PC  C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
    C12N1/19,
PC  C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
    G01N37/00,
PC  C12N15/00,C12N5/00,C12N15/00
CC  Preparation and use of superior vaccines
FH  Key
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FT  Location/Qualifiers
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Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CCATCCAC 8
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Db  8 CCATCCAC 1

RESULT 291
LOCUS      CQ766677      10 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 33 from Patent WO2004005541.
ACCESSION  CQ766677
VERSION    CQ766677.1 GI:44908907
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS   van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.
TITLE     Diagnostic tests for the detection of peripheral neuropathy
JOURNAL   Patent: WO 2004005541-A 33 15-JAN-2004;
          Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)
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    source
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        /organism="synthetic construct"
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        /note="3-intron/exon, exon 3, gene ABTB1"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  12 CTGTGTGA 19
    |||||
Db  2 CTGTGTGA 9

RESULT 292
LOCUS      CQ766737/c      10 bp      DNA      linear      PAT 03-MAR-2004
DEFINITION Sequence 93 from Patent WO2004005541.
ACCESSION  CQ766737
VERSION    CQ766737.1 GI:44908967
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           other sequences; artificial sequences.
REFERENCE  1
AUTHORS   van Broeckhoven,C., de Jonghe,P., Timmerman,V. and Verhoeven,K.
TITLE     Diagnostic tests for the detection of peripheral neuropathy
JOURNAL   Patent: WO 2004005541-A 93 15-JAN-2004;
          Vlaams Interuniversitair Instituut voor Biotechnologie vz; w. (BE)

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FEATURES
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        Location/Qualifiers
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        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="3-intron/exon, exon 4"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 CACCTGCT 13
    |||||
Db  8 CACCTGCT 1

RESULT 293
LOCUS      CQ828565      10 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 283 from Patent WO2004053120.
ACCESSION  CQ828565
VERSION    CQ828565.1 GI:49732048
KEYWORDS   .
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE  1
AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE     Regulatory elements in the 5' region of the vrl gene
JOURNAL   Patent: WO 2004053120-A 283 24-JUN-2004;
          Gruenenthal GmbH (DE)
FEATURES
    source
        Location/Qualifiers
        1..10
        /organism="Rattus norvegicus"
        /mol_type="unassigned DNA"
        /db_xref="taxon:10116"
        /note="V$MYOD Q6"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 CCACCTGC 12
    |||||
Db  2 CCACCTGC 9

RESULT 294
LOCUS      CQ828675/c      10 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 393 from Patent WO2004053120.
ACCESSION  CQ828675
VERSION    CQ828675.1 GI:49732158
KEYWORDS   .
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE  1
AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE     Regulatory elements in the 5' region of the vrl gene
JOURNAL   Patent: WO 2004053120-A 393 24-JUN-2004;
          Gruenenthal GmbH (DE)
FEATURES
    source
        Location/Qualifiers
        1..10
        /organism="Rattus norvegicus"
        /mol_type="unassigned DNA"
        /db_xref="taxon:10116"
        /note="V$AP4 Q5"

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Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CTGCTGTG 16
Db      8 CTGCTGTG 1

RESULT 295
CQ828736
LOCUS      CQ828736          10 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 454 from Patent WO2004053120.
ACCESSION CQ828736
VERSION   CQ828736.1 GI:49732219
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE     Regulatory elements in the 5' region of the vrl gene
JOURNAL   Patent: WO 2004053120-A 454 24-JUN-2004;
           Gruenenthal GmbH (DE)
FEATURES
           source
             1..10
             /organism="Mus musculus"
             /mol_type="unassigned DNA"
             /db_xref="taxon:10090"
             /note="V$WYOD Q6"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CACTGTCT 13
Db      3 CACTGTCT 10

RESULT 296
CQ828850/c
LOCUS      CQ828850          10 bp      DNA      linear      PAT 05-JUL-2004
DEFINITION Sequence 568 from Patent WO2004053120.
ACCESSION CQ828850
VERSION   CQ828850.1 GI:49732333
KEYWORDS
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS   Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE     Regulatory elements in the 5' region of the vrl gene
JOURNAL   Patent: WO 2004053120-A 568 24-JUN-2004;
           Gruenenthal GmbH (DE)
FEATURES
           source
             1..10
             /organism="Mus musculus"
             /mol_type="unassigned DNA"
             /db_xref="taxon:10090"
             /note="V$AP4 Q5"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CTGCTGTG 16
Db      8 CTGCTGTG 1

RESULT 297
E16980/c
LOCUS      E16980          10 bp      DNA      linear      PAT 28-JUL-1999
DEFINITION PCR primer for Acacia sp. genome.
ACCESSION E16980
VERSION   E16980.1 GI:5711663
KEYWORDS
SOURCE    unidentified
ORGANISM  unidentified
           unclassified.
           1 (bases 1 to 10)
           Hiono,T. and Koshiyama,J.
           EARLY DETECTION OF INTERSPECIFIC HYBRIDIZATION IN TROPICAL FAST
           GROWING TREE AND ITS PRIMER
           Patent: JP 1998229898-A 3 02-SEP-1998;
           NETSUTAIRIN SAISEI GIJUTSU KENKYU KUMIAI
           OS None
           OC Artificial sequences.
           PN JP 1998229898-A/3
           PD 02-SEP-1998
           PF 02-DEC-1997 JP 1997345724
           PR 17-DEC-1996 JP 96P 353354
           PI HIONO TAKASHI, KOSHIYAMA JUNKO
           PC C12Q1/68//C12N15/09;
           CC strandedness: Single;
           CC topology: Linear;
           FH Key
           FH Key
           FT source
             1..10
             /organism='Artificial sequences'.
             Location/Qualifiers
               1..10
               /organism="unidentified"
               /mol_type="genomic DNA"
               /db_xref="taxon:32644"

Query Match      27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 GTGACCTG 23
Db      10 GTGACCTG 3

RESULT 298
E28643
LOCUS      E28643          10 bp      DNA      linear      PAT 19-JUN-2001
DEFINITION Microsatellite marker located in the vicinity of semi-dwarf gene
           and method for testing semi-dwarf gene therewith.
ACCESSION E28643
VERSION   E28643.1 GI:13020808
KEYWORDS
SOURCE    unidentified
ORGANISM  unidentified
           unclassified.
           1 (bases 1 to 10)
           Hiromori,A., Akiko,I. and Yumi,Y.
           Microsatellite marker located in the vicinity of semi-dwarf gene
           and method for testing semi-dwarf gene therewith
           Patent: JP 1999253167-A 3 21-SEP-1999;
           MITSUI CHEM INC
           OS Unidentified
           PN JP 1999253167-A/3
           PD 21-SEP-1999
           PF 13-MAR-1998 JP 1998063201
           PR HIROMORI AKAGI,AKIKO INAGAKI,YUMI YOKOZEKI
           PI C12N15/09,C12Q1/68,C12N15/00
           PC C12N15/09,C12Q1/68,C12N15/00
           CC Strandedness: Single;
           CC Topology: Linear;

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FH Key Location/Qualifiers
FT source 1..10 /organism='Unidentified'.
FT Location/Qualifiers
FEATURES
  source 1..10 /organism='unidentified'
  /mol_type='genomic DNA'
  /db_xref='taxon:32644'

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTG 14
  |||||
Db 3 ACCTGCTG 10

RESULT 299
E64716/c E64716 10 bp DNA linear PAT 31-JAN-2002
LOCUS E64716 Method for distinguishing rice variety.
DEFINITION E64716
ACCESSION E64716
VERSION E64716.1 GI:18623011
KEYWORDS JP 2000287691-A/2.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Otsubo,K., Nakamura,S., Teshima,H., Okatome,H. and Kawasaki,S.
TITLE Method for distinguishing rice variety
JOURNAL Patent: JP 2000287691-A 2 17-OCT-2000;
NATL FOOD RES INST,KENICHI OTSUBO,HIDECHIKA TESHIMA,HIROSHI OKATOME
COMMENT OS Oryza sativa L. (rice)
PN JP 2000287691-A/2
PD 17-OCT-2000
PF 09-APR-1999 JP 1999102709
PR KENTCHI OTSUBO,SUMIKO NAKAMURA,HIDECHIKA TESHIMA, PI HIROSHI
OKATOME,
PI SHINJI KAWASAKI
PC C12N15/09,C12Q1/68,G01N33/10,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..10 /organism='Oryza sativa L. (rice)'.
FT Location/Qualifiers
FEATURES
  source 1..10 /organism='unidentified'
  /mol_type='genomic DNA'
  /db_xref='taxon:32644'

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTGCTGTG 16
  |||||
Db 9 CTGCTGTG 2

RESULT 300
AR241991/c AR241991 10 bp DNA linear PAT 20-DEC-2002
LOCUS AR241991 Sequence 279 from patent US 6472154.
DEFINITION AR241991
ACCESSION AR241991
VERSION AR241991.1 GI:27287803
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.

TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 279 29-OCT-2002;
Board of Regents, The University of Texas System; Austin, TX
FEATURES
  source 1..10 Location/Qualifiers
  /organism='unknown'
  /mol_type='genomic DNA'

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCATCCAC 8
  |||||
Db 8 CCATCCAC 1

RESULT 301
AR304497 AR304497 10 bp DNA linear PAT 12-JUN-2003
LOCUS AR304497 Sequence 122 from patent US 6544784.
DEFINITION AR304497
ACCESSION AR304497
VERSION AR304497.1 GI:31693645
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bullerdiek,J., Van de Ven,W.J.M., Schoenmakers,H.F.P.M. and Mols,R.
TITLE Multiple-tumor aberrant growth genes
JOURNAL Patent: US 6544784-A 122 08-APR-2003;
Vlaams Interuniversitair Instituut Voor Biotechnologie VZW;;
EPX;
FEATURES
  source 1..10 Location/Qualifiers
  /organism='unknown'
  /mol_type='genomic DNA'

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCTGCTG 14
  |||||
Db 3 ACCTGCTG 10

RESULT 302
AR306871/c AR306871 10 bp DNA linear PAT 12-JUN-2003
LOCUS AR306871 Sequence 23 from patent US 6551476.
DEFINITION AR306871
ACCESSION AR306871
VERSION AR306871.1 GI:31697271
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Scherba,E.S.
TITLE Noble-metal coated inert anode for aluminum production
JOURNAL Patent: US 6551476-A 23 22-APR-2003;
FEATURES
  source 1..10 Location/Qualifiers
  /organism='unknown'
  /mol_type='genomic DNA'

Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CTGCTGTG 16
  |||||
Db 9 CTGCTGTG 2

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RESULT 303
AX152690
LOCUS AX152690 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 605 from Patent WO0138577.
ACCESSION AX152690
VERSION AX152690.1 GI:14534341
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 605 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTG 16
|||||
Db 1 CTGCTGTG 8

RESULT 304
AX152728
LOCUS AX152728 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 643 from Patent WO0138577.
ACCESSION AX152728
VERSION AX152728.1 GI:14534379
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 643 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CTGCTGTG 16
|||||
Db 1 CTGCTGTG 8

RESULT 305
AX152831
LOCUS AX152831 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 746 from Patent WO0138577.
ACCESSION AX152831
VERSION AX152831.1 GI:14534482
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 746 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCTGTGTG 18
|||||
Db 3 GCTGTGTG 10

RESULT 306
AX152911
LOCUS AX152911 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 826 from Patent WO0138577.
ACCESSION AX152911
VERSION AX152911.1 GI:14534562
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 826 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACCTGCTG 14
|||||
Db 1 ACCTGCTG 8

RESULT 307
AX153356
LOCUS AX153356 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1271 from Patent WO0138577.
ACCESSION AX153356
VERSION AX153356.1 GI:14535007
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 1271 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATCCACC 9
|||||
Db 8 CATCCACC 1

RESULT 308
AX153556
LOCUS AX153556 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1271 from Patent WO0138577.
ACCESSION AX153556
VERSION AX153556.1 GI:14535007
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 1271 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES Location/Qualifiers
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATCCACC 9
|||||
Db 8 CATCCACC 1
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[illegible]

QY		6 CACCTGCT 13 		11 bp DNA		PAT 29-JUL-2004	
Db		4 CACCTGCT 11					
RESULT 314		CQ832674		Sequence 45 from Patent WO2004059002.			
LOCUS		CQ832674		11 bp DNA		PAT 29-JUL-2004	
DEFINITION		CQ832674		Sequence 45 from Patent WO2004059002.			
ACCESSION		CQ832674					
VERSION		CQ832674.1		GI:50832281			
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
REFERENCE		Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,					
AUTHORS		Conrad,M. and Hofmann,K.					
TITLE		Method for determining the homeostasis of hairy skin					
JOURNAL		Patent: WO 2004059002-A 45 15-JUL-2004;					
FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)					
source		1..11					
Location/Qualifiers		/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
Query Match		27.6%; Score 8; DB 1; Length 11;					
Best Local Similarity		100.0%; Pred. No. 1.9e+02;					
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY		11 GCTGTGTG 18 					
Db		3 GCTGTGTG 10					
RESULT 315		CQ832685		Sequence 56 from Patent WO2004059002.			
LOCUS		CQ832685		11 bp DNA		PAT 29-JUL-2004	
DEFINITION		CQ832685		Sequence 56 from Patent WO2004059002.			
ACCESSION		CQ832685					
VERSION		CQ832685.1		GI:50832292			
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
REFERENCE		Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,					
AUTHORS		Conrad,M. and Hofmann,K.					
TITLE		Method for determining the homeostasis of hairy skin					
JOURNAL		Patent: WO 2004059002-A 56 15-JUL-2004;					
FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)					
source		1..11					
Location/Qualifiers		/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
Query Match		27.6%; Score 8; DB 1; Length 11;					
Best Local Similarity		100.0%; Pred. No. 1.9e+02;					
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY		11 GCTGTGTG 18 					
Db		3 GCTGTGTG 10					
RESULT 316		CQ832885/C		Sequence 56 from Patent WO2004059002.			
LOCUS		CQ832885		11 bp DNA		PAT 29-JUL-2004	
DEFINITION		CQ832885		Sequence 56 from Patent WO2004059002.			
ACCESSION		CQ832885					
VERSION		CQ832885.1		GI:50832292			
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
REFERENCE		Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,					
AUTHORS		Conrad,M. and Hofmann,K.					
TITLE		Method for determining the homeostasis of hairy skin					
JOURNAL		Patent: WO 2004059002-A 56 15-JUL-2004;					
FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)					
source		1..11					
Location/Qualifiers		/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
Query Match		27.6%; Score 8; DB 1; Length 11;					
Best Local Similarity		100.0%; Pred. No. 1.9e+02;					
Matches		8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY		11 GCTGTGTG 18 					
Db		3 GCTGTGTG 10					
RESULT 317		CQ832885/C		Sequence 56 from Patent WO2004059002.			
LOCUS		CQ832885		11 bp DNA		PAT 29-JUL-2004	
DEFINITION		CQ832885		Sequence 56 from Patent WO2004059002.			
ACCESSION		CQ832885					
VERSION		CQ832885.1		GI:50832292			
KEYWORDS		Homo sapiens (human)					
SOURCE		Homo sapiens					
ORGANISM		Homo sapiens					
REFERENCE		Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,					
AUTHORS		Conrad,M. and Hofmann,K.					
TITLE		Method for determining the homeostasis of hairy skin					
JOURNAL		Patent: WO 2004059002-A 56 15-JUL-2004;					
FEATURES		Henkel Kommanditgesellschaft auf Aktien (DE)					
source		1..11					

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LOCUS      CQ832885                      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 256 from Patent WO2004059002.
ACCESSION  CQ832885
VERSION    CQ832885.1  GI:50832492
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE     Method for determining the homeostasis of hairy skin
JOURNAL   Patent: WO 2004059002-A 256 15-JUL-2004; (DE)
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CCATCCAC 8
Db  8  CCATCCAC 1

RESULT 317
LOCUS      CQ833280                      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 651 from Patent WO2004059002.
ACCESSION  CQ833280
VERSION    CQ833280.1  GI:50832887
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE     Method for determining the homeostasis of hairy skin
JOURNAL   Patent: WO 2004059002-A 651 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  22  TGGTAAAT 29
Db  11  TGGTAAAT 4

RESULT 318
LOCUS      CQ835128                      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 186 from Patent WO2004059001.
ACCESSION  CQ835128
VERSION    CQ835128.1  GI:50834662
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE     Method for determining markers of human facial skin
JOURNAL   Patent: WO 2004059001-A 186 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  21  CTGGTAAA 28
Db  2  CTGGTAAA 9

RESULT 319
LOCUS      CQ835562                      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 620 from Patent WO2004059001.
ACCESSION  CQ835562
VERSION    CQ835562.1  GI:50835096
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE     Method for determining markers of human facial skin
JOURNAL   Patent: WO 2004059001-A 620 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
            1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  10  TGCTGTGT 17
Db  4  TGCTGTGT 11

RESULT 320
LOCUS      CQ835656/c                    11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 714 from Patent WO2004059001.
ACCESSION  CQ835656
VERSION    CQ835656.1  GI:50835190
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE     Method for determining markers of human facial skin

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JOURNAL	Patent: WO 2004059001-A 714 15-JUL-2004;
FEATURES	Henkel Kommanditgesellschaft auf Aktien (DE)
source	Location/Qualifiers 1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	27.6%; Score 8; DB 1; Length 11;
Best Local Similarity	100.0%; Pred. No. 1.9e+02;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCATCCAC 8
Db	 8 CCATCCAC 1
RESULT 321	PAT 29-JUL-2004
CQ836490	LOCUS CQ836490 11 bp DNA linear
DEFINITION	Sequence 1548 from Patent WO2004059001.
ACCESSION	CQ836490
VERSION	CQ836490.1 GI:50836024
KEYWORDS	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K. Method for determining markers of human facial skin
TITLE	Patent: WO 2004059001-A 1548 15-JUL-2004;
JOURNAL	Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES	Location/Qualifiers 1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Query Match	27.6%; Score 8; DB 1; Length 11;
Best Local Similarity	100.0%; Pred. No. 1.9e+02;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	13 TGTGTGAC 20
Db	 3 TGTGTGAC 10
RESULT 322	PAT 29-JUL-2004
CQ836499	LOCUS CQ836499 11 bp DNA linear
DEFINITION	Sequence 1557 from Patent WO2004059001.
ACCESSION	CQ836499
VERSION	CQ836499.1 GI:50836033
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O., Conradt,M. and Hofmann,K. Method for determining markers of human facial skin
TITLE	Patent: WO 2004059001-A 1557 15-JUL-2004;
JOURNAL	Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES	Location/Qualifiers 1. .11 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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Db      1 TGCTGTGT 8

RESULT 325
CQ837690
LOCUS      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2748 from Patent WO2004059001.
ACCESSION CQ837690
VERSION    CQ837690.1 GI:50837224
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
          Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 2748 15-JUL-2004;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 CCTGGTAA 27
Db      4 CCTGGTAA 11

RESULT 326
CQ837896
LOCUS      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 2954 from Patent WO2004059001.
ACCESSION    CQ837896
VERSION      CQ837896.1 GI:50837430
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
          Conradt,M. and Hofmann,K.
TITLE        Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 2954 15-JUL-2004;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              source
                1..11
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                  /mol_type="unassigned DNA"
                  /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GCTGTGTG 18
Db      2 GCTGTGTG 9

RESULT 327
CQ837956
LOCUS      11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION Sequence 3014 from Patent WO2004059001.

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ACCESSION CQ837956
VERSION    CQ837956.1 GI:50837490
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
          Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 3014 15-JUL-2004;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACCTGCTG 14
Db      1 ACCTGCTG 8

RESULT 328
AR301525
LOCUS      11 bp      DNA      linear      PAT 12-JUN-2003
DEFINITION Sequence 106 from patent US 6538173.
ACCESSION    AR301525
VERSION      AR301525.1 GI:31689327
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Heber-Katz,E.
TITLE        Compositions and methods for wound healing
JOURNAL      Patent: US 6538173-A 106 25-MAR-2003;
          The Wistar Institute; Philadelphia, PA;
          WOX;

FEATURES     Location/Qualifiers
              source
                1..11
                  /organism="unknown"
                  /mol_type="genomic DNA"

Query Match      27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CTGTGTGA 19
Db      2 CTGTGTGA 9

RESULT 329
AR632418
LOCUS      11 bp      DNA      linear      PAT 14-FEB-2005
DEFINITION Sequence 90 from patent US 6846623.
ACCESSION    AR632418
VERSION      AR632418.1 GI:59776728
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Beckmann,J. and Richard,I.
TITLE        IGMD gene coding for a calcium dependent protease
JOURNAL      Patent: US 6846623-A 90 25-JAN-2005;

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Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;

LOCUS AX471109 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 686 from Patent WO02053773.
ACCESSION AX471109
VERSION AX471109.1 GI:22206234
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 686 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCTGCTG 14
|||||||
Db 4 ACCTGCTG 11
RESULT 335
AX471236/c
LOCUS AX471236 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 813 from Patent WO02053773.
ACCESSION AX471236
VERSION AX471236.1 GI:22206361
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 813 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCATCCAC 8
|||||||
Db 8 CCATCCAC 1
RESULT 336
AX471465/c
LOCUS AX471465 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1042 from Patent WO02053773.
ACCESSION AX471465
VERSION AX471465.1 GI:22206590
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1042 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GACCTGGT 25
|||||||
Db 11 GACCTGGT 4
RESULT 337
AX471492
LOCUS AX471492 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1069 from Patent WO02053773.
ACCESSION AX471492
VERSION AX471492.1 GI:22206617
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1069 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 TGTGTGAC 20
|||||||
Db 3 TGTGTGAC 10
RESULT 338
AX482032
LOCUS AX482032 11 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 9 from Patent EP1225233.
ACCESSION AX482032
VERSION AX482032.1 GI:22316754
KEYWORDS synthetic construct
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS van der Kuyl,A.C. and Cornelissen,M.
TITLE Means and methods for treatment evaluation
JOURNAL Patent: EP 1225233-A 9 24-JUL-2002;
Amsterdam Support Diagnostics B.V. (NL)
FEATURES
Location/Qualifiers
source 1..11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Qy 7 ACCTGCTG 14
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db 4 ACCTGCTG 11

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1411 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CATCCACC 9
|||||
Db 10 CATCCACC 3

RESULT 344
AX625507 AX625507 11 bp DNA linear PAT 21-FEB-2003
LOCUS Sequence 2548 from Patent WO02053774.
DEFINITION
ACCESSION AX625507
VERSION AX625507.1 GI:28453448
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2548 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TGTGACCT 22
|||||
Db 1 TGTGACCT 8

RESULT 345
AX625837/c
LOCUS Sequence 2878 from Patent WO02053774.
DEFINITION
ACCESSION AX625837
VERSION AX625837.1 GI:28453778
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2878 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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FEATURES
source
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTGCT 13
|||||
Db 10 CACCTGCT 3

RESULT 346
AX626039/c
LOCUS Sequence 3080 from Patent WO02053774.
DEFINITION
ACCESSION AX626039
VERSION AX626039.1 GI:28454077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3080 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTGCT 13
|||||
Db 10 CACCTGCT 3

RESULT 347
AX626143/c
LOCUS Sequence 3184 from Patent WO02053774.
DEFINITION
ACCESSION AX626143
VERSION AX626143.1 GI:28454181
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3184 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CACCTGCT 13
|||||
Db 10 CACCTGCT 3

RESULT 348
AX626143/c
LOCUS Sequence 3184 from Patent WO02053774.
DEFINITION
ACCESSION AX626143
VERSION AX626143.1 GI:28454181
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3184 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      18 GACCTGGT 25
        |||||
Db      11 GACCTGGT 4

RESULT 348
AX626825
LOCUS   AX626825
DEFINITION Sequence 3866 from Patent WO02053774.
ACCESSION AX626825
VERSION   AX626825.1 GI:28454863
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 3866 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   1..11
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 TGTGTGAC 20
        |||||
Db      3 TGTGTGAC 10

RESULT 349
AX627393/c
LOCUS   AX627393
DEFINITION Sequence 4434 from Patent WO02053774.
ACCESSION AX627393
VERSION   AX627393.1 GI:28455431
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 4434 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   1..11
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 CTGGTAAA 28
        |||||
Db      11 CTGGTAAA 4

RESULT 350
AX627828/c
LOCUS   AX627828
DEFINITION Sequence 5377 from Patent WO02053774.
ACCESSION AX628336
VERSION   AX628336.1 GI:28456374
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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DEFINITION Sequence 4869 from Patent WO02053774.
ACCESSION AX627828
VERSION   AX627828.1 GI:28455866
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 4869 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   1..11
         /organism="Homo sapiens"
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         /db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCATCCAC 8
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Db      8 CCATCCAC 1

RESULT 351
AX628284
LOCUS   AX628284
DEFINITION Sequence 5325 from Patent WO02053774.
ACCESSION AX628284
VERSION   AX628284.1 GI:28456322
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 5325 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source   1..11
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 TGTGACCT 22
        |||||
Db      4 TGTGACCT 11

RESULT 352
AX628336/c
LOCUS   AX628336
DEFINITION Sequence 5377 from Patent WO02053774.
ACCESSION AX628336
VERSION   AX628336.1 GI:28456374
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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REFERENCE
AUTHORS      1 Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5377 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
source       1..11
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match  27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 CATCCACC 9
Db          8 CATCCACC 1
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           |||||

RESULT 353
LOCUS      AX628472                11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5513 from Patent WO02053774.
ACCESSION  AX628472
VERSION     AX628472.1 GI:28456510
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5513 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match  27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          12 CTGTGTGA 19
Db          4 CTGTGTGA 11
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RESULT 354
LOCUS      AX628654                11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5695 from Patent WO02053774.
ACCESSION  AX628654
VERSION     AX628654.1 GI:28456692
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5695 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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Query Match  27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          12 CTGTGTGA 19
Db          4 CTGTGTGA 11
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           |||||

RESULT 355
LOCUS      AX628766                11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5807 from Patent WO02053774.
ACCESSION  AX628766
VERSION     AX628766.1 GI:28456804
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 5807 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match  27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          20 CCTGGTAA 27
Db          4 CCTGGTAA 11
           |||||
           |||||

RESULT 356
LOCUS      AX629030                11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6071 from Patent WO02053774.
ACCESSION  AX629030
VERSION     AX629030.1 GI:28457068
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 6071 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
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Query Match  27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          20 CCTGGTAA 27
Db          4 CCTGGTAA 11
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           |||||

RESULT 357
LOCUS      AX629030                11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6071 from Patent WO02053774.
ACCESSION  AX629030
VERSION     AX629030.1 GI:28457068
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 6071 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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Query Match  27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          8 CCTGCTGT 15
Db          11 CCTGCTGT 4
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RESULT 357
AX629150/c
LOCUS AX629150 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6191 from Patent WO02053774.
ACCESSION AX629150
VERSION AX629150.1 GI:28457188
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6191 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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1. .11
/organism="Homo sapiens"
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Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CATCCACC 9
Db 11 CATCCACC 4
RESULT 358
AX629152
LOCUS AX629152 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6193 from Patent WO02053774.
ACCESSION AX629152
VERSION AX629152.1 GI:28457190
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6193 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source
1. .11
/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ACCTGCTG 14
Db 1 ACCTGCTG 8
RESULT 359
AX629352
LOCUS AX629352 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6393 from Patent WO02053774.
ACCESSION AX629352
VERSION AX629352.1 GI:28457390
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6393 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GCTGTGTG 18
Db 3 GCTGTGTG 10
RESULT 360
AX629742
LOCUS AX629742 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6783 from Patent WO02053774.
ACCESSION AX629742
VERSION AX629742.1 GI:28457780
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6783 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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1. .11
/organism="Homo sapiens"
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Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GCTGTGTG 18
Db 2 GCTGTGTG 9
RESULT 361
AX629813
LOCUS AX629813 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6854 from Patent WO02053774.
ACCESSION AX629813
VERSION AX629813.1 GI:28457851
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6854 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

LOCUS AX630649 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7690 from Patent WO02053774.
ACCESSION AX630649
VERSION AX630649.1 GI:28458687
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7690 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 CTGGTAAA 28
Db 11 CTGGTAAA 4
RESULT 367
AX631791/c
LOCUS AX631791 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8833 from Patent WO02053774.
ACCESSION AX631791
VERSION AX631791.1 GI:28459898
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8833 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CATCCACC 9
Db 10 CATCCACC 3
RESULT 368
AX924272
LOCUS AX924272 11 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 57 from Patent EP1350841.
ACCESSION AX924272
VERSION AX924272.1 GI:40217196
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1

AUTHORS Schoenbrunner,N.J., Myers,T.W. and Gelfland,D.H.
TITLE Thermostable or thermoactive DNA polymerase with attenuated
3'-5' exonuclease activity
JOURNAL Patent: EP 1350841-A 57 08-OCT-2003;
Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1..11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 27.6%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 17 TGACCTGG 24
Db 1 TGACCTGG 8
RESULT 369
A36701/c
LOCUS A36701 11 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 3 from Patent EP0590721.
ACCESSION A36701
VERSION A36701.1 GI:2293973
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
REFERENCE 1 (bases 1 to 11)
AUTHORS Ficca,A.G.
TITLE Method for expressing receptors of the human nervous system in the
yeast Schizosaccharomyces Pombe
JOURNAL Patent: EP 0590721-A 3 06-APR-1994;
ENICHEM SPA (IT)
COMMENT Other publication AT 140484T 960815
Other publication DE 69303685D 960822
Other publication IT 1255697 951110.
FEATURES
source 1..11
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 12 CTGTGTGACCT 22
Db 11 CTGCGTGACGT 1
RESULT 370
BD095127/c
LOCUS BD095127 11 bp DNA linear PAT 27-AUG-2002
DEFINITION A polynucleotide encoding mouse histidine decarboxylase.
ACCESSION BD095127
VERSION BD095127.1 GI:22640715
KEYWORDS WO 0132892-A/20.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 11)
AUTHORS Otsu,H.
TITLE A polynucleotide encoding mouse histidine decarboxylase
JOURNAL Patent: WO 0132892-A 20 10-MAY-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP,HIROSHI OTSU
COMMENT OS Mus sp. (mouse)
PN WO 0132892-A/20

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PD 10-MAY-2001
PF 01-NOV-2000 WO 2000JP007689
PR 02-NOV-1999 JP 99P 312559,23-MAR-2000 JP 00P 082953 PI
HIROSHI OTSU
PC C12N15/60,C12N9/88
CC A polynucleotide encoding mouse histidine decarboxylase FH
KEY Location/Qualifiers
FT source 1..11
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   Location/Qualifiers
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   /organism="Mus sp."
   /mol_type="genomic DNA"
   /db_xref="taxon:10095"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 GTGACCTGGTA 26
Db 11 GTGCCCTGGAA 1

RESULT 371
LOCUS CQ828950 11 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 668 from Patent WO2004053120.
ACCESSION CQ828950
VERSION CQ828950.1 GI:49732433
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Weihe,E., Bieller,A. and Schaefer,M.K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 668 24-JUN-2004;
Gruenthal GmbH (DE)
FEATURES
source 1..11
   /organism="Homo sapiens"
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23
Db 11 TGTGTGTCATG 1

RESULT 372
LOCUS CQ832704 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 75 from Patent WO2004059002.
ACCESSION CQ832704
VERSION CQ832704.1 GI:50832311
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 75 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

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JOURNAL Patent: WO 2004059002-A 75 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source 1..11
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   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGC 12
Db 11 CTCCACCTCC 1

RESULT 373
LOCUS CQ832725 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 96 from Patent WO2004059002.
ACCESSION CQ832725
VERSION CQ832725.1 GI:50832332
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 96 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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   /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CATCCACCTGC 12
Db 1 CATCCTGCTGC 11

RESULT 374
LOCUS CQ833139 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 510 from Patent WO2004059002.
ACCESSION CQ833139
VERSION CQ833139.1 GI:50832746
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 510 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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ACCESSION CQ836644
VERSION CQ836644.1 GI:50836178
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 1702 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GACCTGGTAA 28
Db 1 GCCTGGTAA 11
RESULT 380
CQ837342
LOCUS CQ837342 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2400 from Patent WO2004059001.
ACCESSION CQ837342
VERSION CQ837342.1 GI:50836876
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2400 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 19 ACCTGGTAAAT 29
Db 1 ACTTGATAAAT 11
RESULT 381
CQ837591
LOCUS CQ837591 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2649 from Patent WO2004059001.
ACCESSION CQ837591
VERSION CQ837591.1 GI:50837125
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2649 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 ACCTGCTGTGT 17
Db 1 ACCTGCTGTCT 11
RESULT 382
CQ837743/c
LOCUS CQ837743 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2801 from Patent WO2004059001.
ACCESSION CQ837743
VERSION CQ837743.1 GI:50837277
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2801 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GACCTGGTAA 28
Db 1 GCCTGGTGAA 1
RESULT 383
CQ838096
LOCUS CQ838096 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 3154 from Patent WO2004059001.
ACCESSION CQ838096
VERSION CQ838096.1 GI:50837630
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3154 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)

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  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATCCACTGCT 13
Db 1 ATTTACTGCT 11

RESULT 384
CQ838096/c
LOCUS CQ838096 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 3154 from Patent WO2004059001.
ACCESSION CQ838096
VERSION CQ838096.1 GI:50837630
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
  Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3154 15-JUL-2004;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match
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QY 19 ACCTGGTAAT 29
Db 11 AGCAGGTAAT 1

RESULT 385
CS058269
LOCUS CS058269 11 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 166 from Patent WO2005028671.
ACCESSION CS058269
VERSION CS058269.1 GI:62551452
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
  Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 166 31-MAR-2005;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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        /db_xref="taxon:9606"

Query Match
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  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 ACCTGGTAAT 29
Db 11 AGCAGGTAAT 1

RESULT 386
CS058269
LOCUS CS058269 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 197 from Patent WO02053773.
ACCESSION AX470620
VERSION AX470620.1 GI:22205745
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 197 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  source
    Location/Qualifiers
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        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 26.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCACCTGCTG 14
Db 1 TCATCTGTTG 11

RESULT 388
AX470911
LOCUS AX470911 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 488 from Patent WO02053773.
  
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Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 TGTGTGACCTG 23
Db 1 TTGAGACCTG 11

RESULT 386
AR364168/c
LOCUS AR364168 11 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 12 from patent US 5256558.
ACCESSION AR364168
VERSION AR364168.1 GI:34426497
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS Coruzzi,G.M. and Tsai,F.-Y.
TITLE Gene encoding plant asparagine synthetase
JOURNAL Patent: US 5256558-A 12 26-OCT-1993;
  The Trustees of Rockefeller University; New York, NY
FEATURES
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    Location/Qualifiers
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Query Match
  Best Local Similarity 26.9%; Score 7.8; DB 1; Length 11;
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QY 5 CCACCTGCTGT 15
Db 11 CTACGTGCTGT 1

RESULT 387
AX470620
LOCUS AX470620 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 197 from Patent WO02053773.
ACCESSION AX470620
VERSION AX470620.1 GI:22205745
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 197 11-JUL-2002;
  HENKEL KGAA (DE)
FEATURES
  source
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        /db_xref="taxon:9606"

Query Match
  Best Local Similarity 26.9%; Score 7.8; DB 1; Length 11;
  Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCACCTGCTG 14
Db 1 TCATCTGTTG 11

RESULT 388
AX470911
LOCUS AX470911 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 488 from Patent WO02053773.
  
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ACCESSION AX470911
VERSION AX470911.1 GI:22206036
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 488 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 GACCTGGTAA 28
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Db 1 GAGCTGGTGAA 11
||| |||||
RESULT 389
AX471463
LOCUS AX471463 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1040 from Patent WO02053773.
ACCESSION AX471463
VERSION AX471463.1 GI:22206588
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1040 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CATCCCTGTC 12
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Db 1 CATCCCTGTC 11
||||| |||||
RESULT 390
AX471815
LOCUS AX471815 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1392 from Patent WO02053773.
ACCESSION AX471815
VERSION AX471815.1 GI:22206940
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.
TITLE Method for determining skin stress or skin ageing in vitro
JOURNAL Patent: WO 02053773-A 1392 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 19 ACCTGGTAAAT 29
||| |||||
Db 1 ACTTGATAAAT 11
||| |||||
RESULT 391
AX623055
LOCUS AX623055 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 96 from Patent WO02053774.
ACCESSION AX623055
VERSION AX623055.1 GI:28450996
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 96 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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source Location/Qualifiers
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Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 TGCTGTGTGAC 20
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Db 1 TTCTGTGTGCC 11
||| |||||
RESULT 392
AX623372
LOCUS AX623372 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 413 from Patent WO02053774.
ACCESSION AX623372
VERSION AX623372.1 GI:28451313
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 413 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 CACCTGCTGTG 16
DB      11 CTCCTGCTGAG 1

RESULT 393
AX623975
LOCUS      AX623975      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 1016 from Patent WO02053774.
ACCESSION  AX623975
VERSION     AX623975.1 GI:28451916
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1016 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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            /mol_type="unassigned DNA"
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCATCCACCTG 11
DB      1 CAACTCCTCTG 11

RESULT 394
AX624312
LOCUS      AX624312      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 1353 from Patent WO02053774.
ACCESSION  AX624312
VERSION     AX624312.1 GI:28452253
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 1353 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 GTGTGACCTGG 24
DB      1 GTGAGACCTCG 11

RESULT 397
AX626289
LOCUS      AX626289      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3330 from Patent WO02053774.
ACCESSION  AX626289
VERSION     AX626289.1 GI:28454327
KEYWORDS
SOURCE      Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.

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RESULT 395
AX625384
LOCUS      AX625384      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2425 from Patent WO02053774.
ACCESSION  AX625384
VERSION     AX625384.1 GI:28453325
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2425 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      18 GACCTGGTAAA 28
DB      1 GAGCTGGTGAA 11

RESULT 396
AX625836
LOCUS      AX625836      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2877 from Patent WO02053774.
ACCESSION  AX625836
VERSION     AX625836.1 GI:28453777
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2877 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 GTGTGACCTGG 24
DB      1 GTGAGACCTTG 11

RESULT 397
AX626289/c
LOCUS      AX626289      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3330 from Patent WO02053774.
ACCESSION  AX626289
VERSION     AX626289.1 GI:28454327
KEYWORDS
SOURCE      Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiinae; Homo.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3330 11-JUL-2002; (DE)
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 12 CTGTGTGACCT 22
Db 11 CTGTGTATCT 1
RESULT 398
AX626533/c
LOCUS AX626533 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3574 from Patent WO02053774.
ACCESSION AX626533
VERSION AX626533.1 GI:28454571
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 3574 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CATCCACCTGC 12
Db 11 CATCCACAGC 1
RESULT 399
AX627698/c
LOCUS AX627698 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4739 from Patent WO02053774.
ACCESSION AX627698
VERSION AX627698.1 GI:28455736
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 4739 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES Location/Qualifiers
source 1..11
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/mol_type="unassigned DNA"
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Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 17 TGACCTGGTAA 27
Db 11 TGATATGGTAA 1
RESULT 400
AX627752
LOCUS AX627752 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4793 from Patent WO02053774.
ACCESSION AX627752
VERSION AX627752.1 GI:28455790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 4793 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCCACCTGCTG 14
Db 1 TCCATCTGTG 11
RESULT 401
AX628274
LOCUS AX628274 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5315 from Patent WO02053774.
ACCESSION AX628274
VERSION AX628274.1 GI:28456312
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5315 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCCACCTGCTG 14
Db 1 TCCATCTGTG 11
RESULT 401
AX628274
LOCUS AX628274 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5315 from Patent WO02053774.
ACCESSION AX628274
VERSION AX628274.1 GI:28456312
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 5315 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1 ACCTGCTGTCT 11

RESULT 402
AX628612
LOCUS   AX628612                11 bp    DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 5653 from Patent WO02053774.
ACCESSION
AX628612
VERSION  AX628612.1  GI:28456650
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 5653 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source   1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1 TGATGTTGAC 11

RESULT 403
AX628674/c
LOCUS   AX628674                11 bp    DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 5715 from Patent WO02053774.
ACCESSION
AX628674
VERSION  AX628674.1  GI:28456712
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 5715 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source   1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
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Db      11 CTGCTGGGTTA 1

RESULT 404
AX629060/c
LOCUS   AX629060                11 bp    DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 6101 from Patent WO02053774.
ACCESSION
AX629060
VERSION  AX629060.1  GI:28457098
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 6101 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
Location/Qualifiers
source   1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1 CCCGTTGTGTG 11

RESULT 406
AX629919
LOCUS   AX629919                11 bp    DNA    linear    PAT 21-FEB-2003
DEFINITION
Sequence 6960 from Patent WO02053774.
ACCESSION
AX629919
VERSION  AX629919.1  GI:28457957
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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1
REFERENCE
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 6960 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
source       1..11
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
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RESULT 407
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DEFINITION Sequence 7201 from Patent WO02053774.
ACCESSION  AX630160
VERSION     AX630160.1 GI:28458198
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7201 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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            /db_xref="taxon:9606"

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RESULT 408
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LOCUS      AX630234
DEFINITION Sequence 7275 from Patent WO02053774.
ACCESSION  AX630234
VERSION     AX630234.1 GI:28458272
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7275 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 409
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LOCUS      AX630476
DEFINITION Sequence 7517 from Patent WO02053774.
ACCESSION  AX630476
VERSION     AX630476.1 GI:28458514
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7517 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
source    1..11
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Query Match      26.9%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
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RESULT 410
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LOCUS      AX630793
DEFINITION Sequence 7834 from Patent WO02053774.
ACCESSION  AX630793
VERSION     AX630793.1 GI:28458833
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7834 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 411
AX630793/C
LOCUS      AX630793
DEFINITION Sequence 7834 from Patent WO02053774.
ACCESSION  AX630793
VERSION     AX630793.1 GI:28458833
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.

REFERENCE  1
AUTHORS   Petersohn,D., Conradt,M. and Hofmann,K.
TITLE     Method for determining homeostasis of the skin
JOURNAL   Patent: WO 02053774-A 7834 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
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/db_xref="taxon:9606"
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RESULT 411
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LOCUS AX631396 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8438 from Patent WO02053774.
ACCESSION AX631396
VERSION AX631396.1 GI:28459462
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8438 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
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Db 1 CAATCCTCTG 11

RESULT 412
AX631733
LOCUS AX631733 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8775 from Patent WO02053774.
ACCESSION AX631733
VERSION AX631733.1 GI:28459840
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8775 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
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Best Local Similarity 81.8%; Pred. No. 2.le+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTGAGACCTCG 11

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